

Sn. 08/401, 881



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

Filed: Unassigned

For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

SEQUENCE LISTING

SECTION 1 of 2 SECTIONS,

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Haseltine, William
Rosen, Craig
Ruben, Steve
Dillon, Patrick
Li, Haodong
Earle-Hughes, Julie

(ii) TITLE OF INVENTION: Human Genes, Sequences, and Expression
Products

(iii) NUMBER OF SEQUENCES: 1767

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart, &
Olstein

(B) STREET: 6 Becker Farm Road

(C) CITY: Roseland

(D) STATE: New Jersey

(E) COUNTRY: USA

(F) ZIP: 07068

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 5.0

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/401,881

(B) FILING DATE: March 10, 1995

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Olstein, Elliot

(B) REGISTRATION NUMBER: 24,025

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(B) TELEFAX: (201) 994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|---|-----|
| GGNANAAAGG AGGAGCACGA GGTGGCTGTC CTGGGGGCGC CCCAAAACCC TGCTCCCCCA | 60 |
| ANGTCCACCG TGAATCCAAA TCCGCAGCGA GAACCTCCGT GCCCAACCAT GTGNTGCTGG | 120 |
| TCCCTGTTC AANACCCTCTT AATGAACCCC TGNTGCCTGG GNCTTAANAG CATTCGCCTA | 180 |
| CTCCGTGAAA GTNTAGGGNC AGGAAAGATG GTTGGCGACG TGAACCGGGG CCCAGGNNTA | 240 |
| TGCTTCCACC GNCAAGTGCC TGAAAATTTG GG | 272 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|---|-----|
| GGAANACCAG CTCTGGGGGC ACGGCCANC TTCCTTAAAA ATGTCTACTG TTCCANAAAA | 60 |
| TCCTGTNCAA GCCCAGCTTG AGGGGTAATC ACTCTANACC CCCAAGTCCA TATGGNTCTT | 120 |
| TAAAAGCCTA TNCTAA | 136 |

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|----|
| GGCANAGNAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAANN | 68 |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|---|-----|
| ATCCCCAACG TGNCCGGCCG ACACCAAGCT CTCCAAGATC AAGACTCTGC GCCTAGCCAC | 60 |
| CAGCTNACAT CGCCTGACCT GAATGGACGT GCTGGGCCAA GGGATGCACA GTCTGGGCGA | 120 |
| TNCCAAGGGC CTT | 133 |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| GACTCAATCA TGGNTTGTGG TCTGGTCGCC AGCAACCTGT AATCTCAAAC CTGGAGAGTG | 60 |
| CCTTCGAGTG CNAGGCGAGG TGGCTCCTGC ACGCTAAGAG CTTCGTGCCT GNAACCTGGG | 120 |
| CAAAGACAGC AACANCCTGT NCCTGNACTT ACAACCCTNG CTTCAACGTC NACGAGAACG | 180 |
| CCAACACCAT CGTGTGCAAC AGACAAAGGT ACGGCGGGGC CTGGGGGGAC CGAGCAGCGG | 240 |
| GAGGCTGTCT TTCCTTCCC AGNCTGGAAG TTTTTCGAGG GTGTGCATCA CCTTTGGACC | 300 |
| AGGNCCAACC GCCCTA | 316 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|-----|
| GGCAGAGCCT GTCGGCCACC AAGGTAGTGC ACNGACCCAT GGGNCACCCG CAAGCACCTG | 60 |
| GTGCCCAAGG NACCTGGATA TNCGGCCTGT GAAAGACTCG GAACTCGTCT ATCTGCAGAG | 120 |
| CTGCACCTGA ACTTCTGCAT GAAGNAATGA GAAAGGTGNG CTCCCACGGG ANCACAAGAC | 180 |
| AGGNCAGTGC AACAAGGACA TCCAACGGAA AGCGAACATT GCGAGACCTT GATGTGCCTG | 240 |
| CGGGCGTGGG TGACAACCCC TACACAGGAC CGCNTGGTGC AGCGGTGCCA TGTNAGTTAC | 300 |

333

CATGGTGCTG TTACGTTCAA NNGCCGCAGT NTG

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCAGGAGCC TATCGGCCAC CAAGGTAGTA CACNGACCCA TNGNCACCCG CAAGCACCNN 60
 GTGCCCAAGG ACCTGGATAT CCGG 84

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 220 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GNAGGCAAGG CCAGGGATAA GGNGTGGATG CCGTCACCAA GTTGGGCGCG TTNGTCAAGG 60
 ACATGAAGAT CAAGTCCNGG AGGAGATCNT TCTCTTCTCC TGCCCATTA A GGGTTCAANG 120
 ATCATTGATT TCTTCCTGGG GGCCCTCTCA NGGATGAGGT TTTGAAGATT ATGCCGTNCA 180
 GAAGNAGACC CTGCCGGCCA GNGAACCGGT TNAAGGCTTT 220

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCCCCTTTG GGCATGGCTA TGGGGAGGGG GCTGGAGANG GTATCGATGA TGCTGAGTGG 60
 TGGGTGGCCA GGGACAAGCC CATGTACGAC GAGATCTTCT ACACCCTGTC ACCGGTTGNT 120
 GGCAAGATCA CAGGCGCTAA TNCCAAGANG GAGATGGTGC GCTCCAAGCT GCCCAACAGT 180
 GTGCTGGGCA AGATCTGGAA GCTGGCCGAC ATTGAACAAG GATGGCATGC TGGTACGACC 240
 AACGAGTTTG GCACTGGNCC AACCACCTAC ATNCAAAGTT CAAGCTGGGA GGGGGCACGA 300

GCTNACCCAA CNAGCTGGCC TNACCCACCT

330

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCCAAGAAC GTCATGATGA TCCAGTCCTG CAAATGCAAC TACAACTGCC CGCATGCCAA 60

TGANGCAGCG TTTCCNTCT ACAGNNTGTT CAATGACATT CACAAATTNA GGG 113

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCANAGNAG AACGCAGAGT ACAAGCAATT GCTGGGACAT CAAGACACGC CTGGNGGTGG 60

AGATCNNGAC CTACCGCCGC CTGCTCGATG GAGAGGGAGG TGGTTCTAGT TTTGCAGAAT 120

TTGGTGGTAG AAACCTCAGGA TCTGTAAAC ATGGGATCCA GGGATCTGGT NATCCNGGTG 180

ACTCAAGATC TGGAAGCTGT TCTGGTCAAG GACGAGATTC AAGCAAGACT AGAGTGNACT 240

AAGAACTATN GTTAGAGGNG TTGGTGGATG GCAAGGTTGT CTCGTTCTCC AAGTCCAGCA 300

GTATTTCTGA GGGTNGAAAG TTAAATAAG GGACCTTNCC AGTTCAACAA AAGTGTCTT 360

TTNCAAGGGN ANAAAAATTC CAGG 384

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCAGAGCCC AGAAGAACCA CATCCCTNTT TTAGTCCCG CACTTACAGA CGGNTCGCTG 60

GGCGACATGA TCTTTTCCCA TTCCTACAAG AACCCGGGCC TGGTCCTGGA CATCGTTGAG 120

| | |
|--|-----|
| GACCTGAAGG CTCATCAACA CACAGGCCAT CTTNCCAAG TGCCTGGGN ATGATCATTC | 180 |
| TGGGCGGGG CGTGGTCAAG CACCACATTG CCAATGCCAA CCTCATGCGG AANGGGGCGG | 240 |
| ACTTACGCTG TTTACATCAA CACAGCCCAG GAGTTTGATG GCTCTGAACT CAGGTGCCCCG | 300 |
| ACCAGACGAG GCTGTTNTCC TGGGGCAAGA TNCGGGTGGA TGCACAGNCC GTCAAGGTTT | 360 |
| ATGCTGGAGG CNTNCCTGGG TCTTTCCCCC TGGTT | 395 |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 439 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|--|-----|
| GGCACGAGGC CTTACAGAGA GGTACAGATGC AGAAGCCATT TGAAGACGCC TCGTTTGCGC | 60 |
| TGCGGACGGG GGAGATGAGC GGGCCCGTGT TCACGGATTC CGGCATCCAC ATCATCCTCC | 120 |
| GCACTGAGTG AGGGTGGGGA GCCCAGGCCT GGCCTCGGGG CAGGGCAGGG CGGCTAGGCC | 180 |
| NNCCAGCTCC CCCTTGCCCG CCAGCCAGTG GCCGAACCCC CCACTCCCTG CCACCGTTCA | 240 |
| CACAGTGATT TTATTGTTCC CACAATGGCT GGAAGGGGG CCCTTTCCAG ATTGGGGGCC | 300 |
| CTGGGGTCCC CACTCCCTGT NCCATNCCCC AGTTGGGGCT GNGAACCGCC AATTTTTCCT | 360 |
| TTAAGTATTG NATTTAGNA NGGGTGGGAG GTTCCCAAAC CCAGGCATNT GGTGGGAGGG | 420 |
| GTGTTTCCAA AGAGAAAGG | 439 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | |
|--|-----|
| GGCAGAGNAC AAGGGCCGTG GCCGCTTCGC CCTCATCATC TATGAGAACA TCCTCAAGTA | 60 |
| TGTCAACCTG GACGCCTGGN AACCGGGAGC TGCTGGGACA AGTACTGTGT GGCCTACGGC | 120 |
| GTGGGCATCA TTGGCTTCTT CAAGGCCAAT GAGGAACAGC CTGCTGAGTG CGCATTC AAG | 180 |
| GGCTTTNNCC TGTTCCCTGC ACTCAAACCT GGGCCTGAAG GGACTGCAGC ATCAACCCCA | 240 |
| AGTCCCCGTT GGCTTCTACG TGGACGCGAA CCTNAGGNGA GGGTTGGNAG GAAAGGTTGT | 300 |

TGCTTTCNCC CGGGTNG

317

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | |
|---|-----|
| GGCAGAGCCA ACATTGAGGC CAACGAGAGT AAGGNGGTCC GGCAGTTCCG GAGNACTCTT | 60 |
| TGCCCAGCTG GCTGGAGGAT GACATGGAGG TCAGCGCCAC AGAACTCATG AACATTCTTC | 120 |
| AATAAGGTTG TGAACACGNA CACCCTGATC TGAAAGACTG ATGGTTTTGG CATTGACACA | 180 |
| TGTCGCAGCA TGGTGGCCGT GAATGGGATA GCGNACACCA CAGGCAAGCT GGGCTTTGGA | 240 |
| GGGAATTTCA AGTNACTTGT GGGAACAACC ATTCAAAAAG GTGGNCAGGN CATATTACAA | 300 |
| ACAGTTTCGA CAATGGNACC GATTGNGGGA CCATTT | 336 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | |
|---|-----|
| GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTCAGCGGG | 60 |
| ATGCCTTCGG CCGGGGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGNCA GGCCGCCTGT | 120 |
| GCCAGCACAC GTGTGAGAAA CAACTNCGG CTCCTNACCG CTGTTCTGTC GCCTCCGGGT | 180 |
| TCCTGGCTAG CAGCGGNACG GCAAGCGCTG TGNAAGACGT GAATAAGTGT GAGGCCCANC | 240 |
| GCTGTGAGCC AGGTAGTNTG CCAACATGNT TATGGGNTCC TACCCAGTGG TACTGCCGCC | 300 |
| AGGGGTTACC A | 311 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | |
|---|-----|
| GGCAGAGNAC AAGGGCCGTG GCGCTTCGCC CTCATCATCT ATGAGAACAT CCTCAAGTAT | 60 |
| GTNAACCTGG ACGCCTGGAA CCGGGAGCTG CTGGACAAGT ACTGTGTGGC CTACGGGTGG | 120 |
| GCATCATTGG CTTCTTCAAG GCCAATGNGA ACAGCCTGCT GAGTGCGCAT CAAGGGCTTT | 180 |
| NCCTGTTCTT GCACTCAAAC CTGGGCCTGA AGGACTGCAG CATCAACCCC AAGTCCCCGC | 240 |
| TGCTCTACGT GACGCGACCT AGGGAGGTGG AGAAAGGTGT GCTTCCCCGG NGNAGGACTG | 300 |
| GGACGGTTTT TCCAGTTCAA ATCACTCCAN CTATGGAGCC CATNCTTGTN GGNCANGACG | 360 |
| GGGTTGGTTT TGAAGTTCCA TGCCCACAAC TGGGG | 395 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|---|-----|
| GGCAGAGCCA CAACCTCCCT GGCTCCTACC GCTGTGACTG CAAAGCCGGC TTTNAGCGGG | 60 |
| AATGCCTTCG GCCGGGGCTG CATCGACGTG AATGAAGTGC TGGGCCTCGC CAGGCCGNCC | 120 |
| TGTGCCCAGC ACACGTNTGA AGAAACACAC TTCGGCTCCT ACCGCTGTTC CTGAGACCTC | 180 |
| CGGGTTCCTG CTNAGCAGCG GACGGCAAGC GCTGTGNAAG ACGTGNAATG AAGTGTGAAG | 240 |
| GCCCAGCGNT TGCAGCCAGG NGTNTGGCCA ACATCTTATG NGCTTCCTAA CCCAGTGGNT | 300 |
| ACTNNCCGNC CAGGGNTNAC CAGCTTGGCT TGAAGGGATT GGGGCACAAC TGCAACAGAC | 360 |
| ATTCCGACGA GTTNTGCTTC AAAGGGNGGC CGGAATCCTT TTGNAACTTT CCGTTGTTNT | 420 |
| TNAAAGTTG | 429 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| CTCACTGCCA GTTCGTGCTT GAGCATCGTT CTGTGCAGGA GGAAGCCGGC TTTCACCGGC | 60 |
| AGGCGTGGTG TCAAATGCCC GTTAATTGTT AGCGGACACG AAAACCAGGC CATTACTCAC | 120 |

AGTATAACG

129

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | |
|---|-----|
| CTTACGATC GTTCTGNGCA GGAGGAAGCC GGCTTTCACC GGCAGGCGTN NTGTCAAATG | 60 |
| CCCGATAATT GTTAGCGATA CACGACAAAC CAGNCGCATT CACTCNACAG TATAACGNCA | 120 |
| GGCCAGTCGT CATAAACCGT TCAGGGGAGG AGCCCGGTCA CCCAATTGCG CCCCTGATAA | 180 |
| GTGCNGTNCG ATATTACAAA TTNCACTTGN TCC | 213 |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | |
|---|-----|
| GCCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAAAAAAAAA AANANAANAA AAAAAAAAAA AAAAAANAAA AAANG | 115 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | |
|--|----|
| GGCACGAGCC CCCCTTTTTT TTTTTTTTTT TTTTTTTTTT TTAAANGNT TNANNTTTTT | 60 |
| | 60 |

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | |
|---|-----|
| GGCACGAGCG CATGGGNGTC ATCCTCTGGG GTGACGCTNG GGTACACCAC AAGCACGGAG | 60 |
| ACCTGCCAGT ACCNCAAAGA TTACCTGACA CGGCTGCTGG TCCCCTACGT GGTCAATTTG | 120 |
| TCCTGGGCCA CCGNGTATTG CAGCCNGGCC GAGTGCCATG GCCGTNGNCG GCTGTGTGCN | 180 |
| | 180 |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | |
|---|-----|
| TNCCATGNCA CGATATTTCC GCCAAGGACA TCGACGGGCA CATGGTTAAC CTGGNACAAG | 60 |
| NACCGGGGCT TCATGTGCAT CGTCACCAAC GTGTGNCTCC CAGTGAAGGN AAGAACCGAN | 120 |
| GTAAAACT | 128 |

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | |
|---|-----|
| CACCGCCTAT GGTNCTGACG CCAGGCCTGG GCAGAGCCCG GCGTCTGGA GGCGCTTNGN | 60 |
| NGCCGTNCTT GGGCTGCGGA AAGGCTCAGG ACCCAAGAAG GAGCGGAGAC GCACTGAGAG | 120 |
| CATTAACAGC GCATTCGGNT AGTTGCGCGA GTGCATCCCC AACGTGCCGG CCGACACCAA | 180 |
| GCTCTCCAAG ATCAAGACTC TGCGCCTAAC CACCAGCTTA CATCGTCTAC CTNATGGGAC | 240 |
| GTNNCTGGCC AAGGTGCACA GTCTGGCGAT CCCGAGGGCT TTCANGCTTG GAACTCAAGN | 300 |
| | 300 |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|---|-----|
| TGNGTGAGGT GGCCCTGGGC AGAGAGCACC NTATCANCTT GGACAACCCC AGCTTGAAGA | 60 |
| GGCCACCTCC TGGCTTCGAC AGTNTCATTG CCCGAGGCCA CACCGAGNCT GATCCGACCC | 120 |
| AGGACACTGA GTTGGAGCTG GATGGGCCAG CAAGTGGTGG TNCCCCAGGG CCAGCCTGTN | 180 |
| CCNTGN | 186 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| TCTGNCCNTG TCATCGNAGA CTTCANGGTC TTAGCAGGGG ACAAGAACTT CATCACAGCT | 60 |
| GAGGAGCTGC GGAGAGAGCT GCGGGGCGNC CAGACCGAGT ACTGCATCGC CCGCATGGGG | 120 |
| NCCATACCAG GGCCCTGACG CCGTGNCCGG NGCCCTCGAA CTTACAAGTC CTTCTTCACG | 180 |
| GGCTTTGTAT GGCGAGAGGG NNCTGTGAGG | 210 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|---|-----|
| GGCAGAGGNC AAGCCGAAGA AGCCCAACTA ACCCAATCGN AAGTNCCTGT CAAGTNCGGC | 60 |
| TNAGCATGGC CGNAAGCNMN TGCCTTNANC CCTGGGGAGG GCCACACCCT GCAGGAGCAC | 120 |
| CAAATTGTCC TTGTGGAGGG TGGCCGCACC CAGGAACCTG CAAGGCGTNA AGCTTCACCG | 180 |
| TTNTGCGTGG NAAGTTANGA CTNTGGGCCA CGTGCCAGAA GAAAGTGAAC GGCTNGGGGC | 240 |
| ACAGTGGGCT GGGNGCCCCT NCAGAACATG AAACCTTTCC GNTTCTGGGT TGCNAAAGGG | 300 |
| TTCCTCC | 307 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|---|-----|
| GGCACGAGAG GGCTGGTGCC GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTGAAGC | 60 |
| TGTCAGTGGA GAAGTCCACA GTGCCTGCAG TCTGAGCTGG GAATCCTGTG AAGAGGCTGG | 120 |
| CAGGAGCTGG GAGCCTGAGA AATGAAATGG TGCCTGCTTA CCATCATCCT GCTGGATGCG | 180 |
| GGGCACTGGG ACCCCCTGCT GTNATGAGAA AGGAAGACCC TGGCAGTGAC TTTGGGGACC | 240 |
| CTCAAGGCCG TGGGACCCCA TGCGGGCAAC GTGATCTGGG TTGGACCTGC GCAAAGNTTN | 300 |
| CTTTGCTGGG AGGTTTAGCG TGGTTCAAGA TGGGAGTNAT GCCCAGAGTT GCGTGTGCTT | 360 |
| GGCANCTGGG TTCACAAAGG TTCTTNAANA ATGCTTTTGN CCATTGTTGGG AACAAATTGCT | 420 |
| T | 421 |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|---|-----|
| GGCAGAGCNA ANCCCAGACA CAAGTTTTCA CTCCTTCCTG CGAGCCCTGA GGAAGCCTTA | 60 |
| CTGGGCAGCC CCGGGCTCAT TGAAATGCCC CGGNATGACT TGGCTAGTGC AGAGGGAATT | 120 |
| GAATGGTAAA CCACCGGGGT GAGAAGGGAA GGCTCCCCAT CTNCAGCCAG CCACATCCAC | 180 |
| AAGGTGTGTG TAAGGGTGCA GGCGCCGGCC GGTTTAGGCA AGGCTCTACT GTCTGTTGCC | 240 |
| CCTCCAGGAG AACTTCCAAG GGAGCTTTCC CCAGACATGG CCAACAAGGG TCCTTCCTAT | 300 |
| GGGCATGAGC CCCGNAGTGC AGTTCCAAAA TTCGGGAAGA AGTTNTGACG AGGTAGTTTG | 360 |
| NGGNGCGGTT TGTNGGAGTG GTTCATA | 387 |

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|---|-----|
| GGCAGAGGGA ACACCCAAGG GTTGATATTT GTGGTCGACA GCAATGATCG GGAAGCAAGT | 60 |
| AAATAAGGCC CGGGTAGAGC TGATGNAAA TGCTGGCGGN GGAACGNAGC TCCGGGAATG | 120 |
| GCTGTGACTC CTTGTCTTTG CCAAACAAAC AGGTNTCTGC CTGAATGCTC ATGAANCGNC | 180 |
| TGCTGAGAAT GCACAGACAA GCTGGGCCTG NCATTCCCTT TCGTNCACCG TTAAGTGGTT | 240 |
| ACATTGCAGG CCACCTGTGC CCACCAGCGG GGNACGGGGC TGTNACGAGG GCCTGGTATG | 300 |
| GCTGGGCCAT TCAGCTTCAA AANCAAGAAG TGNAAGCCA GACAGCCCTA ACAAAGTACC | 360 |
| N | 361 |

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | |
|---|-----|
| GGCAGANAAC GGGATCCACT TCCGCAAGNC CCTTTGGNAA GGCCGGGTGG GCCANGCCTC | 60 |
| AAACTATGGC ATGAAACTCC CAATCCTGCG TTCCAACCCT GAAGGACCAG ATCCTGTATC | 120 |
| AAACTGAAGC GGTACAATGA AGGAGACCTT TGGCTACGAA NTGCCCCATT CAAAGAAGGA | 180 |
| GGGGGGACTT ACGTGCTGGT CTTGAAATTT GCAGAGGTCT ACTTTGCACA GTCCCAGCAA | 240 |
| AAGGTATTTG AATGTTACGA TTGANTGGCC ACGTCTGGTG NAAGGGACTT GGGATATCTT | 300 |
| TGAATCGTGT TGGGGCANTA GCACAGTTCA CGGTTGAAAT TATTACCTAT GAAGCATTCA | 360 |
| GAAAGGGGGA AGCTGAGTTT TCCAGGGGGA GGTGTTCCAC CTTTCACAGG GGAACTTTAC | 420 |
| ATTGAGTTTT NTTAAGGGGT ACTTTGGACA TTCCCAGGTT TNTGCACTTT ACATCATGGT | 480 |
| TGGGACCATG GGNTGTTTA | 499 |

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | |
|---|-----|
| GGCAGGAGGG TGAACGTCAT CGCNTCGAAA GCGTCGNAAT AAGACGCACA CGTTGTCCGC | 60 |
| NCGNTGCTGG GTCNAAGGCC TACCACCTTC AGAAGTCGAC CTGTGNCAAA TGTGGGCTAC | 120 |
| CCTGTCA | 127 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | |
|---|-----|
| AGGCCCNTNC CANTTCNGGG CCCCAACCCG TTTNTCCTGG GGGACCGTGA GAAGGTTTGT | 60 |
| TGCCCCAAAA ACCCAGGAGA AGGCCAGGCC GTTTTGGACC GTTTAAAGGT NTTNACGGT | 120 |
| ATCCCACCGN CTTNCGACAA GAAAAAGCGG GNTGGTGGTT TCCTGCTGCC CTAAAGGTCG | 180 |
| TGCGTTNTAN AGCCTAAAAG AAAAGTTTGC CTTTTTTTGG GGGCGGCTTT GGTTTAAGGA | 240 |
| GACTGGTTGN AAGTTACCCA GGNAGTTGAC ANGCCANCTT GGNGGGGGGA | 290 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | |
|---|-----|
| GGCAGAGCTG TTCCCTNCCA CTGGNTGAGG NATCCTGCAC TGCNTACACC CTGAGNTGGA | 60 |
| AACATCGGGN TGTGANAGGT AGCACAGAGG NCTGTNCCCT TTTGTTTATG GTGGNTGTGG | 120 |
| AGGGAATGNC AACCGTTTTG GNAANCCGTG AAGGNACTGA GAAGAGNCCG CTGACCCACC | 180 |
| CCGGGTGGTA ACAGAGACCA GGGGGACAGG TACTTCCCAG GAACTGAGGG NNCAGATTAT | 240 |
| TGNGNTGAGG TTCAGCATCC CCTGGAGGNG TCGGGGTTTC CGCAGAACCC CACTTT | 296 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | |
|---|-----|
| GGCANAGGGA ACTTAAGCAA AAAATCAAAG ACATAAATNA TCAGATGGAT GAGTCTTTCA | 60 |
| GAGAGTTGGA TATGGAATGT GCTCTTTTGG ATGGAGAACA GAAATCTGTA AACAACTGGA | 120 |
| ACTTATGNAA GGAGNAAGGA GATTTTGGAT CATCTAAACC GGNGAATAGC TGANCTGGGA | 180 |
| AAAGAAACAT TGTTGGTGAA AAGACCAAGG ATGCTGACCT GTTTGATGTT GAAAGCAAAC | 240 |
| ACTTTGNAAG ACCTGGGAGT TCCAGCAGCT TGTAACATGA GAGCCGTCTA GATGTAGAAA | 300 |
| AGGTGGAAC TNGACTNCAA CAGCTCCNGC GTGNAAGTTG CTTGNATATT CT | 352 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | |
|---|----|
| GGCAGAGCCC CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNNTTTTN AAGGGGGG | 58 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | |
|--|-----|
| GGCACGAGGT AAATNTGGTG TTTCTCCTAG CTGTAAACTG TGTCCCTAATC AGGATGGAAT | 60 |
| TTNNAAGGAG ACAGATGCTG GAAGATGGGT TCATATTGTT TGTCCCCTGT ATGTNCCTGG | 120 |
| AGTAGCCTTT GGAGATATTG ACAAATTACG ACCAGTAACA CTAACGGAAA TNAACTATTC | 180 |
| CAAATATGGT GCCAAGGAGT GTAGCTTTTN TAAAGACCCT CGCTTTGCTA GANCTGGGGT | 240 |
| TTGCATTAGC TGTGAATGCA GGGATGTNCA GAGCCTATTT CCATGTGAAC CTGTGCTCAA | 300 |
| AAGGAAGGTC TGCTTTCAGA GGCAGCGGGC GGAAGAGGNT ATTAGCAGNT CCATTCTTTG | 360 |
| CTTATTGTAA GCAACTNGCA GNTAGGTTAG TNAGAAAGTG GGA | 403 |

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | |
|--|-----|
| AGGGCGNGGA TTGGCCCGGG CCTGGCGGCC CGCGGGANCC TCAAGCCCAC GGNCAGCAAG | 60 |
| CTNGGCGCTC CGCTGAGNTC CTGCAGGGGC TGCCCAGAGTG CACGCGTTGN GCCACGGTCA | 120 |
| TCGGGNCACC ATCGTCAAGG CACGGGGCAA GCTCNNNCAT CCCGAGTGCT TCATGTGCAG | 180 |
| TGACTGGGG | 189 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | |
|--|-----|
| GCAAACCGCA TCANCTTTCC GGTGGTCAGC GACAACGTGT GGCCCTGGCC CGAAGCCTTG | 60 |
| CGAAGGCCCG AAACCTATTAC TGCTCGATGA GCCGATGGGC GCGCTGGATA AAAAGCTGCG | 120 |
| TGACAGGATG CAGCTTGAAG TGGTGGATAT TCTGGAGCGC GTCGGTGTGA CTTGTGTNAT | 180 |
| GGTCACCCAC GATCAGGAAG AGGCGATGAC CATGGCGGGG CGCATCGCCA TTATGAATCG | 240 |
| TGGGAAATTT GTCCAGATTG GCGAACCGGA AGAGATCTAC GAGCATCCGA CTACCCGCTT | 300 |
| ATAGCGCTTG ACGCNACCGT GGGAAATCAA GACCAAANTC AATCTGATTN CAAAAGCTT | 360 |
| CACGGATTTN TGCCACGGTG TTAACCGCCG CATCTACCGN GCGGNAGTTA TTCAATTTAG | 420 |
| NCCCAGTTCT TCAAAAACCG TTCANTTTTG AAAGTATTCG AAGNCGATTT TGGNTAGTGT | 480 |
| TTTTAAAT | 488 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | |
|---|----|
| GGCAGGAGCC AACCCAGCTA TGGCCTATGC CAACGAGGTG AAACGTGTGG TCAGCAGTGC | 60 |
|---|----|

| | |
|--|-----|
| ACAGGAGAAG GGCAGGAAGA TTGCAGCCTT CTTCGCTGAG TCTCTGCCCCA GTGTGGGAGG | 120 |
| GCAGATCATT CCCCCTGCTG GCTACTTCTC CCAAGTGGCA GAGCACATNC GCAAGGCCGG | 180 |
| AGGGGTCTTT NTTGCAGATG AGATCCAGGT TGGCTTTGGC CGGGTAGGCA AGCACTTCTG | 240 |
| GGCCTTCCAG CTCCAGGGAA AAGACTTCGT CCCTGACATC GTCACCATGG GCAAGTCCAT | 300 |
| TGGCAACGGC CACCCTNTTG CCTGCNTGGC CGCAACCCAG CCTGTGGCGA GGGCATTNA | 360 |
| AGCCACCGGC GTTTGAGTAC TTCANACCG TTGGGGGGCA GCCCAGTGTC CTGCGCTGTG | 420 |
| GGGCTGGCCG TCCTGAATGT NTTNGGAGGA AGGNGCAGCT TCAGGATCAT GNCACCAATT | 480 |
| TAGGCAGTTT CTGA | 494 |

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | |
|---|-----|
| GGCAGANCTG TGGACTGTTC CACCAACAAC CCCTCCNAGG CTAAGCTGCG GCGNGACTCG | 60 |
| ACGAATCCNT CCAGGTCGCT GAGAAGGTTG ACCAGGAAGT ACAACGAAGC TGCTAAAGTC | 120 |
| CTACCANTGG GAAGATGCTC AANACCTCCT CTTGGCTGG AGCAGCTGGA ACGAGCAGTT | 180 |
| TGAACTGGGG TGTGCCCCGC TGGCAAACCT NCACGCANGC GAAGACCAGT ACTGATCTGA | 240 |
| GGGTNACCAC GGTGGGCTTT CCNACACTTT CTGAACTTCG GAACGTTNCC TTCCGGTGT | 300 |
| CACTGANGGT GGTTCGTGAA AGCTCTTNTG AACTTCTGAA TTCCCATCCA CTGTGAACGG | 360 |
| TTCCCTTGTT AGGAANTTTT TNCAGGNAAG NAACCCCTAA AATTTTATGG GAGGACCGTG | 420 |
| GG | 422 |

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|---|-----|
| ACGCCTGCNA TTGGTCAGGC TGACCTGGCC TCCCGTGGGG CCACTCGCTG CCTTAGGTGC | 60 |
| CTTCTGCTCT CTGGAACCAG AGGGACTAGC TGACTTTTGC CAAGGAAGCA GTGCCAAGAG | 120 |

| | |
|---|-----|
| GCATGGTCNT GGTNNCCTGC CTGCCCCCGG GAGNNCACCT CTGTACACTT CCCTGAANAC | 180 |
| CTTCCCAGGT GTGGGTCACT GCCACCTGTG CCCATGGGCA CCCCAGAAGC ACCCACTGTG | 240 |
| AACCACTGNC AGTTTTTCTG CATGGCCCAC AGGCACTGGG CCTGTAANCC TTTCGCAAGG | 300 |
| GGTCCCCGGT CCCTTCCCAA NNAATTTTAG CCTTTNTAA NGGTTGGCAA CCAAAG | 356 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|--|-----|
| CCGACCTACC GAGAAGAAAA TCTTCACCTA CTTTCATGGTG GGCGCCTCCG CCGTCTGCAT | 60 |
| CGTACTCACC ATCTGTNANN CTCTGCTACC TCATCTGCCA CAGGGTCCTG CGAAGGCCTG | 120 |
| CACAAGGACA AGCCTCGAGG GGGTTGCAGC CCCTCGTNCC TCCGCCAGCC GAGCTTCCAC | 180 |
| CTGCCGCTGC CACCACAAGC TGGTGGAGGC TGGGGAGGTG GATCCAGACC CAGGCAATAA | 240 |
| CAAGCTGCAG GTTCAGCACC CAACCTGACC CCCATCTGAC CACAGGGCAG GGTGGGGCAA | 300 |
| CATGCGGGCT GCCATGGGAC ATGCAGGGCG GTNTGGCAAG TGGAGAGGTN CTACAGGGNT | 360 |
| GAGTGACCCA TTTGGAGTTC ATAAGTATGC AATTTGGTTT TGGCAGTATT TTTTGACATG | 420 |
| GGACTNGGNT GTTTGNCGGG TTTAGTAACC CCAGGCCATG GCANCTNAA GGGCATGGTT | 480 |
| TTGAAAAAGG ATTAA | 495 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|---|-----|
| GGCAGAGGGA AACTTTTCCT TTGTCCATCG AGGTGTTTCA TAAGTTTTTT GGTGTGTTTT | 60 |
| CTGGGTCGTC TATGTGTCAT ATGGTTTNAC TTTTCTCTCC TTTTTCGTTT TCAGAACATN | 120 |
| NTTCTGTCTG TTTTGGATTC ACTGCTTCCA TTTNACAGAA TGTGNACTCT TTAGACTCTC | 180 |
| AGTCCATCAT GCCATCGGGT ACTCTTGTTG CAGTGTAATT TTAATNACAT GCGGTTATTT | 240 |
| CCCTAACGAA TGTGCTATTC ACGTTCCATC TTNCAAATC CATTTTCCCA TCCAGCCAGN | 300 |

GTCTACAATT TAGTGCCCNNT GGCTCCNATT TCGGTCCTCC TCCCCGGGGC TTTNCCCTGG 360
CTGCGGTGCT GGGCCAAAAG CAGGGGTTTT ANTC 394

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGCANAGGAG GGCTGGTGCC GGGANTCCAC GACAGACGAG CAGCTATTCA GGTGTAANCT 60
GTCAGTGGAG AAGTCCACAG TNCTGCAGTC TGANCTGGGA ATCCTGTAAG AGGCTGCAGG 120
AGCTGGAGCC TGAAAATAAA TGGTGCCTGC TTACCATCAT CCTGCTGATG CGGGCACTGG 180
ACCCCCTGCT GTATGAGAAA GGNAGACCCT GCAGTACTTC CAGACCCTCA AGGCCGTGGG 240
ACCCCATGCG GGGCAACGTA TCTGGGATGG ACCTGCGGCA AAGTTTCCTT TGCTGGGAGG 300
AATAAGCGTG CTTCAAGAAT GGGAGTNATG CCCGAGGTG CCGTGTNCTT GCACTGGGGT 360
TCACAAGGAT CTGAACAGTG GTTCTGCCAT TTGGGAACAA CTTGTTCTTT GGTCAACCAT 420
TTTTGATTNG TTNACANATC GGCTTCGNAA CCTNG 455

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGCANAGCAA GAAATGGCAC CAGGAACAAC ATTTAACCCG GTCATTGGTG ATTCANCTNT 60
GGATCCAAAA AAGGTTAAGA CCCTCGTTTT CTGCTCCGGC AAACATTTCT ACTCCCTGGT 120
GAACAAAGAG AATCTNTGGG GGCCAAGAAG CATGACTTTG CCATCATCCG AGTAGAGGAA 180
CTCTGGCCCC TTCCCGTTGG ATTCTTTACA GGAAGAGAAT GAGCAAATAC AAACATGTTA 240
AAGATCATAT TTGGAGTNCA GGAGGAACCT CAGAAACATG GGTCCGTGGG TCGTTTGT TT 300
CTNCCAAGGT TTGAAAAGCA GCTGGNCCTG CAAGCTTCCG TTCTGGTTGG GCCGGNCCCC 360
TTTTGNCATG ACCCGNTGTT 380

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CAGTGACCGG TTCTNCAGCA CCCGGTGCTN GAGNTTTNGC AATGTCCCGC ACCGGGACGN 60
TCATCCTGGG GACCTGGTAC ATGGTAGTAA AACCTATTGA AGAGCAATTT GCCTAACTGT 120
GGGAGTGAAC TCATCCAAAC TCCATGCCAG TNNNNAGCNT C 161

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGCACGAGGG TGCCTGAGT CGGAGCCAGA GGCCGCGGGG ACACCGGGCC ATGCACGNCC 60
CCAACTNAAG CTGCATCTCA AAGCCGAAGA TTCCAGCAGC CCAGGGGATT TCAAAGAGCT 120
CAGACTCAGA GGAACATCTN CGGAGAGACC CCCGAAGCCC TCTCCAGGGC AGTCCTCATC 180
CAGACGNTCC GCTAGTGNCA GACAGGAGCG CGCATGGGCC CCCGNNTCGG 230

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGTGGGCCAC CTCACCAAGT GCAGCCATGC NTTCCACCTG CTGTGCCTCC TNGCCATGTA 60
CTGCAACGGC AATAAGGATG GAAGTTTGCA GTGTCCCTCC TGCAAAACCA TCTATGGAGA 120
GAAGACGGGG ACCCAGCCCC AGGGAAAGAT GGAGGTATTA CGGTTCCAGA TGTCGCTCCC 180
CGGCCACGAG GACTGCGGGA CCATCCTCAT AGTTTACAGC ATTCCCCATG GGCATCCAGG 240
GGCCCTGAGC ACCCAATCC CGGAAAGCCG TTCCTGCCA GAGGGTTTTC CCCGCCAGTG 300
GTTACCTTTC CAGACAACGG CCAGGGCCGN AAGTTCTTAG NAGCTTCCTG GAAAGTGGGG 360

CNTNGTAAGA GGNGGGTTCA T

381

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|---|-----|
| CTGCTTGTGT TTAATTCTGC CATTGCCAAC ATGTTACCT GTAACCACAC CCCCATACGG | 60 |
| AGCTGTGCAG CCCGGATGCT GAATTTAACA CCTGCTGACA TCACTGCCTG CCACCTGCAG | 120 |
| CAGCTCAATT ACTCTCTGGG TCCTGGGATG CTCCCCTGTG TGAGGGNACC ATGCCCACCT | 180 |
| GNCAGCTTTC CTGAGGGCTT CTTCCAATGA GACCTTTGAT GGGCTGGGAC TGTCCAGCTG | 240 |
| CAGGGGAGGG TGGCCCTCAA TNTGTANGNA CCCCTGTGAA TNTCTNCTGG TGGTTTGCG | 299 |

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|---|-----|
| GGCAGAGCAC CATCCTATCC AGCCTAACNT TTAATTGAAA GCAACAAAGC ACCTACACCT | 60 |
| TCCAGCTGAA GGNAGTGGA TNGTGGCGTC CCACCTGCGC TCAGCTTACG TTGGTGTCAC | 120 |
| CATCAATGTG CCTGGNACGA GAAATGAACA ACGNACCCTA TATTCAGTGN CCCCTTCCTT | 180 |
| AACACCTCTT NANAAGCTGC TG | 202 |

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| TTAAAANTNA TCCAGCTCTT NCTCAGTGAA AGAGGAAAAT CCCTCCATGG NAGAGGTCAA | 60 |
| CGCCTCGNTG GCATACAGAC TGGGGACCCT GGACATGCGG GNTTTTTTCC GNAACACCCA | 120 |

AGNGGAANAT ATCGATTCTN CCTCGGGAAA GCCCCATCCA ACANTGGATG GTCCATCTGG 180
GAGTTCCAGT ACCGCCCTNG GGGCCCGGTN ATTNATTTCC TGAACAACCA G 231

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGCAGGAGGA GAAGTGGCCT TAACTGTNCC AGGTCACACG TGGAAATAAG TACAAAAGTA 60
ATGACTAAAA TAGGCCAAGT TGTCCGAGCA CTTTGTACAT AGGGGTATTA TACGACTGCA 120
AATTGTGTGA TGTTTAATTG TCACAGANAG AGATACTCGT TTTAAGCACT TTTAGCCTAA 180
TGTNCTGGAA AATTNCTTAA TGGATTTTNA TACTCTATTG GAAACATTTC CATATTGGTG 240
NAAATGCCAC TNCATTCCTT TTNCCTGAGG GGGCAAATCT TGAGTAGGCA ATGGGGAAGG 300
AAAGCCTGGG CAACAGCCAC CATTGTCTT GTGGGACCTG ACATGGTTTA TTCCACCTNG 360
GAAAGGAGG AATTGCTTAA ATGGCACATT GGTTACCCTT TAGGTTAACC NCAGGTTTNC 420
ANTTTGTGCT GGAATTNTTT AGG 443

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGCAAGTTTG GGNATNCTGA CCCTAAAGTA CCCCATTAAG CATGGGATCG TNACCANTTG 60
GAAGGCATGG AGNAGTTCTG GGAACAAAAC TTTTTTAAAA GNAGTTTNGG GTTGGGCCCC 120
G 121

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | |
|---|-----|
| GGCTTTGGGC AGCTTGGAAG TAACCAANAA TAATGGGCAC TACCGTGAAG ATCCCAACTG | 60 |
| GTTTATAAAG AAAGCCCATG AGCATAAAAG GGAATTNANA GAGGGCCAGC TGCAGGNGGG | 120 |
| AAAAGCNTGT N | 131 |

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|---|-----|
| GGCANAGGTT TGTTTCCATT CAGTTTCCTT CNNGCTTATG TTNGTCAGAG TTAGTATCTG | 60 |
| TGGGTTACAA CAAAGAACTC TGATAAACCC AGCAATAATC AATTAAAAGT GCAATAAGAA | 120 |
| GAAGCTGATA TACGTTATCC ATCAGAACCA TCAAGTATCT GGGAATAAAC TTACAAGCAA | 180 |
| GCATGGTAGA CCTTTAGGAA GAAACTATA AATCTTTGCT GAGGCCATAG GGAAAAAACC | 240 |
| CTGANTGGAA GTGGNNCATA ATATTTTCCC TAGTGNGGAA AACTGGGTG GTNTGAAGGT | 300 |
| GTTGAATT | 308 |

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|---|-----|
| GGCANAGCTA CAACAACACA TCCTAATGNG CANTAATTNT CCTTGCAATA CTCCTATTCT | 60 |
| GCCGGTANGA AAAGCCTCTG GGAACCTACC GTCTAGTACA AGATCTTCGC CTCATCAACG | 120 |
| NGGCAGTCAT CCCTACAGTC CCGGTAGTTC CTAATCCATA CACACTCCTC TCTCGCATCC | 180 |
| CCCCAACAG GTCTCACTTC ACTGTTCTGG ACCTTAAAGA TGGNNNTTTC TCTATCCCAC | 240 |
| TAGACCCCGC TTGTAACTT CCTCTTTGCT TTCCACATGG GNAGGACCCA GAACACCGGC | 300 |
| GTNTTTTAAA CAATTCACCT GGGACGGTTC TGNTTACANG GGNTTTAGAG ACAG | 354 |

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|-----|
| CCATGCCATA CTATGTTTGG CAAAATGTNA NTGGNAAAAC TGTATAATAA ACTTTTCATC | 60 |
| TTAAATTTTG GAAACTATCA GTAATACAGT AGATAAAAAT AAACAAATAC CNTTGGAGGT | 120 |
| AGTCTCAGAT CCTGGNATAC TCTCTCTGAT CTAGTTTCTT CCAGCGNATC CATTAGTTTG | 180 |
| ATTACCATAG GTGTGATTAA AATCCACCAG CTGGNGTCCA GTAACATTGG NTCCACCATG | 240 |
| TATGAAACCT CTGAAGGGGA AATNTCCTNG GATTTCTTCT GANAAATTAA TTACCA | 296 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| GGCACGAGCG GTCTGGCTTC ACAGGTCATT TCGCTCCCCC CGTTTCAGGT TGATCTCTCT | 60 |
| CGCCGTGAAT TATCTATTAA TGACGAAGTG ATCAAAGTGA CCGCNTTCGA ATACACCATT | 120 |
| ATGGAAACGT TGATACGCAA TAATGGCAAA GTGGTCAGCA AAGATTCGTT AATGCTCCAA | 180 |
| CTCTATCCGG ATGCGGAGCT GCGGGAAAGC CATACCATTG ATGTACTGAT GGGACGTCTG | 240 |
| CGCAAAAAAA TTCAGGCACA ATATCCCCAA GAAGTGATTA CCACCGTTCG CGGCCAGGGC | 300 |
| TATCTGTTCG AATTGCGCTG ATGGAAAAAT TTAAGTNGGC TTTTTCCTCC CGTTTTTCGT | 360 |
| TGCGGGTACG TTTNCTGTTG GCAACGGCAA CGTAGTACCN GTGCTTTNN | 409 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|-----|
| CTAATGCCCT CACCCCTTAA AACCAGAAAG CGCGCACAAG TTTTSTAANA GGAGACGACG | 60 |
| AGGAAGGGAA AGCTGGAAAT CCAGGTGTAA ATTAATGGTC TTCTGGCTTT CCAGGGNCAG | 120 |

CCCTCCCCCTC CTTCCCGGAT CATAAATCTT NAGCATTTNA AAAATAACTG CANNCTNNGT 180
GTGGTGGNTT GT 192

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAGCTCCGTN NAGTAACGAG CAGGGAAGAG GTGGATGTCC GAAGAGAAAG ACCTTGTGGA 60
GGAAATCAAA AGGAGAACAG GCCAGCCCCT CTGCCATCTN CTGAACTGAA ACAAACTATC 120
AAAGGAAAGG AAGTGGGGAC TGGGCACTTA TTTAAGGTTA AGAACAAACT GCATATGTNC 180
TTANAATTGC TTTGCACTTT TCCCGTTTTN AGCGGAAGGA CCTGAAGAGT GGTNAGNAAC 240
AGAGGCCTTT GAATTTTAAA TTATGGGTTA NTTTNATTGG TTATTAAGT GGCAAAAACG 300
GGCCNGTTAC CAACACCTTT TTTCNATTAC AGGGCCCCCG GGGGNTTTAG TNCCCGTCTG 360
TGCTTCCGGG GTTAAAAGGN CCCC GCNTGA NATGGTCCCC TTTTN 405

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGAATGCATA TGCAGGGAGA ATCCAAAAAC CATGCAGGAA GCTCCGAAGT ATGACGATGT 60
CTTCCAGAA GTGAAATCGC TACTTTATTG AGCAAATAGC ACGTTGCGAG NCAGGCGGGT 120
ATCCAAAAAA GAAATTGTTG CTCGACCCCG GATTTCGGTTT CGGTAAAAAT CTCTCCCAT 180
AACTATTCAT TACTGGCGCG CTTGGGCTGG AATTTGNACC ATTTTCAACC TGCCGCTTGT 240
TGGTGGGTAT GTCACGAAA ATCGGTGGTT GGGCCANCTT GCTGAACGTG GGGGCCNTTC 300
CGAGCGNNTN AGCGGTNGT TCTGGGCCTG TGCCGGGTTC ATTNGCCG 348

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | |
|---|-----|
| CNAGTGGAAT CCCCCGGCCT GCAGGANCAT NATCCCACGC NAAATGCGGT GAAATATTAT | 60 |
| CNCNATCGTA ACCCATGCCG TTAAAGANAT GACGATGCGG CANTTTATCG CNATCGGCCA | 120 |
| GATCGTTAAC TAATGANTTT AATGANCCCT CCTTTTTTGT TTCNAGAAAG TNTAGCCAGA | 180 |
| AACCCTCAGG GGGANTTTTG GTTATTGGNA AAAAANTGTT TNACCCTGTC CCGGGNGGTT | 240 |
| AACCGT | 246 |

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|---|-----|
| GGAANACCTG TTTGGAAGTA ACAATAAGGA GGAGGACAAG GAGGCGGCAC AGCTGCGGGA | 60 |
| AGGAGCGGCT ANNGNAGTAC GCGGAAGNAA GNAAGGCCAA GAAGCCTGC | 109 |

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | |
|---|-----|
| GGAAGACCNC TATTGGNCTA CCGAAAGAAT GGTGTAACCC CATATATAAT TTCNTTTAAG | 60 |
| GNTGGTTTAG AAANTGGAAA ANTGTTAACA AATGTGGCAA TTTTNTNGGN TGTATGCACC | 120 |
| TGTGNATGCA TA | 132 |

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|---|-----|
| GGAAGACCNC TGGCGCCGTT TTTNGNACAA NAAGGTGCTG CTGTCCTTTG GAAAGGCCTT | 60 |
| CAAGTGTAAG GAGCCTGGTT GGTTTCCCTT TGTTTTCTAA AACCAGGTCC ACCGGTTTTG | 120 |
| CCTGGNTGAA GCCAGNCTGC TTTTNCNAGC CCAGTNCCTT AACTG | 165 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|---|-----|
| GAGNTNAACA TGGNCANNNC CAGCCAGACC NTGGCCACCT TCCTAGNTNN NCTGGCGCAG | 60 |
| AAGCTAAAGC CCCTGGGGNA GCAGGAGANT CGCGGTGATT NTGGAGCTNA TTNCNTGCGG | 120 |
| AGTGCGAGCC CCGGGGCCTG CCCTTCNACG GCCGCATCCT TGCCTGGAAC ATGCGCTACT | 180 |
| ACATGAACCA GGTGGAGGAG ACGCGCTACT GCTTGGACCA NAACCTNCTC AAGGAGTACT | 240 |
| TCCCCTTNCA GGTGGTCACG NACGGGCTTC TTGGGATCTA CCAGGAGCTC CTGGGGGTTG | 300 |
| GCTTCCACCA CGAGGANGGT GCANTNCCTT | 330 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|---|----|
| GGCACGAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANNNN | 58 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | |
|--|----|
| AACANANCTN GAACTCCAC CCGATCAGAC GCCTCCTAAA NCTAGTGGAA TCCCCCGGCC | 60 |
|--|----|

| | |
|---|-----|
| TGGTTTAACG ATGAACGAAT TNACCGAATC GCCTCGGTAA ATTTNCCCGT AATATGGGCA | 120 |
| ACGTTAAGAA ATTGGAGCTT TTCCCCTACN AAGAGCTGGG NAAACANAAA TGGG | 174 |

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | |
|---|----|
| TGGCGCCGNT TTTNGGACAA CAAGGTGCTG CTGTCCTTTG GNAAGGCCTT CAAGTGTA | 60 |
| AAAGAGCTGGG NAAACANAAA TGGG | 75 |

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | |
|---|-----|
| GGCAGAGNCA ATTAATAAAC AAGCTAGATA CCCAGTCTAT TTTCTTTTGA GGATATTTTC | 60 |
| CTGTAGGTCA TTTTAATTGA TTTGTTTGAC ATGACTACAT TTATAATAAT CTANTATGGT | 120 |
| AAACCTAAGC ATCCTACATC TTGTCTTTAG CTTATAAAGA ATTTCCCTTT CTTGGAAGCA | 180 |
| TTAAGTGACT TCTGGTCCCT TAAAATATTC AAATGTGTTG TTTTGGCCAA AATTNCCATA | 240 |
| GGCAAAGAAG AATGGAGAAA AGAAATTGTA AAATGGTTCT CGGAGCTTCT TTGGGTAA | 300 |
| GGGTCTAATG CCAGGGACCA GCATAAAGT TNCGAGTTGG TGCTGTGGGG GGACCCCGGT | 360 |
| TTGTGAGTTC CAGAGGGTGT GTTTGNGNAC AGGCCAGTG GAGGCTCACA CCACACNGTT | 420 |
| CTGGGTCCG CTCAAGGTNG NGGCCGCCAG TG | 452 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | |
|--|-----|
| GGCAGAGCAG GTCTCAACTT CCAGCGAGAG AATGANAGCC CTGTGGTGCG GGCCANGGGT | 60 |
| GCCANCCCTTG ACCCTGGGTG AAGCAAGAAC GCCGACGNGG CCCTGCAAAA CCTCCGGGTG | 120 |
| GGTCATGAAC AGTGCACAGG NTTCCATCAA GCAANTGGTT TCCGGAGCTT GAGGACANTG | 180 |
| AATTTTGTN CCGAAATCCT TAAATCTTTA GGCAGAATTT TTNAAGTTAA AGACGGGGGA | 240 |
| GGAAGGCTTT TNAGGGACCC CTGGGTGTTC TTAAGCATNA AGNTTCGNGT TNTACCCTGA | 300 |
| GGTTAACCAC GGTTCGATCT TAA | 323 |

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | |
|---|-----|
| GATACGCCCT TTGGCAAAGA ACCTGGNGTN TAGANATGTG GTGTTTCGNT CCATAATTNT | 60 |
| GGAGATCCAA AAAGGAAGAG GCTGTGGCCC TAAAAAAAAT CACGTTTACC TGCCAGCTGC | 120 |
| ACCACCTACN TCCAAANCAG CTGGCCACGN GCCTTGCCTT GGGAATTTNA AAANACAGCN | 180 |
| ATGAATCTTG GCTGGCNTGG ACGTNACGAN GAGCCGATCC TTGTCCTCCC CACCGTGCCA | 240 |
| TTATAAACAT GGGCGGNATT TCCNACCAAC TTACAAGGGG CAGGTTCTNG AGGGCACGTG | 300 |
| AATTGGNCCA GGNTTCAAAT T | 321 |

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | |
|---|----|
| GGCAGAGGTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GNAATTTTTT TTTTTTTTNN | 60 |
| GGGN | 64 |

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCACGNGAA CGGGCTGGGC CGAGCCCGCA CTNTCGCGGN TCCGAGAGGA CNNGCGTCGC 60
ATCGTGCTGC CAGCCATCGA CAANATCAAG TACAGCACGT TTAAGGTGCA GCAGTATGCG 120
AGACGNNGCC CATGGCTACA ACTGGGGCCT CTGGTGCATN TACATNATAT CCCCCGCAGT 180
ACTGGANTGG ACC 193

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCANAGGGA GGAAATGTGT TACAAAGATA TATGTACAAG TGTATTCATC ATTTTCCTGT 60
TTATAATTAA TAAAATGAAA ATGAGNNGGN ATGTTGGGTT NTANGGTTTG N 111

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCAGAGCAA ACTTCAGGGA AAGCCATGCN CATTGGAGCA GAGGTTTACC ACAACCTGAA 60
GNAATGTCAT CAAGGAGAAA TATTTTTTTT TNGGGGTGNG 100

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AACAATTAGC TCCAGGAAAT AACAGTTATT TNATCATAAA ACAGTCCCTT CAAACACACC 60
CCNNCCGTTT GTNT 74

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | |
|---|-----|
| GTACCATTG TCTGACCTCT NTAAAAAATG TGATCCTACA GAAGTGGAGC TGGNATAATC | 60 |
| NGNTAGTTAC TGCTACCCAN AGCAATATCT GTGAATGAAG ACAGTGCTAC AGAGGACCTG | 120 |
| GCTACACTTA TNNACAGAAA CAAGTGCTAC ACAGCTGTGG ANCCCACTCG NGATATGGTG | 180 |
| GTGNAGAACC ANAATGGTGG TAAACAGCCT TTAACCCAG AATGCCTGGC TNATCCTGGA | 240 |
| CTGANTTTGA AGTCATTGCT GGAATGCNTA GCGCTTTTTC CTTNGAGAGG | 290 |

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | |
|--|----|
| NGTAGNGGNT CAGACCCAAA GNCTATGAAG TTAATGCTAC TCTGAAGTCT CTCAACA | 57 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | |
|---|-----|
| GGCAGAGGNA GACCCCGGTN TNACGGAGTT AACGTACATG ACCTACGTAA GGGAAGACCT | 60 |
| GCGNGTGCTG CAACTGTNAN AAGCGCTGTG GNCNCTGGAA CGTGGTCTTC GTAATCAANA | 120 |
| GCTCCAAAAG CATTGGGTAC ACCAACTTNA CACTGGNGAA GAAACTTCGT GAATCAACGT | 180 |
| GGTCAACAGG CTGGGTGCCA TCGCTAAAGG ACCCCAAGTC CGNGAACAGG GACGCGTGTG | 240 |
| GGCGTGGTGC CAGTACAGCC ACGAGGGCAC CNTTGAGANN CATNCCA | 287 |

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | |
|---|-----|
| GGCANAGCAA CCCCATAGGC GGGATCAGCA AGACGGACCT CAGGGCCTTC GTCCAGTTCT | 60 |
| GCATCCAGCG CTTCCAGCTT CCTGCCCTGC AAGCATCCTG TTGGCGCCGG CCACCGCAGA | 120 |
| AGCTGGTAGC CCTTGGCTGG ATGGACAGGT GTNCCAAACC GACGAGGAAG ATATGGGGAT | 180 |
| GACATATGCG GAGTCTTCGG TCTATGGGAA ACTCAGGAAG GTGGCCAAGA TGGGGCCCTA | 240 |
| CAGCATGTTA CTGCAAATC CTCGGCATGT GGGAGACACA TCTGNCACCC CGAGACAGGT | 300 |
| CGCTGACAAA TGAAGGGGTT TTTTTTCCAA GTACTCCATG AACAGACACA NGATGACCAC | 360 |
| G TTCACAACC GNGTTACCAG TCGAGGAACT ACAGCCCTGA GNCANCAGT TTNATTTG | 418 |

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | |
|---|-----|
| GGCAGAGCTG ACTGAGTGGG ATTGAAGGGG AGGTAGGGTG GGTGTGCCCT ATGAATGTAG | 60 |
| GGCCTGCTGC ACCCTGGGGA GGGGACCCGG ATGCAGTNNA TGCCCAAGTT CCAGCGTTCA | 120 |
| GACTGCCTGG GAAGCCCTGA GAACTCCCTG NACCCAGCAG GACGCCCCAT CCTTGGGTTT | 180 |
| NNGGGGGTAG A | 191 |

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | |
|---|-----|
| GGCANAGGTA TCATCAAGAG CCACCAGGGC CTGGACCGNC AGTAGCTGAG CTTTGGANCC | 60 |
| CGGTCCTTCT ACTACAAGCT GCGTGCCGCT GAAGCAGTAC ACACCCANGG NCAAGTACCA | 120 |

| | |
|---|-----|
| TGGCAACGTG ATGCTACTGC GCGCCAAGAA CGGGTGGCGN CTACGGCAGG GNNCCTGGGC | 180 |
| GCGGACTACA ACCTTTNCCA GGTATGCAAC GGGAAAGTAT NCGT | 224 |

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | |
|---|-----|
| GGCANAGCGG GATCCCGGGG ACCTCTGGCG ATCCACAGAT GCTGGAGACT TAGATCTACT | 60 |
| TGGAAGAACC ACGTTTCTGG CTCTTCTCAG GCACGGGAGA CCTACTAACA GAACGGGACT | 120 |
| TGCTCCGGCT CCGGCTCCTG CTCCTGCTTC TTGACCGGCT GTANGATTTG CGACTACGGG | 180 |
| AACGGGNATC GGCTACGAGA CCTGAGAGGA ACTTCTGGTC CGGGATCGAG ACCTGNCTTC | 240 |
| TTGNACCTAC TGTGNNCTTT TGCTGCCTT | 269 |

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | |
|---|-----|
| CGNGCACAGG ACCAGGNCCT TGGTGAGAAA TTCCCAACCT GGGCNAACAA CCAAACCAGA | 60 |
| ATTAGAACTN CTGGGGCACA ACCCGAGGAG AAGANGAATC ACCTCCAGCT TTACGATCGG | 120 |
| TTTAAGAGGA CTCATCAATC TTGGCAACAC GTGCTTTATG AACTGCATTG TCCAGGCCCT | 180 |
| CACCCACACG NCGNTACTGA GAGATTTCTT TCTCTCTGAC AGGCACCGGT GTGAGATGCC | 240 |
| GAGTCCCGAG TTGTTGTCTG GTTCTGTGAG ATGTCGTCGC TGTTCGCGG GAGTTGTTAT | 300 |
| TCTNGGAAAC CCGTNTTCTT GATGTGGCCC TATAAGGTNA CTGGCAACTG GTGGTGGGAT | 360 |
| ACANGGCCNG GCATTTT | 377 |

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | |
|---|-----|
| GGCANAGGNA AAAAAAGGAA ACACCGCAAA CGGTCCCGGG ATCGAAAGAA AAAGTCTGAT | 60 |
| GCCAATGCAA GTTACTTAAG AGCAGCTCGA GCTGGTACAC CTTGAAAAGG CCCTCGACTA | 120 |
| CATAAAAAAT GGAGTTGACA TCAACATTTG CAATCAGAAT GGGTTGAACG CTCTCCACCT | 180 |
| TGCTTCCAAA GAAGGCCATG TAGAGGTTGT TTCTGAGCTG CTGCAGAGAG AAGCCAATGT | 240 |
| GGATGCAGCT ACAAAGAAAG GAAACACAGC ATTGCACATT CGNATCTTTG GCTGGGCAAG | 300 |
| CAGAGGTNGG TAAAGTCTTT GNTTACAATG GGGGCCATGT TCATGGANCA TTTN | 354 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | |
|---|-----|
| AAAGCTGGCA TCCCTNACCT CCTGATCTGA AAAGAAAAGC TTTCAGGNAT TCATCACTAA | 60 |
| GCATTTNGTC CACTGTNTGT TTGTCTTAAG ATTGCCTTTA TCAGATTAAG GAATGTNCAT | 120 |
| TTNATTCCTA GTTTGCCGAG AATTTTTTATT GTCATAGGAT GTTTAATTG GCCACATCTT | 180 |
| TTTCTGCATC TGTTGGGAGT AATCAAATTA TTTTAGCTTA TAATCNCTTA ATATGGTGGT | 240 |
| TTACATTNGG TTTTATAAAN GTTAANCCAA ACAGGGTGGT CTGGTATATT GCCANGGTAA | 300 |
| | 300 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | |
|--|-----|
| GGCANACCCG GATTGAATAG TNTTAACCAG CTTCCNTGGC TTGCTGAACT GCATGAGGCT | 60 |
| CTNACGCACT TGTTAAGCGG CCCCTCCACC AGCACCTTCT GCTCCTNATA GTAGTTCAGC | 120 |
| AGGTGGTTCC AAAGCGGCTG CTTTGAATAG TGCCCTTCGG GTTGCCCAACA ATGAATGACG | 180 |
| CCATACCTTG CTCTGGTCAG GGCCACGTTN AGACGCCTGG GGTCATTTAA AAAGCCAATG | 240 |

CCTTGGTGCT CGTTGGCCCG NACACAGGGN CAGGNTGNTG AAGTCCTTTT GG

292

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | |
|---|-----|
| TCTCTCTCCA GTGTAAACTC TTTAATGTCG TGTAAGGCAC GNAAGTCGAC TAAATACCTT | 60 |
| GCCACAGTNA CTGCATTGTG AAGGTTTCTC TCCAGTATGT ATTCTCTAAT GTNGTGCAAG | 120 |
| GTGTGAATTG TAACTNAAGA CTTTGCCACA TTCATTACAT TTGTNTTNTT TTGTTTGTTT | 180 |
| GTTTGTTTTT NTTTTTT | 197 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | |
|---|-----|
| GACACGAGCT NGAGCCCACC CTGGAGGGAG GAAGAGGTNG TCACCCCTGA CTTCCAGGAG | 60 |
| CCTCNGGTGT CCAGTGGGGT AAGAAGAAAC CCTGNATTTT GGTAGGTAGA AGCANGAGTC | 120 |
| TCAACANACC CTNCAGCCCT GACCCCTGGG GGANCCCATG ACTGGACCT | 169 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | |
|---|-----|
| CTTCCTGCAC AGGAAGGACG TCCTCGGTNN CTCGNAGGAG GAGGNCATGG GGCTCCNNGA | 60 |
| GGTCAGCGTT TCGNACATCA AGCCNCCAGC CCCANAGCTG GGCCCCATGC NANANGGCCT | 120 |
| NNGCCCTCAG NAGGTGGTCC GGAGGCATAT CCTGGGCTCC ATCGTGCAGA GCGAAGNCAG | 180 |
| CTACGTGGAG TCTCTNAAGN GGATACTCCA NGNCTACCGC AACCCCTAA T | 231 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | |
|--|-----|
| NGTTTGAATT GANCCCTCAC TAAAGGGGCA AAAGCTGGAG CTCGCGCGCC CAGAGCGAAG | 60 |
| NTGCGGACCG CGCCGCGACC TTGGNTTGAG CGCATTNGTT TGCTGGAACA CGCCAACCGT | 120 |
| CAGGCGAGTA ACCTGGCCTA TGGTGACCAG CGCCGTCTTG AGATTGCCCCG CTGCATGGTG | 180 |
| ACGCAGCCGG AGATTTTAAT GCTCGACGAA CCTGCGGCAG GTCTTAACCC GAAAGAGACG | 240 |
| AAAGAGCTGG ATGAGCTGAT TGCCGAAC TN CGCAATCATC ACAACACCAC TATCTTGTTG | 300 |
| ATTGAACACG ATATGAAGCT GGTGATNGGA ATTTCGGACC GAATTTACGT GGTCAATCAG | 360 |
| GGNACGCCGC TGGCAAACGG TACGCCGGAG CAGATCCGTG AATAACCCGG ACGTGATCCG | 420 |
| TGCCTATTTA GGTGAGGCAT TAANATGNGA AAAANTNCAT GTTTGTCCTT TGGACAAAGT | 480 |
| CAGGCGTCCA CTTANGGTAN ANTNCCAAGG CGGTTGCATG AGGGTGAGCC TTCATATTCA | 540 |
| ATTCAGGGGC GNGATTTT | 558 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | |
|---|-----|
| GGCACGAGGG AGCNCAAGCA GGATTCTTCC CGAGTCCCTG GCATCCTCAG AAGCTTCAAC | 60 |
| TCTGGAGGCA ATGGGTCGAA AGGGAGAAGA TGACTGCAGT NCCTGGAAGA AACAGACCAC | 120 |
| CAACATCCGG AAAACCTTCA TTTTATGGA AGTNCTGGGA TCAGGAGCTT TCTCAGAAGT | 180 |
| TTTCTGGTG AAGCAAAGAC TGACTGGGAA GCTCTTTGCT CTGAAGTGCA TCAAGAAGTC | 240 |
| ACCTGCCTTC CGGGACAGCA GCCTGGAGAA TGAGAATTNC TGTGTTGAAA AAGTTTCAAG | 300 |
| CATGAAAACA TTGTGAACCC TGGGAGGACA TCTNTGAGAA GCACCACCCA CTAATAACCT | 360 |
| GGTTCATTNC AGCTTGTTNT CTGNGTGGGG NAGCTCTTTG AACCGNNTTC CTGGGAGCGG | 420 |
| GGTGTCTNCA CAGAGNAAGG ATTCCCAGTT TTTGTCANTN CCAGTAGGTT TTTGTCGGGC | 480 |

AGTGNAATA CCTACATGGG GGATTGGGAT GTCC

514

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | |
|--|-----|
| AGCAGGTATG GTGTTCCAGC AGTTTTACCT CTNCCCGCAT CTGNACAGCG CTGGNAAAAC | 60 |
| GTCATGTTTG GNCCGCTACG GTGTCGTNGC GCGAACAAAG AAGAGGCGGA AAAACTGGCA | 120 |
| CGTGAGCTGC TGGCGAAAGT CGGTCTNGCA GAACGTGCAC ATCACTACCC NTCCGAAC TT | 180 |
| TCTGGTGGTC AACAGNAACG TGTGGCGATT NNCCGCGCGC TGGA | 224 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | |
|---|-----|
| GGAACAAAAG CNTNAGCTCG TGCCGCCGGC AGGTGCACAC TAGTGGATCC AAAGAATTCC | 60 |
| NGCANAGTCA CAGCTGATTC CTGGGNAGAG GCTGAGAGGC ACTCCTGGNA TCTCTGGAGA | 120 |
| GNGGCGTCTC CCAGCTGT | 138 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | |
|---|-----|
| GCTGTAGNTN GTCAGANAGG TAGCGAGGAA CAAGAAGCGA AATTAGTTGC CGTTCATTTA | 60 |
| ATCGCGGCAA ACCTGGCAGN GCATGNTTCA CATGGTATTT GGANCATCCC AAGNTATGTA | 120 |
| CGN | 123 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | |
|---|-----|
| GNGTAGCNNG GAAGNCACAG CGCATCTCCC CGCTGTAGGN TTCCTCCCAC AGAACCCGTT | 60 |
| TCGGACCTTC AAAGCGTCTG GTGGAGATGC TGTGCCGCT GCTGCTGCTG CTAACCCATG | 120 |
| TGCCTGGGCC GTTNAGNTC AAGAAGGCC CNGGGCGTNN TCCCT | 165 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | |
|---|-----|
| AACCCTNCAC TGAAAGGGCA NCAAAAGCTG GGGCNCGGGC GCNCTGCAGG TTCGTACACT | 60 |
| AGTGGATCCA AAGAATTCGG CACAGTTGTG GTTTNTCTCA NCGCCTNGGT AGCCGGTAAC | 120 |
| AAACGNGGGT TCCCNNGAT TGGACCGACG CAGCCANGCC NCTGTGGACT TGTTATCAAA | 180 |
| AGAAAGCTAA CTGCTAGATC TTTATCGAGT TAAGAGTGTG GATCTGCATC CTACAGAGCC | 240 |
| ATGGGATGTT GGCAAGTCTT NNACANNGGN | 270 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | |
|---|-----|
| AGCCCNNGGA TGTGCCACTG AGCCTCGGCC CCATCGTGGG GAGCTNTNCC CATCCNGCCT | 60 |
| GTAACCCACC TCTGGNCCCC ATCCATAGAT GATAGGGACC TCTCAACTNT AGG | 113 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | |
|---|-----|
| TGNCTTNGGC TTTGTCCAGC ATNAAAAGGC AGAGCGAACG TTTTCACTGC AGGCTGTTTC | 60 |
| CCNCCAGGGC AAGTGGGACA GGGCGAGTNC TGACGTCTGC AGGCATGGTG TGCATTTAGG | 120 |
| GGTGGGCGGC ACCGAGGGGG CATCATTTGG CATAGGCGGG CCCGGGGGTC ACTGGGCTAG | 180 |
| ATGACTGGCT GGTGCTGGG GGCAGGTGTC ACAGCCTTTG CTGNGCACCC TTTAAGTNGA | 240 |
| GGACAGAACA TTGTTGGGAG GAGTCCAGGC ATAAAGTNAC ATAAACAGCG NCGGNGAATG | 300 |
| GGACCAGCGC ACCTTNAGAG GTGGATTCAT TAGCCTTNAG TCAACTGGGG T | 351 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | |
|---|-----|
| GTGGNACACT TTCCACGGCC TCTTCAAGTC CACGCTGGTN TGCCCCGATT GTGGCAATGT | 60 |
| ATCTNTNACC TTCGACCCCT TCTGCTACCT CAGTGTTCCA CTGNCTATNA GCCACAAGAG | 120 |
| GGNCTTGGAG GTCTTCTTTA TCCCCATGGA TCCGNGNCGC AAGNCAGAGC AGCACTGGGT | 180 |
| CGTGGTTCCC CAAGAAAGGC AAGATCTTCG GGTCTAATGT GTGGCTCTGN ACAAACACAC | 240 |
| GGGGNAT | 247 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | |
|---|-----|
| AGGCAGGTGT CCAAATGGGC AATNCCTGCT GGGAAGCNCT ATTGNTTGGG AACATGGGTT | 60 |
| TNACCCTGNT GGGCAGATGC CAGTGAACAA GACCATTGGT GGAGGGGACG ACTCCTTCAC | 120 |
| CACCTTCTTC CTGTNAAANT GGTGCTGGAA AANACGTACC CCGGGCAGTT TTTGTGAGNT | 180 |
| CTGGAGCCTA CGGTCATTGA ATGAGAATCC GAAATGNGCC CANACCGACA GTCCTTNCCA | 240 |

NCCAGAGCAG CTCC

254

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| GGCACGAGGT GCGTGATGN CTCCCGGGGC CACGGTGGGG TGAAGGATGG CGAGCCGGAC | 60 |
| ATACCATTNT TGGATGTATT TTTTTTAAAA CAGCAATAAT TAGCCATTTT AAAGGAGGGA | 120 |
| TGTACCTGTN TGTGTNCATG TCCACGTNTT TGAGCGTGTG TNTGTGTGTN CAAGTGGGTT | 180 |
| CTTGATATG TGTAGTGTGA GCATGTGTGC ATGTNTGAGC CTGTGCACGT GCATGTTGTA | 240 |
| GGTGCATAAG CATGTACACG CGTGACATGC ATGTCCGTGT ACACGTNTAT AGGTGTACAT | 300 |
| GTNCATGAGT TGTGTACATG CGTGACACGT GTATAGGATG TACGTGTGTN TNCGCATGTG | 360 |
| TGCGNGTAAC ATGTNTTTGT GNTCTTGGGG TATGCATAAG CCATACACGT G | 411 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|--|-----|
| GGGCACGNGC AGAAGTCAAG GTCANTTAAA TGAAAAGCCC TTACCTGAAG GTTGGGAAAT | 60 |
| GAGATTCACA GTGGATGGAA TTCCATATTT TGTGGNCCAC AATAGAAGAA CTACCACCTA | 120 |
| TATAGATCCC CGNACAGGAA AATCTGCCCT AGNCAATGGA CCTCAGATAG CCTATGTTTCG | 180 |
| GGACTTCAAN GCAAAGGTTT AGTATTTCCG GTTCTGGTGT CAGCAACTGG CCATNCCACA | 240 |
| GCACATTNAN GATTACAGTG NCAAGAAAAA CATTGTTT | 278 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|-----|
| TGGGGCAGGA CCAAAGGCAA GATCCATGCC AACGCTGCTG ACCAACCCCC AAAACCAAGC | 60 |
| TGGCTTTGGG TCTGTGTCTG GTGCCACTGG GCAATGTGGC CTAGATGGAA GGGTGAAGGG | 120 |
| GTCCCACTCT CAGTGTCTCT CCTGTGTTCT TCCTCCTTCC ATCTTATCTC TATCTCTGGG | 180 |
| CTGGTTTGTN AGCTGAAAGA GTTCACACAT ACCTGGGGTG GGCCTCTGTC TCCTCGACAG | 240 |
| AGTGGGACTG AGGAGCGAGG CCTGAAGCAT TACTGGTTCA CATCCTGGCC CGGACCAGAA | 300 |
| GACCCAGAC CGGGCCCCC CACTCCTGTA CCTGGTGCGG GAGGTTNGAG GAGGCAGCCC | 360 |
| AGCAGGAGGG GNCCCACTNT TGCCCCCATT CATCGTCCAC TGGCAGGTGG GGTNCTCCCA | 420 |
| GCCAGCCATG GN | 432 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|---|-----|
| TTGNCAGGTN CGACACTAGT GGATCCAAAG AATTCGGCAN AGCTGATNTG ATGCGTCACA | 60 |
| TGNTTATGGC CAACCCCCAG ATGCAGCAGT TGATGGAGCG GAACCCGTNG ATCAGCCACA | 120 |
| TGNTCAATAA CCCTGAACTC ATGAGGCAGA CAATGGAGCT TGCTCGGGAA TCCAGCCATG | 180 |
| GATGCAAGAG AATGNTGCGG AACCAGGACC GGGNCCTGAG CAACCTTNTN GAGCATCGCT | 240 |
| GGGGGGTATA ATGCCCTCNG CCGTATGTAC ACGGGACATN CAGGAGCCCA TGTTTCAGTG | 300 |
| CTGCCCCGGG AACAGTTTTG GCAACANTCC NTNCT | 335 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | |
|---|-----|
| ACCTTCTTTA AATCCGTCAA TAGCCTGCCA GCCAGTAAGC TGTGCCAGTT TGTCAACAAT | 60 |
| CGCAGGCCGG GTACNGGNTG NATATAGACG ATTTTTTTTC CCGGCGTGGC TTTCAGCTCA | 120 |
| AGCGGGGCCG CCCCAGCCAC CCGTTCCTTC CTCATATCGA CTTTACCTAC ATTACCACTA | 180 |

| | |
|--|-----|
| TTTCAATGCT GGT'TTTCGCG GTTGGCGGAG CAGNAGNAAG ATTTCTCCTT ACGTTAATCA | 240 |
| AACGCGCAAC CCAGGAAAAG AATTTCCAAA AGGGATGTTA TGCCTGGCGG TGGATGGTTG | 300 |
| CGGTTTGTGN CCATTCTGGG CTCGCTGGCG ATGGGGGATG GATGTTTTGA TTCGNGTAAT | 360 |
| ATCCCGGATG GACTTTAATG GACCCAAGGT CANTTATTTA CGGCCTTTCC ANAAGTTNGG | 420 |
| GNNG | 424 |

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|-----|
| NNNAGNGCCT NCAGGTCGAC ACTAGTGGAT CCAAAGAATT CGGCAGAGAA AAAAACAAAG | 60 |
| CCATTGACAA GTTACAGATT TCCAGGAAGA AGGCAAAAGA AAAAGGAGCT TAGACAGGGA | 120 |
| AGGAAGAGTC CCCTCTATCC TTAAGTTCTC CCATGTCCGT TGTAAAAGGG CTCCACAGCT | 180 |
| CCACAGAAGA AGAGGGNAGG AAGGACAAGC GCTGGTCAAG GTTATGCAAT CCCAACCTGC | 240 |
| CATCTTCACT GCACCATTAA GCTGGNTATT CTGAAATATG CTTCTTTCTC GACTTTCCGG | 300 |
| CANATTTTAA ATTNAACATT AGAATCCAAC CGGTCGACCT GNTNGTCATT G | 351 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|---|-----|
| GGCACGAGGA ACTGTGGATC TCCTACAATT TTATTGAGAA GTTGAAAGGG ATCCACATAA | 60 |
| TGAAGAAATT GAAGATTCTC TACATGTCTA ATAACCTGGT AAAAGACTGG GCTGAGTTTG | 120 |
| TGAAGCTGGC AGAACTGNCA TGCCTCGAAG ACCTGGTGTT TGTAGGCAAT CCCTTGGAAG | 180 |
| AGAAACATTC TGCTGAGAAT AACTGGATTG AAGAAGCAAC CAAGAGAGTG CCCAACTGA | 240 |
| AAAAGCTGGA TGGTACTCCA GTAATTAAAG GGGATGAGGA AGAAGACAAC TAATGCCACG | 300 |
| CTTTCCACTG TGTGTAACT TATTTGAAAT GTCCNTAGGA NCATTAGATA ATTTTATGTG | 360 |
| ATTGTNNNTT TTAAGATTCT GTATGGGGCA AAGTTTCNTA AGTTAAACCG TTCANNCNTC | 420 |

NCCANCTTTT TTTTCCCTTA ACCTATTCCG TGNTTTNCCC CCAAACCTGGT ANGGCCANCC 480
TNTATATCCC TTCCCNTTT TAGGAACCCN CAATTTTC 518

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCGNNAGNGN CTNCAGGTCG ACAGCGCTTC CTGTCCACGA ATCATATCCG CTATTTTCTC 60
GCCAATCATA ATTGTCTGG CGTTCAAATT CCCGGTGATA ATCTGCGGCT TAATCGACGC 120
ATCCACCACA CGCATGCCTT CTAACCCGTG TACGCGGCCT TCGCCGTCAA CCACGGACAT 180
CTCGTCGTAA CCCATTTTGC AGGTACCGCA CGGATGGGAA GGCGGTTTCG GCGTGGTTAC 240
GCACGAACTC ATCGAGCTGT TCATCCGTCT GGCATTCGAC ACCGGGGCTG ATTTTCGCGGC 300
AACGATACTN ATCCAGCGCG GGTGATGCA TGATNTCGCG GGTGATGCGA ATTGCGTCGC 360
GGGAACTCCT GCCAGTGCCT GCTCGTGCGA CATGTGNTTG AAACAGAATN CGCCGGATGG 420
TAGTGCGGGT AGCGGGGTTT NATGCCGNAC NGG 453

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AGGGCNAGCT NACTGANGC TACCAGGAGA TCTCCANGCG AAACCTCAGCC TCCTCCCAAG 60
CTCCCTNTGG GATCCTAGCC ACAAGCTCTC CAACAATTAC TATTGCACTC GAGAATGGCC 120
GCCGGGGAAT CTNAGCCCN TTGCCATCAT GCATNTGCGT TCNACAGAAG NNGCTGGTGT 180
GCAGGCAAGA CAGCAGAGAG CTCTGCTGTG AGCTGACCAC TGAGCNGGNA GGCGNTGCNT 240
CCANNTTCTT NTATTAAAGA GNTTGGGGCT TNNCTTCGGG CCACCTTTAN CTGTTTACAC 300
TGCAANCTTN AGGGNCACCG GATGANTTNG CCNCCTTTGG GATTTTCNAC CAGGGGGGTT 360
TTGGACNCAN TTTTNTGGNC AACTAGGGGG GNTTGGGTTT CNNTTGGGTT TTTTTTGN 420
AATTTAAAN AAGGGGGNGT TTTTAAAAA AAA 453

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | |
|--|-----|
| TTTTTNCGC GGNCGGTGGC GCGGCAACCG CCAGANGATC CAGAAGAAAA GCAGATNGTT | 60 |
| GGCGAAGATG GAAATCGCCA GGCCAATCAN TCGCCACGTC GGTTTCAGCC ACTCANTGCT | 120 |
| GTTCAGGTGC AGGGCGCTAA TAATCATTTG CTGCGCCGAA CCGGCAACCG AGGTGATCGA | 180 |
| AAGCTTCACA ATCAGCGCAA TCAACAAACC AATCAGCGAA ATAAAATCTC GCAGATATTT | 240 |
| TACCCAGAAC TTCTCCTGAT CTTGCGGCGA GCNTTCCCAG ACATCGCGCG NACTGGGCCA | 300 |
| CGATTCTGTTT CACGCAGGTT AACCCATCCA NTTGATGCCG GNANTAAAGT GCCACCGCCA | 360 |
| GTCCGACAAG CCCTACAGTC GTTACGCTGC TGGNACGGTG GTGTTGNNGG TGT'TTTTNCA | 420 |
| ACGTGGTGGC TNNCGTGGG TNCNTGNNGT TTTTGCAGAA TTTTTCGNA GATTNTCCNG | 480 |
| TAGGCAACAT GGNTGGGGAG GNCCAGCAAC AAGGCCCCNG NGGGCAAANG ACANCNTCAA | 540 |
| AATGGTNT | 548 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | |
|--|-----|
| CCATCAGAGA GGCTGGCTCC AGCATCTTAC GCATGTCCAC ATTGTGGTCA GTTTGCAAGA | 60 |
| AGTCACCCGT GATATGTGGC AAAACAGCCG GACTCCCGAC ATAAAGTGCT GGAAGGAAGA | 120 |
| CTGTGAGGGA CACAGTTGTA AAGGTTCTCG AATTGTATCT GTCTGATCAG AGAAACAATT | 180 |
| TAATGTCCCA GATCAAAGTC GAGAGGCAGG CTCTGGGAAC TGGGCTGTGA GCAGCCAGAG | 240 |
| AAAGGCGGCA GAACCAAGTTT CTTCAGGGCA GGTCTCTTTT ATCTGCTTGT CTGGATTGCC | 300 |
| TAGTGGACAC TCCATTGGCT CCCAGAGGCC TTCCTGGTNC ATNTCNTCCC TCTGGCTGGG | 360 |
| TCCTTGATCT TTGCAGATGG CTGCGTCCCT GGGGCCAGGA GCACCAATGT GTGCCGNTGC | 420 |
| TGGNCAGGTA NGGNGGTATN CNAGGTNATG TTNTTCCAGG TTCACCNGTG CTTGGTGTG | 480 |

CGGTTTATTG AGTGAANTCN GT

502

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|---|-----|
| GGCAGAGCC AAACACTCCA GAGACCGACG AGTCCCTGNT CGACCCCAAC ATCTTGTCCTC | 60 |
| TCAACATCCT CTCTTCCGGA TACATCCACC CAGCCCAAGA TGACCGGACC TTTTACCAAT | 120 |
| TTGAGGCTGC GTGGGACAGC TCCATGCACA ACTCTCTCCT GCTGAACCGG GTCACCCCTT | 180 |
| ATCGAGAGAA AATCTACATG AACACTCTCC GCTTATTATC GAGATGGAGA ACTGCACCCA | 240 |
| GCCGGCTGTT GTCACCAAGG AACTTCTGGC ATGGTCTTCT ATTCCCGTGA ATGCCAAGCT | 300 |
| GGCCAGCCTN CGNGGCTNCC ATNCCGCAAC CTNTTTTGGN CAGTGGGGAG GCCTTTCGGG | 360 |
| CCTNCAGAGA GTGAACCTGT GNANTGGTGT GTTANNAGNT TCAGCNTGTG GCCACGTGGC | 420 |
| TGANGCGGGN CAGCCCAGGG NTGCAGCGNC GGNGCCGNAG NGTTCNGGGA CACATTGTGG | 480 |
| GCTNTGTTCC GGGCGAGGAG AACTGGCAGN TG | 512 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | |
|---|-----|
| GGCANGAGCG AAATACACAG AAATGGACTA CGCCCGACCT GGTAACAAAG CAGCTTTCAC | 60 |
| TGTAAGCCTG GATCCAGGGC CCCTGGAGCA GTTCCCNCAN TCCATGGAGC CACAGCTCAG | 120 |
| GCAGCTGGGC CTGCCCACCG CCCTCAAGAG AGGTGTGGTG ACTCTGCCTG TCTGACTACG | 180 |
| AAGGTGTGCA AGNGGGCGA TGTGCTGACC CCAGAGCAGG CTCGNNTCCT GAAGCTTTTT | 240 |
| GGGTATGAGA ATGGCTGAAT TCAAGGTGAC CATCAAATAC ATGTGGGATT CACAGTTCGG | 300 |
| GAAGGTTTCC AGCAGATGGG NAGACGGATT TGNCCAAAGA AGCGCATTTT AAGTTCCACA | 360 |
| GAAGNGTTCA GATTCCAGAA GGTTGNNTGA TTGAAAAGGG NNTTCGGGAC TTAAGGTNTT | 420 |
| CCTGGGAAGT TTTTGGGTTT TCATTGGGCC CTTCAGGATT TTTTCCGCC CTTTGGNGAG | 480 |

GGCAGTTTTT TATTTNTTCT TAGNAA

506

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | |
|---|-----|
| GGTCAACATG GNGCCCGACC AGTACCANAT GGGGAGCACC AAGGTNTTTT TCAAGAACCC | 60 |
| ANAGTCGCTT TTTCTCCTG GTAGGTAGNT GCGAGAAGCA AAAAGTTCCG ATGGGTTTTT | 120 |
| GCCCGTAAAC CCATNCCCAG GAAGGTTCTN GTCGTGCGGN CACGTTGGGT CTGTTNCC | 178 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|---|-----|
| CGGTGACCAT GTNTGGCCTG GGNTGTAAGA AGTACGTGGN GGCCAACATC TCCCATAAGT | 60 |
| AACGCACAAC TGTNAAATAT ACAATNAAGA CTCTAGCCAG CTGTNCTGAG ACCGTAATCT | 120 |
| TNATGCTGCT TGGNATCTNA GCCGTGGACT CTTCTAAGTG GGCCTGGGNT TCTGGGCTGG | 180 |
| TGCTGGGCAC CCTCATCTTC ATCCTGTNCT TCCGAGCCCT CGGTATTGCT GGCACCCTCT | 240 |
| GCTTTCCAC TCTNCCTTCC TGTCCCGCCC CTCCCTGCAG CTCATCTCCC TATGTGAAGT | 300 |
| CCACATCTTT GTNAATTCCT AAAGCCTCCT CTTGTTGCTC ACCTGTCCCA GCCCTGTAAA | 360 |
| GACCTCAGCC CAGATAATTG GGTCCCATCG GGTCCCAAGT CCTTCAA | 407 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|---|----|
| GGCAGAGCTT NGTGGGAGCC TCGAGCCTTC ATCATGCAGT GTATTTNTTT CTGTNGTAAT | 60 |
|---|----|

| | |
|---|-----|
| CCAGCTGATC CATTGATCAG TGGGGTTGGG GACGCTTCTN TNCTGCTCAT TTATTGCTGT | 120 |
| GTACAAACCA CCTCTAAGTG AAGGGCTTTA AAACAAGATC GTTCATTTCT TTTGCACATG | 180 |
| GGCATTGGGG TANCTGGGCG CACTACGGCA CTTCTTACCT GGGGCCTCAT CAGTNNAGAT | 240 |
| GGGGCCAGGT TGGGTTAGCC CCAAGGCTTC TGGCATTGGN CTAAGAAGGC CTTCAGAACA | 300 |
| ATGAGGGCTT TGGGCGGCTG GGGGCTCCCC ACCAACAACC CTTNCACCTT CGTGGGGCCT | 360 |
| TCCAGGTTAG CCTGTTCCAC CTGNCNCAGA ACACACACAN CCAGTCCCAC AGGTTCANCC | 420 |
| CTT | 423 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | |
|---|-----|
| GGCAGAGGNC AAGATGGCCA CTGTNATCCC TGNNCCCCTG AGCCTAGGCG AGGANTTCTA | 60 |
| CCGCGAGCCA TCGAGCACTG CCGCAGTTAC AACGNCGGCC TGTNNCGTAG CGCAGCCTGN | 120 |
| NAACTGCCCT TCCTCGACTC GCAGACCGGC GTGGCCCAGA ACAACTGCTA CATCTGGATG | 180 |
| GAGAAGACCC ACCGCGGGCC GGGTTTNGCC CCGGNACAG ATTTACACGT ACCCCGCCCCG | 240 |
| CTGTTGGAGG AAGAAACGGA GNCTCAACAT CCTGGAGGAC CCCAGACTTC AGGCCCTGCG | 300 |
| AAGTTACAAG ATCGACTGTG AAAGCACCCC TGGAAGAAGG AGGGTNGCCT TCCGGNAAGG | 360 |
| GCCGGTTNCT TCGAGGGTTT TATTGTTNTG CCANAGTACG GGGGGAGAAA GAAAGGTTT | 419 |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | |
|---|-----|
| AGTGGTATCC AAAGAATTNG GCANAGGNCG GAAGATCTNA AGACACAAAG GCCCAGTCCT | 60 |
| ATGGGAGAGG GAGCTGCAGG GNGCGGGAGC TGGGACATCC CANGGNTCAT GAAGTGGGGG | 120 |
| NGCAGCCCCC ACGCTGGNA AGCTGAGGGA AGGGCTCATC TCCCCTNTAT GGGGGGNCAG | 180 |
| GAAGGGANTA CCTGNNCCCT GACTTNGTTG GGATTGGGAA CTNAACCCTG GGNGGCCCT | 240 |

CTGAGAGCCC ACCAGCCACA GGNCANTGAA TGCCAACAAA GAGCCCGTTG CTGGAAAGGT 300
CTGTAGCCTG NGA CTCAGTG GNGCTGCCTC CTGN 334

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGCANAGGGN GAGGGCAGAG GAGGAGAGTC GCGGGCGGCC GCTTGGGCGC ACTTNCCGGG 60
TCACCTTGTC CCGGAGGAGN AAATGGCTTC CCTGAGGCAA GTGTACCTAC ATTCCCAGCC 120
CACCAGCCTG ACGCCCAGCC AGGGAAGAGA GTACCATGGA TGGCATCATT GGAACAGAAG 180
AGCATGCTGG TGCACAGTGA AAATCAGTGA TGCTGGCAAG AGGAATGGTT TAATTGAACA 240
CCAGAACTT GATGGCCGAG AGCAGAGATG GTCTGGTGTC TGTTTACCCA GCGCCCCAGT 300
ACCAGAGCCA CCGGGTNGGG GGCCAGCACA GTGNCGGNCA GTCTGGNACA GCAGCAGGAG 360
TTAAGCCNTT TGTCAGCAGT TGGTT 385

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TGGCINNAGGA CCAGCCATCG GAGGTGACTG ANAGATATAA TTTGGGACAG GTCATCAAGA 60
CTGAGGAGTT TTGTAAAATC TTCCGGGCCA AGGACAAGAC GACAGGCAAG CTGCACACCT 120
NCAAGAAGTT CCAGAAGCGG GACGGCCGCA AGTGTCGGAA AGCTGCCAAG AACGAGATTA 180
GGTATCCTCA AGATGGTGAA GCATCCCAAC ATCCTACAGC TGGTGGATGT NTTTTNTGAAC 240
CCGCAAGAGT TACTTTAATN CTTCTGGGA GCTGGCCACG GGGAGGGAGG TGTTTNACTG 300
GNATCCTGGG ACCAGGG 317

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | |
|---|-----|
| GCGCCTGCAG GTCGACACTA GTGGATCCAA AGAATTCTGC ACNAGGTNTT NTTGGTGTG | 60 |
| GGNNGCTGGT CTGGGGACAG GTCATTGCCA CCATCCCCAC CAGCCAGCTC AAGTGCCTGT | 120 |
| NGGAAGCCGG GCACGGGCCN GGNAAGGGAC GAGATGACCG ACGTAGGGAG CTGGCCGAAG | 180 |
| GAGGTAAGAG AATCGACCAT GTCGAGCGGG AACTCCGCAG GGGNCCCAGA TCCTCTGGTT | 240 |
| CCGGGGCCTG AACCGNATTC AAACGCAGCC TGGGCCTCTN CCCACCACTT CCCAGAAAC | 300 |
| GGCGCTCGTC TNAGGNCCTG GGAAGGCTGC CTTTCCGGTT CGTGGGGGTA CGGGGNTGTT | 360 |
| CCCGCAATG GGTTCCTGG TCT | 383 |

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | |
|---|-----|
| ACCTGCGCGG GGNCATCCCG AATNCNTTTN AGCACATCTN CACCCACATC TCCCGCTCCC | 60 |
| AGAACCAACA GTACCTGGTC CGGGCCTCCT ATTTGGAGAT CTACCAGGAA GAGATTCGAG | 120 |
| AACCTNCNCT CCAAGGAGCC GGGNCAAGAG NGCTAGAGCT GGAANGAGAA ACCCCGAGAA | 180 |
| CTGGCGTCTT ACATGCAAGG GACCTCTTCC TGCCTTGTT CACCAAGNAA TGNG | 234 |

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | |
|---|-----|
| GAACATGNCG AGGCCATCGT AAGCNGGAAG CAGGAGGTGC TGCAGGNTTG GAAANAGCTG | 60 |
| CTGTAACTTG TNAAGGTTGC CCGCTTGCTT GTTAAGCTCC ACAGCCGNCG CCCTGGCCTT | 120 |
| CCACAGCCAA GTCCGCGAAC CTGNTCTCCT GGTGTTGGT CATCGCCGCN AGANTTGGGG | 180 |
| CAGCCGNCAA GCCCAGGTGC CCCTNAATCC CTCCTGGGGC TTCCNGCCTC CCCCTGGTGG | 240 |

GCCTACCCCT GGCAACCCCC AGCCC

265

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | |
|---|-----|
| CTGCTGTNCG AGGCCGGNCC CCGGTGGGCT GNNAACGCTG GGACCTGCAG AAGCACTCTT | 60 |
| TCCTAATTNT AATCGGCGAT ATCGGTACAG AGAGTCANCT GNGGGCCGTG CGGGCCAACC | 120 |
| TTAAACAAGG GAATTCTTTC CTGGTAACAT TGACCTGTNA TCCTTTGANT TGAACCAACA | 180 |
| GTTGAAACTC TTCATTACCC GGCACCTAGC TCACTTCTCC TCAAAGGTCA AAGGCCAGAG | 240 |
| GACCCTTTGC CACCAGAGTG AAGATCCTAG AGACCATCAT CCTGGTAAAT CCCAGTGNCA | 300 |
| GACAGCATCA GCTCTGAGGT TTCATCATCT TCTTTAGGCA GTTCNTCAGT TTATAAACTA | 360 |
| TTATTTTGAA TGGGGCAAAG TTTTNGGAGC CTNGGGGGGN GACCTNAT | 408 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | |
|--|-----|
| GGCGCNCCTGC GGGAGNNGGG CTTCCCGTAC ATNACGCCGG TGCAGTCCGC AACCATCCCT | 60 |
| CTNTTCATGC GAAACAAAGA TGTCGCTGCA GAAGCGGTCA CAGGTAGTGG NAAAACTC | 120 |
| GCTTTTNTNA TCCCCATCCT GGAAATTNTT CTNAGAAGAG AAGAGAAGTT AAAAAAGAGT | 180 |
| CAGGTTGGAG CCATAATCAT CACCCCCACT CGAGAGCTGG CCATTCAAAT AGACGAGGTC | 240 |
| CTGTGCATT TNACGGAAGC ACTTCCCCGA GTTCAGGTGG AATTGGATGC AGTGTCCCTG | 300 |
| TTAAGTTCAT GGGGCTGTTT TNTCGAACTT NAATCAAAGG CTGTTTTTCT TGTGTAGNC | 360 |
| CAGTTTCTTT TTGGATTCCG AGGCAGGAAT TCTGGAGGAA NTTTTTGAGA GGTTTAAGGC | 420 |
| AANAAGGTNG GGGACCATCA TNTTGGGCCA TTCCAAGGCC GTTTTGGNGG ACATTTT | 477 |

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

| | |
|---|-----|
| GCCAGCACCC GAACATNATC ACCCTCAAGG ATGTCTATAN TGGTGGCAGG TTTGTGTACC | 60 |
| TGGTAATNGA GCTGNATGCN TGGTGGGGAA GCTCCTGGAC CGCATCCTCC GGCAGAGATC | 120 |
| ACTTCTCGGA GCGGCCN | 137 |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | |
|---|-----|
| GGCAGAGCAG ACTGTCCCCG TGTTGTCTGA GGCAGACCCC TCAGGTTGGT GAGCAGGGTG | 60 |
| CTNTGTGGCC GAGGGCTGGG TGGGCTGGCC TTTGCAGTCA TCTCACCATC TTCACGAGCT | 120 |
| TNTNTCTCTT CAGTCACGCC GATGATGGAG CTGAAGCCCA ACGCAGTNAG CNACCGTGCG | 180 |
| CTGGGTCTGG NAACACCCAC GCTGGACTTC GGCCGACGAG TGCCCCAAGC CAGAGCTGCT | 240 |
| GGCCATCCGT TTTCTNGAA TGCTGAGAAG TGAAGCCAAG GCCCTGGGNG ACCTGGCCTT | 300 |
| GACTTNGGGG NTTACCTGN | 320 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | |
|---|-----|
| GGCAGAGGTT GGTCTTTGCC ATGTCCTTTG TCCCGNCAG NTTCACTCTT GTCCTCATTG | 60 |
| AGGAGCGAGT CACCCGAGCC AAGCACCTGC AGTCATGGG GGGCCTGTCC CCACCCTCTA | 120 |
| CTGGCTTGGC AACTTTNTCT GGGAACATGG TCGGGGGGCT GCTTGGACGG GTGGGGGGCC | 180 |
| AGCCACTGCT TGCCACTGCC CTGTNTGGNC CCTTGTNAGN CAGGGGCTTG TCCAAGATGG | 240 |
| CCTGGGTAAA GTTTGTAGGG ATTGTGGGAG ACTTTNTGGC CTTCTAATT CAAAAAGCAA | 300 |

GGNGGTTCAA GGTGGGAACA GGGCTNAGGG TGGGCAGTGC CCAACTNNTT TTAGGGTTGA 360
TAAAAGGT 368

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAGGGCCATT CAGTGNATGG GGAAAGGTGA ACATNCCATC GTGTACCTCA AGCCCAGCTA 60
TGGTTTTTGG TAAGTNTTGG GGANGGAAAA NTTCCAAATC CCACCAAATG CTGGAGCTGG 120
NA 122

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTCAAACCTCG CCTGGNAGCA CCCATCATCC CCNTGCCGGT CCTNACCTCT NCCTGGAGCN 60
GTCCCCCGC TTCCTTCCCC ATCCAAGGAG GAGGAGGGAC TAAGGGCTCA GGTGCGGGAC 120
CTNGAGGAGA AACTAGAGAC CCTGAGCACT TNAACGGGCA GNAGACAANG CAAAGTTAAA 180
AGAAGCTGGA GAAACANAAA 200

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

TGTGCTACAT CACCTACGTN AGCAATCAGA CCTACCAGGA GCGGACCTAT AAGCAGCTNC 60
TCCAGGAGAA GGCAGCTTTC CGGGAAGCTG ATCGCNCATA GGAGCTCGAC CCCAAGTGCA 120
GGGGGCTGCC CTTCTCCTCC TTCCTCATCC TGCCTTTCCA GAGGATCACA CGCCTCAAGC 180

| | |
|--|-----|
| TGTTGGTCCA GAACATCCTG AAGAGGGTAG AAGAAAGGTC TAAGCGGGAG TNCAGTGT | 240 |
| TTGGAATGCTC ANAAGGGNGC TGGAAAATGG TGGTAAAGGC ATGNAACGAG GGCCTTCAGG | 300 |
| NAAAATGAGC CGCACGGAAC AGATGATCAG CNTTTCAG | 338 |

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | |
|---|-----|
| ATGCGCTNCT GGTGTTCTNA GTGGCCAAAG TCTNTGCCCA GCCCAACNTG GCTGAAATGA | 60 |
| TTCAAAAAGG TGAGCAGNTA TTCCTGGTAG CCAGAGCTGT GTTCATNG | 108 |

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | |
|---|-----|
| AAGCCCACAT NGCCACCCCG GAGCAGCTCT ATCCNGNCTA CNTTGGGGGC TATAAGCAAT | 60 |
| GTAATGCTGG CTGGNTTGG GATCAAACCG TAAGTTATCC CATCCAGACC CCACGAAAGG | 120 |
| CCTNNAACGG GGACATNGNT GG | 142 |

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | |
|---|-----|
| AATNCANTCT TAAGGCCAG GGGAACACAA TGAAGTATGN ATTGACTGAA TGCAGAACCT | 60 |
| GGTTGTGGNA GAGCNAGCTG AATGTTTGGC CCAGAAGAAG CCTGTTCTGT TTTGGGAGCA | 120 |
| GTNANAACCA GNATATGACG TGAGAAA | 147 |

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GGCAGAGNCT GCAGTTTGCA GNGCCCGGAT AACCGAGGCA GTGGCCCCTC CCGCGTCCCC    60
AGGTTTCAAG GACGCTAGGN CTCTCCGCGG CCCTGAGGCT TCGCACTGGG GAGTGGGGCC    120
GCCAGATGGG ACGTGTTTCAT GAAGGGCCTG TCCATGGCCA AGGAGGGCGT TGTGGCANCC    180
GCGGAGAAAA CCAAGCAGGG GGTCAACGAN GCGGCGGAG AAGNCCAAGG AGGGCGTCCT    240
CTACGTCGGA AGCAAGACCC CNGAAGGTGT TGTACAANGT NTTGGCTTTC AATGG        295
```

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
NANGNGCTCT GCCAGGTNCG NACACTAGTG GATCCAAAGT AATTCGGCAG AGGATGGAGC    60
GGCAGGTCCT CCCAGACCCC GAGGTGCTGG AAGTGTGGGG GACAGGCAGG ATGGGCTAAG    120
GGAACAGCTG CAGGCCCCAG TGCCTCCTGA CAGTNTCCCC AGCCTGCAAA ANATGGGTCT    180
TCTGCTGGAC AAGCTGGCCA AGGAGAACCA GGACATCCGG NTGCTGCAGG CCCAGCTGCA    240
NGCCCCAAAG GGAAGAGCTT CANAGCCTNA TGCACCAGCC CAAAGGTTAG GAGGGAGGAG    300
AATGCCCAGC TNCGGGGGGG GTTCTGNAGC A                                331
```

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GAGGCGCTGC GTCTTTCCAG CGTTTCGCAT CCGGAATACA TTGGACGCGT CGGAAGTTCT    60
TTAGCGATAT CGGCGGGCGG GCGCTACTAA TGCATGGTAC TGAAGGTGAA GTGTATGCTA    120
```

| | |
|---|-----|
| ATCCGCAGCG CTGCCCCGAG ATCAATCTCA TTGACCGTGA AAGGGATGCG GGTGCTGTAT | 180 |
| GAAAAACAGG ACACTGCTGG TAGCGAGTTA CTGCCACAAG CAAAAGATCC GGAAACCACG | 240 |
| GCGCATGGGT TGAGCCGTTG CCTTGCTGGG AGCGGAACCG ATTCCCGAAT CGCTGAAAAT | 300 |
| CCAGATGGNT TNCTNGCCTG GTGGTTACGG GTTAAGCGGG CAACTTTTCA GCGACGGNCT | 360 |
| TGGGGGCGTT TAATCCGGGC ATTNAATTC CTTTTCTCTA | 400 |

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|--|-----|
| GGCAGAGCCC CACCGTGTTT AAAAATACTACA CTGCAAGCTT TNAATCGAN AAGCGCCGCA | 60 |
| TTGAGCTCAA CATGTGGGAA CATTGAGTT CCTCTNACTA TGAATAATNT CCGGCCTCTG | 120 |
| GCTNATNCCT GAATTCTGAA TGCTGTGCTC ATTCTGCTTC GAACATTAGN CGACCAGANA | 180 |
| CACTGGGACA GTGTTNCTTC AAGANAGNGG CCAAGNGGNG ATTTCAAGAG TTCCTGNCCC | 240 |
| CATGCCCAAG GTTGTGCCTG GTTGGGCTGT TAAACTGGGA CATGNGGGAC TTGAACCTGG | 300 |
| GCCCACACTG MNGGGAGCTG TTCCAGGCAG AGGGCTTATN CCCTGTTAAC ACATGNGCCA | 360 |
| AGGGCACTGT GCCTGGGCCA GCAGGTGGGG GGGTGTGTGC CNATGTTGNG TGGTNCT | 417 |

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|---|-----|
| GGCAGAGTGG TGCTGGACAG TGACCAGCNG GTCAGTGCAG CTAGNCCACT NGCCCACGCC | 60 |
| TACTTNGGCC AGTACCACGA CCCCAGGAT GAGCCAGAGG | 100 |

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|---|-----|
| TACCTGGATA TNCNCGTNTA ACGCCGTGGG GGTCTGGNCC TAAGTGTGTA AGCNTTGCAC | 60 |
| GCCGTGGAGA AAGACGTGTG GACCGCCTGT GCCAGATGGC ATCCCCCACA AACTCGCNCT | 120 |
| ATGGGCAGAA GGAGTCCTCG GAATCAAAAC TTCGACTACA TGTTCAAAAT TCTNAATCAT | 180 |
| CGGCAACAGC AGCGTGGGCA AGACGTCCTT CCTCTTCCGC TAATGCTGAC GAACTTCGTT | 240 |
| TCAGGNCTGN TCTTCGTNAG CACCGTGGGG CATCGACTTT CAAAGGTTCA AGACCATCTA | 300 |
| TTCGCAACGT CCAAGAGGNT TCAAGTTGGC AGNTTTGGGG ACACAGCAAG GGCAAGAGCC | 360 |
| GGTTNCCGGN NCCTT | 375 |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| GGCANANCGG CAGGAGGCTC NATACTACAA GCTGGGGGAG ACCACCCTGG AGGAGTGGAA | 60 |
| GAGGCGTATC CAGGAGAATC CAGGGCCCTG GGGAGAGCTG GCCACGGACA ACATCATNT | 120 |
| AACCGTGCCG ACTGCAAATT TTCGTACTCT GGAGAACCTT GAGCCCGNTG CTCCGCCTCT | 180 |
| GGGAATGAGG TGATGCAGGC TGTGGCGCGA CTGGNAAGCT GAGCCCTTCC CTTTGCGCCT | 240 |
| GCTTCAAAGG ATNTTGCCG ACGTGCAGAT CTTCACTGGG NTGGGATGCA TNCAGGTAC | 300 |
| CCCATCCATG TGCCATCTGG AGTTCAATGN CAGGAGCTTC ATTCAACGGG GAAGCTCCTT | 360 |
| CAGGAACCAA GGGGCTGTTG GGGGCCCCGT TCCATGAGCT GGGGCCGCAA CCAGCAGTGG | 420 |
| CAGGAGTTGG GGAGTTCCCA GGGACAATAC CAACGGGGGC NACTTGGAAN CTGTTGGTGG | 480 |
| TGTGTTATGT GCATGANAAC GTCTTTGGGG NNTTCTT | 517 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| AGCTGGNTNN CGCGCGCCTG AATTCGCCAG GAAGCAGGTA TGGNGTTCCA GCAGTTTTAC | 60 |
| CTCTTCCCGC ATCTNACAGC GCTGGAAAAC GTCATGTTTG GCCCGCTACG GTGCGTGGNG | 120 |
| CGAACAAAGA AGAGGCGGAA AACTGGCAC GTNAGCTGCT GGCGAAAGTN GGTCTGGCAG | 180 |
| AACGTGGCAC ATCACTACCC TTCCGAACCT TCTGGTGGTG AACNGTCAGC GTGTGGCGAT | 240 |
| TNNCCGCGCN GTGGCGGTGG AAGCTGNNGG | 270 |

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| GGCACAGTTT CATTCCTGGT TTTAAGGAGT TCACGGGCCA TGTGGATCGC ATCTTTGAGG | 60 |
| ATGTCAAAGA GCTCACTGGA GGCAAAGTGG CAGCCTACAT CCCTCAGCTG GCCAAGTCAA | 120 |
| ACCCAGACCT NTGGGGTGTG TCCCTGTGCA CTGTGGATGG TCAACGGGCA CTGTGTGGGG | 180 |
| CCACACAGGG ATNCCCTTCT GCCTGGCAGT GCCTGGTNTG NNAGCCCCTN ACCTATGNCC | 240 |
| ATCTCCATGA AGGCACCCTN AGGCACTGGA CTTACGTGTC ACAANGTTTT NTGGGNCAAA | 300 |
| AGAGCCCAAG TGGGCCTGGC GCTTACGAAC A | 331 |

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|--|-----|
| TTGNAGGTCG AACTAGTGG ATCCAAAGAA TNTGGCNGAG CNAGGGGTGA AGTCCTTNAG | 60 |
| GCCCTGAATG GTCAGCTTGT CCACAGGGTG AATCTTGTTG TAGTCAGCCG GGTCANNNAG | 120 |
| GTNAGAGGCA GCAGGACCTG TTTNNTTCAGG TTGGTCTCTG GAAAGCAGGC GGCATTCCGT | 180 |
| CATCGGGGGC CTNACTAGCC TGGAGAGCTT CATTTTCTAA ACCCATCTGG GGCTCTGGGA | 240 |
| AGATGCCCCCT TAATCCTGNT GCCTGGGAAC AATNCCCGGG TCAGTGAAC TATGGGNGCC | 300 |
| CTGGGTGCTG CTTCCCTTTC AACTAGGGGT NCCCCTAGCA AGTNTGACGC TGGGTGCTGG | 360 |
| AGGTTTGCAA GGNCTTTCCT NGTTGGCACA TTGCATGGAT N | 401 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| ACTCACAAGC TTGNNTTTGA NCACCAGCCA GGTGACATCT TTGGCTGTNT GGCCGACATC | 60 |
| GGNTGGTTTA CAGGACACAG CTACGTGGTG TATGGGCCTC TCTNCAATGG TGCCACCAGC | 120 |
| GTCCTTTTTG AGNAGCACCC CAGTTTATCC CAATGNCTGG TCGGTACTGG GAAGACANTA | 180 |
| GAGAGGTTGA AGATCAATCA GTTCTATGGC GCCCCAACGG GCTGTGCCGG CTGTTGCTGA | 240 |
| AATACGGTGN ATGGCCTGGG GTGGAAGAAA GTGATGGATC GGTCCNTGCC CTGNGGGACC | 300 |
| CTGGGGGTCA NTNGGG | 316 |

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

| | |
|---|-----|
| GATCATTATG CTAAGNTNGT NTGNGNCTCC AGGTCGACAC TAGTGGATCC AAAGAATTCC | 60 |
| GCACGAGCAG TTGGTGAGG ACAGAAGGTC CGGTGGTTAA AGAAGGAAAT GGAGAAATAC | 120 |
| GCTGACCGGG AGGATATGAT CATCATGTTT GTGGATAGCT ACGACGTGAT TCTGGCCGGC | 180 |
| AGCCCCACAG AGCTGCTGAA GAAGTTCGTC CAGAGTGGCA GCCGNTGCN CTTCTNTGCA | 240 |
| GAGAGCTTCT GCTGGCCCGA GTGGGGGCTG GCGGACAGTA CCCTGAGGTG GGCACGGGGA | 300 |
| AGCGCTTCCT CAATTCTGGT GGATTCATCG GTTTTGCCAC CACCATCCAC CAAATCGTGC | 360 |
| GCCANTGGAA GTACAAGGAT GATNGACGAC GACCAGCTGT TCTACACACG GNTCTACCTG | 420 |
| GNCCCAGGAC TGAGGGAGAA ACTNAGCCTT AAATCTGGAT CATAAATTNT GGGATCTTTC | 480 |
| AGAACCTCAA CGGGGCTTTT AGATGNAATG GGTTTTAAAA GTTTTAATNG GGAACCGGGT | 540 |
| GCGTATNCGG AANGNGGGCT AAGGACAAGG T | 571 |

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

| | |
|---|-----|
| GGGAACATNG AGACTTGGGC CACCCAATTN GAGAGGATCT TGGACAGAAA CCCCTTCATA | 60 |
| AAACCTNAGC CTCAAAGGGC TTCNCTGACT GTGANAAAAA AAAAAAAAAA ANTCC | 115 |

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | |
|--|-----|
| GGTCNTGATT AACCTCATGA AGGGGCCAAA GNTCGGGGNC NGCGCCTGCG GGTCGACACT | 60 |
| AGTGGATCCA AAGAATTCGG CAGAGCAGCT TTTTNGATGCC TTTNAAGATG ATAGGTATCT | 120 |
| GTNCATGGTA ATGGAGTACA TGCCTGGTGG AGACCTTGTA AACCTTATGA GTAATTATGN | 180 |
| ATGTGCCTGA AAAATGGGCC AAATTTTACA CTGNTGAAGT TGTCTTGCT CCTGGATGCA | 240 |
| ATACACTCCA TGGGNTTAAA TTACACAGNG GTGTGNAAGC CTGACAACAT GCTCTTGGGA | 300 |
| TNAANCATGG GACATCTAAA ATTTAGGCAG ATTTTGGGCA CGTGTATGAG GGTGGATGAA | 360 |
| ACAGGGCATG GTTACATTGT GNATACGGCA GTTTGGGAAC ACCGGATTTA TATNNTCACC | 420 |
| TGAGGGTTNC TGAAAATCCA CAAGGGGGGT TGATGGGTTT TCTTATGGGG CGGN | 474 |

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | |
|---|-----|
| TACAGCGATC TNCGAGTGGN ACATGNTGGG TCCAAAGANT CGGCANAGGG ACAATCTCTA | 60 |
| ACTAGTGTCA TGGCTCCATC TGGGGCTGGG CTGGGGTCAG GACTCCGTCT GAGGCTGTNT | 120 |
| TTTGACTGTN AGGTAGCCCA GGCTGGGCTG ACTCCTGATT GTGCAGTTTT GCATCTTCTC | 180 |
| CCTGCTGAGA GTCCACCAAA GTNTTCTATG GTAGACCCAG TNTCTGGAAG TNATCATCAN | 240 |

| | |
|---|-----|
| GCAGCAGCAA CAGGGNGTGT TGTAGGTCAG CAATGGGGAG ATAGGCAATG CAGAGGTGTC | 300 |
| TNTTCCAGNN CCCTGGAGAG CCATTTTGTC GGNANTTGGA GCTGGTNAAT NAGAGGNTGC | 360 |
| TTGAGCAGTG TCGGAATAAT CCCGTCAGGA CAGCTGCTAG TTCAAGCTGG TTTGGTGAAT | 420 |
| GTATGGANTA CTGAGAGGTG AGTGCAAAAG GTTGGCTGCT TCTAAGTTTG GTGAGTCATT | 480 |
| GTTTTNTTGC TNATTGCATG TTGGGNAAGA TACCACCTCA NTGCTTACGT TATCAGCN | 538 |

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | |
|---|-----|
| GGCAGAGGTC ATGATGGAGG TCGAGTCCTC CTACTCGGAC TTCATCTCCT GTAACCGGAC | 60 |
| AGGCCGTCGG AATGCGGTCC CTGANATCCA GGGAGACTCA AAGGCTGTAA GCGTAAGGNA | 120 |
| AGCTGGCTGG AGACATGGGC GAGCTGGCAC TCGAGGGGGC AGAAGGACAG GTGGAGGGGA | 180 |
| AGCGCCCCAA ACAAGGAAAG CTGGGCAACC AGCCCCAGAG CAGCGATGGG NACCACCTTC | 240 |
| GTTTTTGAAA TCTGAACCTT GTTCCAAGAA GGCTTGACG AGAGACCCTT NTGTTCCCCT | 300 |
| TCCCANAGGG GGGGAACCTT GGGCAATTGG GCCCANAAAN GCTTTTTTTTT TTN | 353 |

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| GGCAGAGCCC AGCAGGGAAT AAAATTTTTN NAAACCCTAG TGCCATATGN TGAAGGGGCC | 60 |
| CCTGCTTTTA AGGGAAGGGC TCCTGCCTTT NCTNACGCTT CTNTCCACCC CAGGTATGAT | 120 |
| CTCATGTACC AGTGCCTGGA GTGCTGACCC CAAGCAGCGC CCGANCTTTA CTTGTCTGCG | 180 |
| AAATGGGAAC TGGGAGAACA TCTTGGGCCA GCTGTCTGTG CTNATCTGCC AGNCAGGACC | 240 |
| CCTTATGACA TCAACATCGA GAGAGCTGAG GAGCCCACTG CGGGGAGGCA GCCTGGAGCT | 300 |
| ANCTGGCAGG GGNTCAGCCC TACATGGGGG TTGGGGATGG CATTGGCNTN GGGGCATGGG | 360 |
| GTGGCACTNC CCAT | 374 |

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

| | |
|---|-----|
| GGCACGAGCA ACTGCTGGTT CTCCTAGAGG CCTCTCCTCA AACTCGCAGN CTGCCTGATC | 60 |
| ATTGCTACAG AATGAACTCT AGCCCAGCTG GGAACCCCAA GTCCACAGCC CTCCAGGGCC | 120 |
| AATGGGAAAC ATCAACCTGG GGCCTTCAGC CAACCCAAAT GCCCAGCCCA CGGACTTCGA | 180 |
| CTTCCTCAAA GTCATCGGCA AAGGGAATA CGGGGAAGGT CCTACTGGCC AAGCGCAAGT | 240 |
| TTGGATGGGG CGTTCTATGC AGTGAAAGGT ACTACAGAAA AAGTCCATCT TTAAAGAAGN | 300 |
| AAGAGAGCCA CATTATGGG CAGAGCGCCA TMTGGCTTTC TGAAAGAACG TCGGGGCACC | 360 |
| CCTTNCTTGT GGGGNGCTGN GCTNATTCCT TTCCAGAACA AC | 402 |

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|---|-----|
| CAGACGCTGT CCAGCTGGNA GTAACAGTGG GGCCTGGTGA ACGTCGGATC GGCCCAGGGG | 60 |
| AGCCCTTGGN AACTCCTGTG CAATGTGTCA GGGGCACTTC CCCCAGCAGG CCGTCATGCT | 120 |
| GCATACTCTG TAGGTTGGGA AGATGGCACC TGCGAGGGCA CCTGGGCCCT GGCCGCCTGG | 180 |
| TAAGCCCAGC TGGACACAAA GGGTGTGGGN CAGCCTGGGC CCTGGCTATG AAGGGCCGAC | 240 |
| ACATTGCCAT GGNGCAAGGT GGCATCCAGA ACATACCGGN TTAGNGTTAG AGGCTGCCAG | 300 |
| GNCTGGGTGA TGCGGGCAAC TNACCGTTGT CTTG | 334 |

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | |
|---|-----|
| GGCAGAGTTT GTTTTGAAGG AGACCGGNTG GCATTCTTCG GGACAGAGAT ATCTTTCAGA | 60 |
| TCCAATGGAG AAGCACTCCA GCAGCTATAA TCAAGGTGGT TACAACCANG ACAGCTATGG | 120 |
| ATCAAGCAGT GGGTACAGTC AGCAGGCGAG TTTGGGGCCA NNCTCAGATG AGTTTGGCCA | 180 |
| ACAGCCTACT GGCCCCACTT CCTTTACCAA TCAGATTTAA CAGAGTAGCA TTTGCATTCT | 240 |
| TCTGCAGTGC GCCTCACCAT CTTCCATTTT AGTGGGCAGA AGAATTTTTT AAGGGTTTCA | 300 |
| ATCAATTATT ANTGCAGAGA GTATTGANTG TNAATGCAGA GCTCTCTAGT NTTNCATTAA | 360 |
| GGCAGCAAT | 369 |

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | |
|---|-----|
| GGCAGAGCCA AGGCGNTGGC TNGAGGGAGT CAGCGGCCTC GGGCTTGGGG GCCTGTTGGA | 60 |
| GGAGGAAGGA GCCGGGGCAG GTGCTGCCAA GAAGGAGGTG CTGGAGCCTG GCAGGGAAC | 120 |
| CTCCACCCTC NTGGAGGCCG CAGCCTGNAT GGTGAAGGCC AGCCAGACAG AAGACGTGGA | 180 |
| TGGNACCTGG GGCTCTTCAG CAGCCAGGTG GAGCGAATCA GGGGGCCAGC ACAGACTTNT | 240 |
| CGGCGACCCT CCAAGGCCC TCCTGCCAGA TCCCCAGTT CAGGACTTTT TCCTTCATTG | 300 |
| AGGACACCGA GATCCTCGAA CANTNCCCAT GTTATCGGGA GCCGTGCCAA TTTGGGGGCG | 360 |
| CAATTTTGG GGGCAACGGG GCCCCGGTCC ATTCGGNCTG GGGGGTTACT TTGGGNCTTT | 420 |
| NGGGGNAGC ANAATTCGGA TG | 442 |

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|-----|
| CGGCTTTATT TGTAGGCGAG ATCTTTGTNC GCNTCATATG GTCCACACGG GAGATCAGCC | 60 |
| CTATTATTGT NAGAGTGTGG GAGTGCTNCG ATAGGCCNCG TGTCTTTGAN ACATCAGAGA | 120 |

GNCCCCGTGG AGA

133

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

| | |
|---|-----|
| GGCACGAGAA CACCTATGGN TTTCCAATGG ATCTAACTGG ACTAATTGNT GAAGAGAAGG | 60 |
| GCCTGGTGGT AGACATGGTT GGCTTTAAAG AGGAGAGGAA ACTGGCCCAG CTGAAATCAC | 120 |
| AGGGGCAAGG GAAGCTGGTG GGAAGACCT CATTATGCTG GACATTTACG CTNATCGAAG | 180 |
| AGCTCCGGGG CACGGNGTCT GGAGGTCACA GATGATTCCC CAAAGTTACA ATTNACCATT | 240 |
| TGGNGCTCCA GTGGTAGCTA ATGTATTTNA AGANACACAG TGGGCTACGG GTGAATGGTT | 300 |
| TCTGCGNCAG GGGAGNAAGA TGTTCCTGG GGAGAGGTGT TCCCACAGGT CCAGGAGTTG | 360 |
| TTGGGAGTTG GTTGCNTGGG ACAAGANCCN GTTTTT | 396 |

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|---|-----|
| TGGCACGAGT GCGACGCGGT GGTCACCATG TGGATCTTGG GTCTGAGGAA AGAATTTNAG | 60 |
| GAAGCCAGGA AGTGGGTGTC GAAGAAGTTA CACTTTGAAA AGGACGTGGA CGTCAACCTG | 120 |
| TTTNAGAAGC ACGATCCGCA TCCTGGGGGG GCTCCTGANT GCCTACCACC TGTTTGGGGA | 180 |
| CAGCCTCTTC CTGAGGAAAG CTGAGGATTT TGGAAATCGG CTAATGCCTG CTTTTCAGAA | 240 |
| CACCATCCAA GATTCCTTAA CTTCGGGATG TGAAACATCG GTNACTGGGA GTTGCCCACC | 300 |
| CGTNACGGT GGAACCTCC GACAGCACTN TGGGCCGAGG TGACCAGCAT TTCAGCTGGN | 360 |
| AGTTTCCCGG GAGCTCTNCC CGTTTTTCAC AGGGGGATNA AGNAAGTTTT TCAAGGGGG | 419 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|---|-----|
| NNANACTGAG TGGATCCAAA NAATTCGGCA GAGCAGTGA AGATCAAAGC AATCGGGCAT | 60 |
| GTAATAGAGG ANGGCGGTGT CAAAATAAAG CTAACCGTAA TCANCACCCC AGGCTTTGGA | 120 |
| GACCAAATCA ACAATGAAAA CTGCTGGGAA GCCCATTAAG AAAGTACATC AATGAAGNCA | 180 |
| GTACGNGAAA GTTCCTGAAA GGAGGNGGTT CAACATCGCC AGGTAGGAAA CGCATCCCTG | 240 |
| AAAACTNCGT GTCCACTGNT GCCTTTGACT TGCATCTCTC CCACAGGNCA CTCCTTGCGA | 300 |
| ACCTCTGGGA TCTTGAAGTT NCATGAAACA CCTTCGGCAA GGTNTGANA CCTCATCCCT | 360 |
| GTTCAATTGCT TANGGCNTGG ACACCCTGGA CCCTGGTGGG TGAANGTCT GATTTTCAAG | 420 |
| CCAAGGGTTT CGCCAAGG | 438 |

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|--|-----|
| NTNTGACTNC AGGTCGACAC TAGTGGATCC ANAGAATTTCG GCACGAGAGC CGGCTCGGGG | 60 |
| AGAAGCAGCT CANCTGGGAC ATAAGGTGAC ACAACTGGCA AGCTATTTTA AGCCCTTNAN | 120 |
| CTTAGCCGCA GTTGGTGTGG CCTCCAAGAT TCTTGATCAT CAGCAGCAGA TGACGGTGCT | 180 |
| GGACCAGACC AAGACTCTCG CAGAGTCTGC CTTGCAGATG TTGTATGCAG CCAAAGAAGG | 240 |
| TGGCGGAAAC CCCAAGGCAC AACACACCCA TGACGCCATC ACAGAGGCCG CCCAGTTGAT | 300 |
| GAAGGAAGCC GTGGATGACA TCATGGTGAC GCTGAACGAA GCTGCCAGTG AAGTGGGGCT | 360 |
| GGTTGGGGGC ATNGTGGACG CCATTNCAGA AGCCATGAGC AAGCTNGATT GAAGGCACTC | 420 |
| CTCCAGAACC AAAGGGNAAC ATTTTTTCGA CTATCAGACG ANTGTGGTTT AAATACTCCA | 480 |
| AAGCCATTTG CGGTTGANCA GCNTNAGGGA AATGATGACT AAGTCGGTTT ACTAACCCGG | 540 |
| AGGGNGTTTG GGAG | 554 |

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|--|-----|
| GGCACGAGGG CCCNCGGCAC TAAGTCATCT TGGAGTTATT AACCACTGGG CCCTAGGCAC | 60 |
| TAAGTNATTT GTGGAATGTA AAGGTTCCCTA GCGAGCATCT CACCCCAGGC TCCAGGGCCT | 120 |
| CCTGAGTGCA CTGAATTTAT TTTGCACAAT ATCGTGCACA TGAGCTCATC TGNGAAGAGC | 180 |
| ATCCAGTCTT CATCAGTCTA CCAAACCTCA GGAACCACCG TTTCCCCCTC AGTTCCTTGC | 240 |
| AATCTGTTCA TTTAAGGATG AGGAACCAAA GTCCAGGAAA GAGGAAGGGG TTGCCCAGGG | 300 |
| TACTGGATAG TMTTCTGCAG AGTGGGACAA GGGCTCTCTG GGTNTTCTTG ACTNCACCAN | 360 |
| ATCTNGTTCA CCCCTGNACC TGGACCTCCT TGAACCTCA GTTCTCCCT GAGGGGACCC | 420 |
| TGCACACCCA CAACTTCANA ACAACATTTT CTTANAANCT AGNGG | 465 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|---|-----|
| ATNANTTTAG AGTCAAGTAT GAAACANACC TGGCCATGCC CCANTTTGTG GAGAACGANA | 60 |
| TCCATGGGCC TCCGCAAGTC CATTGAATGA CACCAATATC ACACGACTGC GAGCTGGAGA | 120 |
| CAGAGAATCG AGGCTCTCAA GGAGGAGCTG CTCTTNATGA AAGAAGAACC ACGAGGAGGT | 180 |
| AAGTTAAAAG GCCTTACAAG CCCAGATTGC NAGCTCCTGG GTTGAACCGT GGAGGTTAGA | 240 |
| TGCCCCAAA TTTTNAGGGA CCTCGCCAAG NTCATGGNCA GACNTCCGGG CCCCAATATG | 300 |
| AACGAGCTGG CTCNGTAGGA | 320 |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|---|----|
| GGCACGAGAT GATCCTTNAG TNCCTNAAAT TGATCGGATC TACAAAACAG ATAGAGAAAA | 60 |
|---|----|

TTACATCGCA TACTTCTGAA GTCCATTCCN GAGCTATTCT GTTGTGACTT TTNTCGNGAC 120
CGATTCCGGCA GGAAGACANC TGATNCCTGT CCGG 154

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGCACGAGAA GCCTGAGACT AGGGAGGAGA GGGTTGCTCC AAAGTGGTTC CTACACAACC 60
AGGAGGCAGC CCTAGGAACT TCAGATCAAA GCGGATGGAC TTTGGATTAC AGGAGAAATA 120
TTTAGTGGTA TCTGGAAAAG AAATACATTA AAAAGAATAA AATAACTTTG AAATTAAAAA 180
ATCCCAACAA TCTTTTGTTC CACATTTTAG CTGCGGATCA GCATTTAGGG TAAAGGTGTA 240
ACTTCCTCCT GAAGGTACAT CCTTGGCTAG AAATCTGAAA GGCCAGGTCA TTNCTTTGGT 300
TCTCTGGAAC CGGATTTAGG CATAGTTTCC ATTCAAGTTT TTCTNGGTNC TTTGAAGTNA 360
ACCTTTTCCA NTATTATTCC ANTGGGTTTA GGGCTTAGTT ATTATGAATG TNCCCTCAGA 420
TGGGCAACTC CGGTTTTTCAN CCNTCAGGTC TAGCCCTGGG GAAGGAAGNA GGAGGGCCAG 480
GTTTCNGGTGG GTTCAAA 497

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GGCACGAGGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AANAAAAAAAA AANAANANAN 80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|---|-----|
| GGCAGAGCC ATGCCCCGCT ACGCCGACGC GTCGNNACGC AACACGCTTA GCGGCTTCTC | 60 |
| CTCAGNCCAC ATGGGCAGTN ACGTTCCAG CCCCANAGCC AGGGTCACCA CGCTGTNCAA | 120 |
| CCCCATNGTG GNCTCGGTCT CCAGACGGAC CGCACCCCGA GGTAAGTGGG GCAGTGTCCG | 180 |
| GACCAGTGTG ANGNAGCAGT GGTCTTGGCA CCGATGTGGG CTCCCGGNTA GCTGGCAGAG | 240 |
| AACGCGCTNG NCCCACCCCA GG | 262 |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | |
|---|-----|
| AGAGCGCGCC TAACCGTAAA GGTCGTTACC TGTATATGGA ACCCAAGCCC TACCTGGAAG | 60 |
| TCTNCCTGCA CTNGGAGCCC CGGNCCAATN TGAGNAACTG ATCGG | 105 |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

| | |
|---|-----|
| CACGNNNCGG CACGNCACCG TTCACCTTCC AGCCAGAAGG GGTCACGTGG CGGGAGCAGA | 60 |
| AGGAGCAGCG GGCCGCCCTC ATGGTGGGCA TGNTCGTTGG CGTGTTCGNG CTCNGCTGGT | 120 |
| ATCCCCTTCT TTCTCACCGA GTCATCAGT CCCCTGCGGC TCCTGNGACA TCCCCGGCCA | 180 |
| NCTGGAAAAG CANCT | 195 |

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

| | |
|--|-----|
| GGCACGAGCA CACACGNACC ANCATCTACA GGACGTGGAC ATTNAGCCCT ACGTCAGCAA | 60 |
| GATGCTAGGC ACTGGCAAGC TGGGTTTNTC CTTCGTACGC ATCACGGNCC TGCTTGTTNGC | 120 |
| GGGCAGCCGG CTCTGGGTGG GCACCGGCAA CGAAGTGTTG CATCTCCATC CCCCTGAACA | 180 |
| GAGACTGTGG TCCTGACACC GAGGCCAGCT CCTGGGGNTC CGAGCCAATT AAGAACATCC | 240 |
| CCCACCTCTG GGGAGGGCGC CCGTCCCGGG GGCATCATCC ACGTGTATNN GCGATGACAG | 300 |
| CANTNAACAG GGGGGGNCAA CAG | 323 |

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | |
|---|-----|
| CCAACCCTGG TGTGGTACCA NCCCGATGGC ACTCGGGTGG TCAGTNAGGG ACACACTTTG | 60 |
| GAGAACTGCT GCTACCAGGG AAGAGTGCGG GGATATGCAG GTCCTGGGT GTCCATCTGN | 120 |
| CACCTGCTCT GGGCTCAAAG GCTTNGTGGT CCTGAACCCC AGAGAGAAGC TATACCCTGG | 180 |
| AGCAGGGGGC CTGGGGACCT TCNAGGGTNC TGNCCATTAA TTTNNGCGGA ATCCAAGATC | 240 |
| TCCACCTG | 248 |

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

| | |
|---|-----|
| GGCACGAGCC AATGTGGCAG CCGCCCTGGG GGTGGCAGAG CTCCTNTTCC TGCTGGGGAT | 60 |
| TCACAGGACC CACAATCAGN ACCTTCGNGT GGNTCTTCGT GCAGGGGCTG CACCTNTACC | 120 |
| GCATGCAGGT TGAGCCACGN AACGTGGACC GTGGCGCCAT GGCTTGCTAC CATGCCCTGG | 180 |
| GCTNNGGCGT CCCTGGCTTT GCTGCTGGGC CTGCTGTGG GGCCTGGACC NTNAGGGNCT | 240 |
| NT | 242 |

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

| | |
|---|-----|
| TGAAGGAGTN CTTNCTTNA ACGAAACGCT CCAACGANTA CCACCTGATT AATTGTCCCC | 60 |
| AGTACTTCCT GGACAAAATC GACGTGAATC AAGCAGGCTG ACTATTTCCC GAGCAATCAG | 120 |
| GACCTGTTTC GNTGCCGTTT CCTGATTTCT GGAATNTTTG AGANCCAAGT TCCAGGTGGA | 180 |
| NAANGTAAAC TTCCACAT | 198 |

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | |
|--|-----|
| AGGGCCAGCG GGACAGGGCA GAGNTCATCN TTTGCAGAA TNTGGGGGGT GGGGAGGCAG | 60 |
| GGCCACAGGA AATAATTGGG GTNCAGCTCC AGCCCCCTCCA ACCAGCCCCA GAAGTAACCA | 120 |
| CGGTCCAGCT CCAGCCAGCG CANGAGGTGA CCACAGTCCA GCTCCAGCCA GCACAGGAAG | 180 |
| TAACCACGGT CCAGCTCCAN CCAGCACAGG AGGTGACCAC GGTCCAGCTC CAGCCCGTGG | 240 |
| CCGGCCAGNT NTCCAATTCC ANTGGGGGAG CTNTGG | 276 |

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | |
|---|-----|
| GGCAGGACCT CGTCCAGCGA CTCAAGTCTC ANCGGATTGC AAAGTTCGCC TTAACTATG | 60 |
| CCACCAAGAA GGGGCGGGGC AAGGTCACTG CTGTCCACAA GGCCAACATC ATGTGANGGG | 120 |
| GCATGGCTTT GTNTAGGGAT GGGTTCCTGG GAAGGTAGCC CCTGTACTTT CTNGGGTAAT | 180 |
| TCTGTCCNCT TTGGGCNATG GGACAGGTAA ACTT | 214 |

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

| | |
|---|-----|
| GGCACGAGGC AGGATGAGCG CTGGCAAGAC CTCAATGTGA TCAGCAGCCT GCTCAAGTCC | 60 |
| TTNTTCCGAA AGCTGCCCCG GCCTNTTTTN ACTGATGACA AATACAACGA CTTCATNGAG | 120 |
| GCCAACCGCA TTGAGGACGC GCGGGAGCAA TAAGGACGNT GCGGAAGTTG ATCCGGGGAT | 180 |
| CTCCCAGGAC ANTACTATGA AANGNTTCAA ATTCCTTGTG GGGCCATNTT TAAGACCATG | 240 |
| GGTGGACCAC TTTNAGTTCA CCCTTT | 266 |

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | |
|---|----|
| TTCCAGAGGG CCACANAGGT GCTCNGCGCC GCCCAAGGAG ACCATNTCCC TGGCCGAGCA | 60 |
| | 60 |

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | |
|---|-----|
| GGCANNGGGA AAGTGGGGNT TAAAAAGGGA GAAGCAGACC TCTGNATGNA TCTGCCGCTT | 60 |
| GAACATGTCA GCTTTNAGCT GAAACCTCCC GACGCGCCAT CTCCTCATTC AAAGGTCTGC | 120 |
| NTCTCCCTTT TCAACCCCAA CTTTCCTTCT NNAAGGGTTT TCCTGNAGAC TGCATTCNT | 180 |
| GGGTTTTCCT | 190 |

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

```
GGCANAGACA ACCGTGAGAA GCTCAGCGAG TCGGTGCTGA TGAAGGGGGA GCGGGTNATC      60
GCNATCCTAA AGCTCATTGA GCACCCCCAC GTCCTAAAGC TGCACGACGT TTNATGAAAA      120
ACAAAAAATA TTTGTNACCT GGGTGGCTCA GGAGACCAAN ANTGTN                      166
```

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

```
GGCAGAGGTG TGGACGGCAT AAATGTAATA NNATATGCTG TGTGGATAAG GAGCACAAGT      60
NTCCTTTGAT TTGTGGGAGG AAATCCGTT GTGGCCTTCA TAGGTGTGAA AGGAACCTTG      120
TNCATCGTGG GAAACTGCCC CCAGANGCAA TGCGGTTTGN NTTTTTN                      167
```

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

```
GGCANAGCGG CANGAGCCAC AATGAAACCA AGGAGGTAGA AGATGACTGG AAATACGTGG      60
CCATGGTGTT GGACAGAGTA TTTCTTTGGG TATTTATAAT TGTNTGTNTA TTTGGNAACT      120
GCAGGGCTTA TTTCTACAGN CCCACTTACT TTGGGGGGGG GGN                          163
```

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | |
|---|-----|
| GGCACAGCAA GCNTTCACAG GTGGTGGNAT TTTTGGGGGC CCAGCTAAGC CCAGCCCGCC | 60 |
| GGCGGCAGCA CATGCAGGAG CGCAGAGCCA CCCAAACCTC TCCACTATTT AATCAGGAAG | 120 |
| GGTCCCCCTA GCCCTAAGGC TTCTTTTTCG TTCCAGGTGA AACACAGNAA GANTCAGCCT | 180 |
| TCCCAGCAGC CNGGGGGGAG ACCCACAAGC CCCTAAAAGC NTGCACTCAA GAGGGGGCCC | 240 |
| AGTNTTCACC AGGAACCTTG GAGGAAGTTC CCACAGGGAG CGCAAAGTNC GGCAGGCATC | 300 |
| GNCCTTCCGG GGCTTCTTNT TNTGGCATT | 329 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | |
|---|-----|
| AGCAAGGNAG CTCTGGCTGA NACCACCGGN NAGACGCACC TCCGGGACCA CACCCACCAA | 60 |
| GGCTCCTGCC CCTNTTGTTT CTGGGGTCCC CAGTTGTTCT TAGGGCCTNC TGTGGGGCCA | 120 |
| GGCCCCGANTG NGCTGTGNGA GCACTTCATT ACCGAAAGG | 159 |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | |
|---|-----|
| GGCACGAGGC GCTTTCTNCC NATTGTNTGG TTTTACTTTT GTNCTGGTAT GAATTCGATT | 60 |
| CCATTTTAAT NCATCCTGTT AAATNAAGTT AAATGAGGGG AAANCAAAAC CAAAAGGNAA | 120 |
| AAAAGGCACA GAGTGAGAGA CAACCCAGCA CAGGACCCCC AGGAAGGCAA GCAGTAACGC | 180 |
| TCCAGCAGCC GGGTTGTGCT GCCTGGGCCC AGGCTTCTGC NAGGTGGTTT ACAGGCGGGA | 240 |
| ACCATTGNTA CCACAACCAC CAAAGGNGGT GGGAGTNCTG TGTGTGCCCC CTTTACAGAA | 300 |
| GAGGAGACCG NGNNCTCAGA GAAGATCCAG CAGTAAGATT TAGAGTCAAG GTT | 353 |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | |
|--|-----|
| GGCACGAGGC CAGCNTTCGC CAATNNTTGG AGAGTGGGGT TNTGGGGTCA GGTGGGGGAC | 60 |
| CCCCACGGGG TCTGGANTTC TNCCGGGAGG AGATCACCAC CTTTCATCGAT GAGACACCTC | 120 |
| TCCTTTCTCC GACTGCTTCA CCAGGGCACT CTCCTCGTCG GCCCCGGCCA CTGGGNCTNT | 180 |
| AACCCCGCCG ACTCTTCCCT TGGNTCCCT GAGAAGCAGA GCCGTTGGAC TTCCTTTGGG | 240 |
| AACTGAAGCG CAGGGAGACG CTGCTCCCTG ACGGGGGGTG AAGAAAGTNC CAAGGGCTTG | 300 |
| GGGAGGATCC TGGGGCCCAG GCAACCCCAT NTTTTCCCA GNTGACCTGT NAAGCCCAAG | 360 |
| CAGGNTGTTG NAACTTCAGA GGAGAAAGTT GA | 392 |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | |
|---|-----|
| GGCACGAGCT GGGCTCATTC CCAGCCAGCT GCTGGAGGAG AAGCGGAAAG CATTTNTNAA | 60 |
| GAGGGACCTG GAGCTGACAC CAAACTCNGG GACCCTATGC GGCACCTTTT AGGAAAGAAA | 120 |
| AAGAAGCGAA TGAATGTATT TNACCACCAA GNAATGCAGC CTGGTGAGCA GCGCNATCTC | 180 |
| CCTGTNTCCA GAGTTTGACC GTNATGAGCT GCTCATTTAT GAGGAGGTGG CCCGCATGCC | 240 |
| CCCGTTCCGC CGGAAAACCC TGGTACTGAT TGGGGGCTCA GGGCGTGGGA ACGGCGCACT | 300 |
| GGATAGGAAC AAGCTCCTTC ATGTGGGGAT TCCAGATTCG NTATGNGCAC CAAGGGTGCC | 360 |
| CTAAAACTT CCCGNGGGNC CGNAAAAAT CAGAGCGGGG AAGGTCAGG GTTTAACAGT | 420 |
| TTTTTNTTCC CCTTGGGGGA AGATGGNAGG | 450 |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | |
|---|-----|
| GGGCAGGGAC GCCCTGGCGC CTCTNTAGGC CGACTNCTCG AGCTGCTTAC CAAGCTGGGC | 60 |
| CGCGACGACG TGCTGCTGGA GCTGGGACCC AGCATTGAGG AGGATTGCCA AAAGTATATC | 120 |
| TTGAAGCAGC AGCAGGAGGA GGCTGAGAAG CTTTACAGG TGGCCGCTGT AGACAGCAGT | 180 |
| NTCCACGGA CAGCCAGAGC TGGGCGGGGC ATCACCACAC TTGAATGACC CCCTGGGGCA | 240 |
| TATGCCTGAG CCGTTTTCGA TGCCTTCATC TGCTNATTGC CCCAGCGAAC ATCCAGTTTG | 300 |
| TGGTAGGAGA ATGATNCCGG GNAACTGGAA CAGACAACT ATCGACTGAA ATTGTGTGTG | 360 |
| NTTTNGACCG GATGTTCTTG CCTGGNA | 387 |

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | |
|---|-----|
| TCACCGATTG GGATTNNGAC ATTGGAAAAT TCCGACGTTT TCTTTGGTGG TGTGGTTCTG | 60 |
| GGAATCCACG CCAANGGGAA GCGCATAANG NACTGGTTTG ACTGC | 105 |

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | |
|--|-----|
| GGCAGGAGN AGAGCTCAGC ATCACCCTCA CGCTGCGGAT GCTGATGCAC GGGNAGGAAG | 60 |
| TGGGCAGCAT CATCGGGAAG AAGGGCGAGA NTGTAAAGCG AATCCGGGAG CAGAGCAGTG | 120 |
| CCCGGNTCAC CATCTCCAAG GGCTCCTGCC TGCAACGCAT CACCACCATC ACCGGGTCTA | 180 |
| CAGCAGCTGT TTTCCATGCA GTCTCCATGA TTGCTTTCAA ACTGGATGAG GACCTTTTGTG | 240 |
| CCTGCTCCTG CAAATGGTGG AAATNTCTCC AGGCCTCCAG TGAACCCTGN GGCCTTGTTN | 300 |
| ATCCCTGGCC AGTTCNTTTN GGCTCACTGG TTTGGG | 336 |

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | |
|---|-----|
| GGCAGAGGTA AGCCATATGT NTTCGACAGA GTGCTACCTC CCAACACGAC CCAAGAGCAG | 60 |
| GTTTACAATG CATGTCCGAN AAATTGTCAA AGATGTCCTT GAAGGTTATA ACGGGACGAT | 120 |
| TTTTGCGTAT GGGCAGACTT CATCAGGAAA AACCCACACC ATGGAGGGGA AGCTGCATGA | 180 |
| CCCCCAGCTC ATGGGGATCA TCCCACGANT TGCCCATGAT ATCTTTGACC ATATCTACTC | 240 |
| CATGGGATGA GAAACCTGGG AGTTTCACAT AAAGGTTTCC TATTTTGAGN ATCTTACTTG | 300 |
| GGACAAAATA AGGGACTTTA CTTGATTGTT TTCCAAGACC AACTTGGGCT GTTCNTGAA | 360 |
| GGTTAAAAAC AGGTNCCCTN TGTAAGGGG GTTNCATNGG GCGG | 404 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | |
|--|-----|
| GGCANAGGGT GGAGAAGCTC NACTACAAGA TGGAGCTCTN CAAGGAGATC CGNGAGGNAC | 60 |
| ACCTGGCCGC ACTGGCGAGG GGCTGCGCGA GNAAGGAGCT GCACGNGGNC GAGGTGCGCA | 120 |
| NGAACAAAGGA GCAGCGAGAA GAGATGTCGG GCTAAGGGCC CGNNACGNGG TCGCCCATGC | 180 |
| CTGACGAACG TNAACACGTT CGGGTTTTTG GTTTGTTTC GTTCACCTCT GTTTAGATGC | 240 |
| AACTTTTGTT CCTCCTCCCN CANCCNGGNC CCCAGGTTCA TG | 282 |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | |
|---|-----|
| GGCACGAGCT TTCTTGGGCG GGTCTGTAAG AGAGAGGCCA CGGTCCTGAG CTACGATGGC | 60 |
| TCCATGTACA TGAAGATCAT GCTGCCTAAC GCCATGCACA CGGAGGCAGA GGATGTNTCC | 120 |

| | |
|---|-----|
| CTGCNTTTNA TGTCCCAGCG GGCTTACGGA CTCATGAATG GCCANCACTT CCAGGGAGTC | 180 |
| TGCCGACACC CTACGCCTGG AGCTGGATGG GGGGCAGATG AAGCTTNACT GTCAACCTCG | 240 |
| ACTGCCTGCG CGTNGGCTGC GCACCNAGTN AAAGGNCCCG AAACGNTGTT TGCGGGGTAC | 300 |
| AAGTTCATTG ACATGAGTGG NCACAGGNTT GAGGGTGGTC CGGCCGTGGG CAAGAGNCTT | 360 |
| GCAATTGTTT TTGGGACAAC GTGGACTTTN GGAGGGGACA ATTNG | 405 |

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | |
|---|-----|
| GGCAGAGCAG ATAACAGCCA TGTTGTTGAC TAAGCTGAAG GAAACTCCTG AAAACAGCCT | 60 |
| CAAGAAACCA GTAACAGATT GTTTTATTTT AGTCCCCTCC TTCTTTACAG ATGCTGAGAG | 120 |
| GCGATCTGTG TTAGATGCTG CACAGATTGT TGGCCTAAAC TGTTTAAGAA CTTATGAAAT | 180 |
| GNCATGACAG CTGTTGCTTT GNAATTACGG AATTTATAAG CAGGATCTCC CAAGCCTGGA | 240 |
| TGAGAAANCN TCGGATAGTG GGTTTTTNGT TTGGTTAGGG GGCCATTCCA GCTTTTCCAA | 300 |
| GTGGTCNNGC TTTGTGCTTT TTTAACCAAG GGGGAAA | 337 |

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

| | |
|---|-----|
| CTTCNAGGTG AGCCAGCTCT ATNACTGNAN ACTGGATCGT GGTCAACTGC TCCACACCGG | 60 |
| CCAACTACTT CCACGTNCTG CGCCGGCAAA TCCTGCTGCC CTTCCGCAAG CGCGCTGAAT | 120 |
| TATNTTCACA CCTGAAATCT CTGCTGAGGC ACCCAGAGGC CAAGTCCAGC TTTGAACCAA | 180 |
| ATGGTATCCG GGACCAGNTT CCAGGGGGTG AATTCCTGAA GATGGGGCCG AAGNACGGGC | 240 |
| CCTTGANCNA GGTGAAGGGG TTAATTTTTT GAAAGGGNAA GGTTTAT | 287 |

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | |
|---|-----|
| GGCAGAGCTT CTNCAAAGCT GCCCTCTNCC ACTTCATAGT AGNCGAGTTG AATGCCAAGC | 60 |
| TTGCNCTTNA GAAATATGAG GAAATGTTTC CAGCATTNNN NGNTTCAAGA GNNTGTAAAT | 120 |
| NNTTGAAAAA ACTCCTAGAA GCTCATGGAA GAACAGNNCA GTGNAAGCTT AACTGAAGC | 180 |
| AGTGTAAGGA ATTTGAACTC AATATCTCGC TTGGNTCAGT GGCTGNCCAC CATGTTGCTT | 240 |
| CGCATCAAAA AGTCCATCCA AGGGGNTGGA GAAGGAGATG GAGACCTAAA ATGNNTGTTT | 300 |
| TTGGNCTTTG TGGGCATGCA GCTAACTCCT CTTTAGTTTT GTTCTTAGGG TCCAAGTGAT | 360 |
| CTTTTATGGG GATGCCNCTT TTAATGGGT TAATTTTGTT TGGNATATGA GGCCCAACGG | 420 |
| GCCNGTGNN A | 432 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | |
|---|-----|
| GGCACGAGTA CGAGTCCCTT CAAACCGCCA AAAAGAAGGA TGAAGNCAA ATTGCCAAGC | 60 |
| CTGTTTCGCT GCTTGAGAAA AGNCGCCCCC CAGTGGTGCC AAGGCAAACT GCAGGCTCAT | 120 |
| CTCGTAGNTC AAATAACCT GCTCCGAAAT CAGGCCGAGG AGGAGNTCAN CAAAGCCCAG | 180 |
| AAGGTGTTTG AGGAGATGAA TGTGGATCTG CAGGAGGAGC TGCCGTCCCT GTGGAACAAC | 240 |
| CGCGTAGGTT TCTATGTCAA CACGTTCCAG TGGCATCGGG NGCCTGGTGG AAAAATTNC | 300 |
| ACAAGGAGAT GAGCAAGNTC AACCAGTNCC TCAATGANTG TGCTGGTTCG GNCTGGNNGA | 360 |
| AGCAACAGGG GNGCAAACAN CTTTCACGGT NAAGGCCCCG NCCNTTGAC AACGGGNCTT | 420 |
| GAAAAGGGGT ACAAGGGGCC TTTTAACTTC CAGTTGGTTC CCTTGCNGGN ANCCCCGGGG | 480 |
| TTCCGGGTTA ACCAGGGGCC A | 501 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| GGGCACGAGT GCAGATGAAG ATGTTGATCG GAAACACTGG GGCAAGTTTC TGGCTTTTTA | 60 |
| TCAGTATGCA AAATCATTTA ACTCAGATGA CTTTGNTTAT NAAGANCTGA AGAATGGAGA | 120 |
| CTACGTCTNG ATGAGGTGGA AGGAACAGTT TCTGGTCCCA GATCACACGA TCAAAGACAT | 180 |
| CAGTGGTGCT TCTTTTGCCG GGTTCTACTA CATCTGCTTT CAGAAGTCAG CAGCCTCCAT | 240 |
| AGAGGGCTAC TACTACCATA GGAGTTCAGA ATGGTATCAG TCCCTCAATC TAACCCATGT | 300 |
| TCCTGAACAC AGTGCACCCA TCTTATGAAT TCCGGTGACA ACGGGTTNAG NNCAGCAACC | 360 |
| AAATTAAAC TNGAACTTNG GCAAAAAAG | 389 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | |
|---|-----|
| GGCAGGAGGA CACTGCCGTG GAGAACATGC CCAGCCTGAA GATGAAGGTG GTGGAGGTGC | 60 |
| TGGCTGGCCA CGGTCACCTG TATTCCCGCA TCCNAGGCCT NCTCAGCCCC CATCCCNTGC | 120 |
| TGCAGCTGAG CTACACGGNC ACCGACCGCC ACCCCCAGGC CCTGGAGGCT GNCCAGGCCG | 180 |
| AGCTGCAGCA GCACGANGTT GNCCAGGGCC AGTGGGATCC CGNAGACCCT GCCNCAGCG | 240 |
| | 240 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | |
|---|-----|
| GGNACGAGCC CGACGGAAGN ATCCAGGGCA CCCCANAGGN TACCAGCTCC TTAACCCACT | 60 |
| TNAACCTGAT CCCTGTGGGC CTCCGTNTGG TCACCATCCA NAGCGNCAAG CTGGGTNACT | 120 |
| ACATGGCCAT GANTGCTGAG GGAAGTCTCT ACAGTTNGCC GCATTNACA GCTGANTGTC | 180 |

| | |
|---|-----|
| GCTTTAAGGA GTGTGTCTTT ANGAATTACT ACGTCCTGTA CGCCTCTCCT CTCTACCGCC | 240 |
| AGCNTCGTTG TGGCCGGGCC TGGTACCTCG GCCTGGACAA GGAGGGCCAG GTCATGNAAG | 300 |
| GGAAACCGAG TTAAGAAGNC CAAGGNAGCT GCCCACTTTT TNCCCAAATT TCTGGNAGGT | 360 |
| | 360 |

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | |
|---|-----|
| AGGAGGCCGG CCTCACCTTA ATGAGGACGT TNTCGTAGCT GGTGGGATTN ATGACGTCAT | 60 |
| AGCAGATGAC CACGAGGTGG GTGTNCTGGT AGGACAGGGG CCGCAGCCGG TTNATAGTNT | 120 |
| TNTTGCCCTG AANGCACAGA GCAGCGGGGG TNAGGGGACG TCCCCTTCCC TGTTTGGA | 180 |
| CTGAACGGGT GAAGGGGAAG GGGCCAGGCA AGTAAACCCT GNCTTTAGGG CCTTCAATTT | 240 |
| CCCTCATCTT ATGACAATGG GGCAGCAAAG CCAGGTAGTG CTGGCACGGG CTNTNTGGGT | 300 |
| CGCAAATTGT TTGGGAAGGC TTNAGGNCNG | 330 |

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | |
|---|-----|
| GGCACGAGCA GCCTGTACCC TAAAATGAGT GCCCATAAGC GCTCCTTGGA TTCCTCATT | 60 |
| NAACTGCTGC ACAAGGATCA GCTGGATGAA ACTGTNAATG TGGAGCCTCT AACCAAGGCC | 120 |
| ATCAAGTACT ATNAGCATCT GTGACAGCAT CCACCTTGGC CGAACAGCCT GAGGACTGTA | 180 |
| ACTATGNCAG CTGGCTGACC ACATTAAAGT TCCACGGCAG AAGTTGGCCT TTTTGGTNT | 240 |
| TNGNN | 245 |

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | |
|--|-----|
| ACCAGGCTTT GGCTCAAAAG AATGGATGGN GTTTCCTCT TGTTGCCAG GCTGAAGAGC | 60 |
| AATGGCGCGA TCTTGGCTCA CCNCAACCTC CACCTCCAN GCCGGGGTGC TCNTNNCACT | 120 |
| GCCGGGNAAG GTGATAGCCG CTCCNAACG CTAATTAATG CGNCTACCTC ATGATGCGGG | 180 |
| AGAAGNTGGG NCGTCAATCT GCCCTGAGCA TCGTGAGGTC AGAACNTGA | 230 |

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | |
|---|-----|
| GGCAGGACG GCGCGCAGC CAACCCCGA GGAGCGGCCG GNTGGCGTCC GNGCGCCCAG | 60 |
| GAAGTTGGGG ATGTCCTACA AACCCATCGC CCCTGCTCCC AGCANCACCC CTGGNTCCAG | 120 |
| CACCCCTGGG NCCGGGCACC CCGGTCCCTN ACAGGTAAGC NTCCCGTCGC CGTCGGGCTT | 180 |
| CAGTGCCAGG NAGCCGGCGC CTCCTTTGAA AACCGCTGTT TTNAACGNAC TTTTG | 235 |

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

| | |
|---|-----|
| ATCAGGGGAA ATCAAACGGA CTGTCACAAG GATCCTGCCA GATCCTGATG ATCCAAGTAA | 60 |
| GTCCCCTGTT GGGTCACCTC TAGGGNGCGC CATTGCAGAG GNCCCCAGCG AGATGCCAGG | 120 |
| GGATGAGGTG CCTGTGGAAG AGCACTTTCC TGAGGCAGGC ACAAATTCAG GGAGCCCCCA | 180 |
| GGGGGCCAGG TAAAGGGGAC GAGAGCATGA CAAAGGCCAG TAACTCGTCA TCTCCCAGCT | 240 |
| GCANTTCTGG GGCCGGGTC CCAAAGGGGG CTTGNCCCAG GTTTNACAGA CAGGCANGAA | 300 |
| GCAACAGNGC ACAG | 314 |

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | |
|---|-----|
| GGCANAGGTC CCCGCAGAGG AACNTNCTGC CCAACCGGTT GCTGACCAAG GTGGCCGAGA | 60 |
| TGGCGCANAG CNATCCTGGT CTGCAGAAGC AAGACCTGTG CCAGGAGCAC CACGAGCCCC | 120 |
| TCAAGCTTTT NTGCCAGAAG GACCAGAGCC CCATCTGTGT GGTGTGCAGG GAGTCCNGGG | 180 |
| TGCACCGGCT GCACAGGGTG TGCCCCCGCA GGAGGCAGTG CAGGGGTACA AGTTGAAGCT | 240 |
| GGAGGAGGAC ATGGAGTACC TTCGGGGAGC AGATTCACCA GGACAGGNAA TTTGCAGGCC | 300 |
| AGGGAGGAGC AGAGNTTAGC CGAGTGGCAN GGTCAAGGTN GAAGNAGC | 348 |

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | |
|---|-----|
| ATCCAGACCG ACTTCCGCTG CTGTGGCGTC TCCAACTACA CTNACTGGTT CGAGGTGTAC | 60 |
| AACGCCACGC GGGTACCTNA CTCCTGCTGC TTGGAGTTCA GTNAGAGCTG TGGGCTGCAC | 120 |
| GCCCNCGGCA CCTGNTG | 137 |

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | |
|---|-----|
| GGCAGAGCC GCCTCCTCCC GCCGAGTCAG CAGCAGCAGT GAGCTGGACC TGCCCTCGGG | 60 |
| NGACCACTGC NAGGTTGGGN TCCTGCAGCT CGACGTGCCC CTNCTCCGCA CCCAGCTCCG | 120 |
| CGGCTCCCGC CTGCTCGATG CCATGCGCAT GTACCGCCAA GGTTACCCTG ACCACATGGT | 180 |
| GTTTTCCGAG TTCCGCCGCC GCTTTGATGT CCTGGCCCCG CACCTGACCA AGAAACACGG | 240 |

| | |
|---|-----|
| CGGTAAGTAT ATCGTGGTGG ATGAAAGGCG GGCAGTGGAG GAGCTGCTGG AGTGCTTNGG | 300 |
| ATNTGGAGAA GAGCAGCTTG NTGCATGGGC CTGAGCCGGG TNTTCTTCCG GGTGGGNACC | 360 |
| TTT | 363 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|---|-----|
| GGCAGGAGGG CTCCAGGGNA GCCCTCTTCC CGGTGGCTTT AATATGAGTN TCGAGGGAGG | 60 |
| TCAGGGTAGG GGCAGCTACC ACGCCTGAAG CCCTAGAGGT CACCAGGCGG CGCGGGTAGA | 120 |
| TTCGGGGGAA GCGCGCAGGG CTGCGCTAGG GACCCGCCGG GTCACCCTGG TACATGGNTG | 180 |
| GCTTTTNTTT ACAGTTTGTT CTAAACATCA GAAATGTTTG TCCGCTTTTA AAAACAAAAT | 240 |
| TGGCAGTAAC AGTTTATTAT TGGGTAGCTT GATGGAACCT GTGGATTACT TAATTAAAAA | 300 |
| ATTAATAATC TGNCTTTTTA ATTGGGGNTT TACCANTTTA GTGTTNTTGG GNTTTAAAA | 359 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

| | |
|---|-----|
| GGCANAGCTG CCGCCGTCGC CGCCACCCGA GCCGGAGCGN GCTGGGCCGC CAAGGCAAGA | 60 |
| TGGTGGACTA CAGCGTGTGG GACCACATTG AGGTGTCTNA TGATGAAGAC GAGACGCACC | 120 |
| CCAACATCGA CACGGCCAGT NTCTTCCGCT GGCGGCATCA GGCCCGGNTG GAACGCATGG | 180 |
| AGCAGTTCCA GAAGGNGAAG GAGGAACTGG ACAGGGGCTG CCGCGAAGTT CAAGCGCAAG | 240 |
| GTGGCCGAGT GCCAGAGGAN ACTGAAGGAG CTGGAGGTGG CCGAGGGCGG CAAGGCAGAG | 300 |
| CTTGAGCGC TCTNCCANGC CGNAGGTANA G | 331 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | |
|---|-----|
| CCAGAGGTTT GCTGGCCACT GTCAGTGTGT GTNTGAGGCT GATCGCCAAG CGCATGGTCC | 60 |
| GGANGAACTN CCTNGTGATG AACCTGGTGN CTGTAGAAAC CCTGGGGTCN ACGTCCACCA | 120 |
| TCTTCTCAGA TAAGACAGGG NANTNTNACT NAGATCCGCA TGATAGTCGC TNTCATGTGG | 180 |
| TTTGACAACC AGTTCCACGA GGCTGACACC ACTGAGGTNC CAGTCAGGGG ACCTCATTTG | 240 |
| ACAAGAGTTC TNTACACCTN GGTGGTTCCT NTNTTCA | 277 |

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | |
|---|-----|
| CTTGAAGGGG GCCAAACCCA AGCTGATGTC GGCCATCTCC AAGACCTTCT NGCCGGCCCA | 60 |
| CAANAGCTAC ATCATCGNTG GTNGTNTGGG TGGCTTCGGC CT | 102 |

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | |
|--|-----|
| CTTTGCGTCC TCAATTGCCN CGGGGCTCNC GCTGGGGCAC AAACNACTCG ACGCAGCGCA | 60 |
| GACGCCCAAG GTGAAGGTTG CCCACGGGGA TTGCCCCGGTC CATGNCCAAT GCCATGGGNG | 120 |
| TGCAACTGCT ATGTTCCATC CGNNCAANCC GCGT | 154 |

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|---|-----|
| GGCACGACCG GGCTCGAGAG CCNCCNCGCA TGCCAGTNCC CATNCGGGGC CGCCGCCAGT | 60 |
| NAACGNCGGA GAGGTGTTCC CCCACACTG GGGCTCCCAC TACTGCGAAG GAGTGACCCA | 120 |
| CGAAGGCCAC AGAGATGGCC GGGGCTTCGG TGAAGGTGGC GGTGCGGGTC CGCCCNTTCA | 180 |
| ATTCCCGGGN AAATAAGCCG TGNACTCCAA GTGNCATCAT TGCAGATGTT TGGTAAGCAC | 240 |
| CACCACCATT GTTAAACCCC AAACAGCCCA AGGGAGACGC CCAAAGGTT TCAGCTTTGG | 300 |
| NACTNATTGC TAACTGGGTT TGGGACAATC TNGNACCTNG A | 341 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | |
|---|-----|
| CTNACTGGTG CTTNCTGCCG TCGACTGGTA TGCAGTCAGC ACTGTGAGCC ACTTACCTNC | 60 |
| AGGTGTNANC TCGGGGCCAG CCCCTTGCAT GTGGACCTGG CCACCCTNNG AGAAGCTTAA | 120 |
| G | 121 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | |
|---|-----|
| GGCACGNGGT AAATGCTATG AAAATAGTTA CTACACTATT GTTTATNTGT ATTTTTATTG | 60 |
| AATTGTTTTG GGGTGGGGGG CAGCTGTATC TTTCTTAGTA ATAGAACCCC TGGTTTTAGC | 120 |
| TGGGCACATG AACTGCCNTC AATAAAGATT AAAGTACCCC AGCCTTCCTT GAGATTGTGG | 180 |
| CCATGTGACT GAACTTTAGA CAGTGAAGAT ATAAGCAGAT ATCTNCTGTG GCAGTGTTAG | 240 |
| GAAACTATTA AAGACAGTAA GGAACATTGC CCTTGCCTT CTTGTTCCT TNCTTCATTT | 300 |
| TTCTGCCTGG GAATGCAANG TGNATGGNTA ACACCCTAGC AGNCTTTT | 348 |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

| | |
|---|-----|
| CCTGGACCCA CAGTCGGCCA GTGGGTACCT GCAGCTGTCA GAGGTCTGNA AGNGCGTAAC | 60 |
| CTACACCAGC CTGTACAAGA GTGCCTACCT TCACCCCCAG CAGTTTGGAC TNGTAAGCCT | 120 |
| GGGGTNTTGG GCAGCAAGGG GTTCACCTGG GGCAAGGTCT ACTAGGTAAG TGGAAGTNGA | 180 |
| GNGTGNAGTT NCTGGTTCTT AAGGGATGAA GTAAG | 215 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | |
|---|-----|
| AAAAAAAACC CAACTTGACC TAGTTGTCAT TTATAGANCA CTCCATCCAA CAACAGNAAA | 60 |
| ACACATAATT TTTTTCAAAT GTACACGGAA CATTTGNAAG ATAGNCCACA TTCTGGTCTA | 120 |
| TAAACAAGG CTCAGTAAGT TTAGAAGGNT TCAAGTTATA CAAAATATAT TCTCTGACCA | 180 |
| CAATTGANTT AAATAAAAAA TACCNGAAAG NTATCTAGNG ATTCCCCAAA TATTT | 235 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | |
|---|-----|
| GGCACGAGNA GTTGGAGGAG AAGAATCAAG AACTGCAGCG GGCAAGGCAA AGAGAAAAAA | 60 |
| TGAACGAGNA ACATAATAAA CGTTTATCAG ACACTGTTGA CAAGCTGCTT TCAGAATCTA | 120 |
| ATGAGAGGCT TCAACTTCAT CTTAAAGAGA GAATGGCTGC TTTGGAAGAT AAGAACTCTC | 180 |
| TTTTAAGAGA AGTTGAAAGT GCAAAAAAGC AGTTAGAAGA AACACAACAC GATAAGGATC | 240 |
| AGCTTGTCCT AAACATTGAA GCACTGAGGG CTGAACTAGA CCACATGAGA CTTAAGAGGT | 300 |
| GCTTNCACTT TCATCCATGG GCCGACCCCA CTTGGGGCAG TGTTCCCGA TTTTCAGGTT | 360 |

TCCCCATGGC AGACGGGNCA CACAGACTTC NTACCAGCAN CCAGTGCAGT NGTTGCGGGN 420
GCCCACAGAA A 431

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGCACGAGCC GTGATGCCAA GCTGCCAGCC TCGCGCTCCA TCCGCAACCT CTTTGGCAGT 60
GGGAGCCTTC GGGCCTCAAA GAGTAACCGT GTGACTGGTG TNTACGAGCT CAGCCTGTGC 120
CACGTGGCTG ACGCGGGCAG CCCAGGGATG CAGCGCCGGC GCCGACGAGT CCTGNACACA 180
TNTGTGGCCT GATGTCCGGG GCGAGGAGAA CCTGGGCAGG CTNNTAGGCC CCGGAGTNGA 240
CAGTTTTTCAT T 251

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TGGGTNCCCC GGGNTGCANG AATTNGGCAG AGGTACAAGC TCGNTGCCTA TAAAGCTGAT 60
GATCCAACAA TGGGGGAGGG CCCAGACAAG GCACGTTCCC AGCTCCTGGA TCCTGGATCG 120
AGGCTTTGAC CCCAGCTCCC CTGTGCTCCA TGNAATTGAC TTTTCAGGCT ATGAAGTTAT 180
GAATCTGGCT GCCTATCGAA AATGNTGTAT ACAAGTATGA GACCANNGGC ATCGGGGGAG 240
GNACGTGTNA AGGGGGTTCT C 261

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

| | |
|---|-----|
| GGCAGAGGNA CAAGCTCGAT GCCTATAAAG CTGATGATCC AACAATGGGG GAGGGCCCAG | 60 |
| ACAAGGCACG CTCCCAGCTC CTGATCCTGG ATCGAGGCTT TNACCCCAGC TCCCCTGTGC | 120 |
| TCCATGNAAT TGACTTTTCA GGCTATGAGT TATGATCTGC TGCCTATCGA AAATAATGTA | 180 |
| TACAAGTATG AGAACCAGCG GCATCGGGGA GGCACGGGTG AAGGAGGTGC TCCTGGAACG | 240 |
| AGGACGACGA CCTGTGGGAT AGCACTGCGC CACAAGCACA TCGCNGAGGT GTTCCCAGGA | 300 |
| AGTTCAACCG GTTTTTGNAA AGATTTTTTC TTTTAGCAAG NGGATTGAAT TACTGGAGGG | 360 |
| AAGGCCACC NTGCGGGACC TNTNCCCAAT TG | 392 |

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

| | |
|--|-----|
| GGCAGAGCCC GACGGAAGCA TCCAGGGCAC CCCAGAGGAT ACCAGCTCCT TNACCCACTT | 60 |
| NAACCTGATC CCTGTGGNCC TCCNTTTGGT CACCATCCAG AGCGCCAAGC TGGGTCACTA | 120 |
| CATGGCCATG AAATGCTGAG GGA CTGCTCT ACAGTTCGCC GCATTTNACA GCTGANTGTC | 180 |
| GCTTTAAGGA GTGTGTCTTT GAAGAATTAC TACGTCCTGT ACGCCTCTGC TCTCTACCGC | 240 |
| CAGGTTTCGTT NTGGCCGGGN CTGGTACCTC GGCCTGGACA AGGAGGGCCA GGTCATGAAG | 300 |
| GGAAACCGAG TTAAAGAAGA CCAAGGCAGN TGNCCAATTT TTNCCAAGA TNCTGGGAGG | 360 |
| TTGGNCCATG TAACCAGGGG | 380 |

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

| | |
|---|-----|
| GTACTGCTTC CAGTTCCTGC CCTTTGGCAA AGGCCTCATC AAGAAGTGCC GGACCAGCCC | 60 |
| TAATGCCTTT NTGCAGATCG CGCTGCAGCT GGCTCACTTC CGGGAACAGG GGTAAGTTCT | 120 |
| GCCTGACCTA TGAAGGCCTC AATGAACCAG NAATGTTCCG GGAAGGGAAC GGACTGAGAA | 180 |
| CTGTGNCGTT CCTGTNACCA GCGAAGTTCC ACAGCCTTTN TGGCAGGCCA TGNATGGGAG | 240 |

| | |
|---|-----|
| GGGTCCCACA CAAAAGCCAG ACCTGCAAGA ATCTTTTTTC AGAAAGGCTT GCTNAGNAAG | 300 |
| CACCCAGGAA TATGTNACCN GCCTGGGNCC ATGAAACCGG GGGCAGGGG ATTCGNAAAN | 360 |
| GGCANCTTTT TTTTGGCCTT TTAATTTGGG TTNTTCCAAG TTAACCTAGG GGGTTCANTT | 420 |
| TTTCCTTTTT CCTTGNTTGA GGGTGGTTTT NGGGGAANCC TTGGGGGNTT TTTTCCAACC | 480 |
| AGGCCAGT | 488 |

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

| | |
|--|-----|
| GGCAGAGGNC AGGACGAGCT CAGCTTTAAG GCCGGAGACG AACTCACCAA GCTGGGNGAG | 60 |
| GAGGATGAGC AGGGCTGGTG CCGTGGGCGG CTGGGACAGC GGGCAGCTGG CCCTCTNACC | 120 |
| CTGCCNAACT AACGTGGAAG GCTATCTAGA AGGCCNCCTN CCCTGCCATA CTGCCCCGTTA | 180 |
| ACTCCTCCCC ACTGCCGCCC CTCCCCCTNC CCACTNCTGC GTNCTCCTTC CCCTCGCCAT | 240 |
| AGAAGTTTCC AGACATATTT TCCCGAATTC AAGCTTTTTT ATTTTTTTTAA AAAGTTCAAA | 300 |
| ACCAGGAACA AAAACAAAAG TNATGCCANG AGGACAGAGN CATTTNGCAG GGGCCCANCT | 360 |
| GGNAGGGTTT GGGGTGCTTG GGGGTTTTTG GGAGTGGGGC CCCCAGGGTT AGGTTAACCA | 420 |
| GTTNTTNAGG TANTTTAGGC CCCAAGCATT CAACAAACAT CTGGGTTCTT TTTCTGGGGT | 480 |
| TTCCACCCAA AN | 492 |

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

| | |
|---|----|
| TTCCATAATG GCTGTNCTGA TTTACATTCT CATCAACAAT GNACAAGTGC CCTTTNCTCT | 60 |
| GCATTCTCCC TAGCATTTTT TTTTTTTTNT CTTTTNG | 97 |

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

| | |
|---|-----|
| GGCAGAGGG ACCCGCCCGC NATGGGGGAC GAGGACGACG ATGAGAGCTN CGCCGTGGAG | 60 |
| CTGCGGATCA CAGAAGCCAA CCTGNACCGG GCACGAGGAG AAGGTGAGCN TGGAGAACTT | 120 |
| CGAGCTGCTC AAGGTGCTGG GCAGGGAAGN CTACGGCAAG GTNTTCCTGG TGCGGAAAGG | 180 |
| CGGGTCGGGC ACNACGCGGG GTAAGCTNTA CGCCATGAAG GTGCTGCGCA AGGTGGNCGC | 240 |
| TGGTTGNCAG GGCCCAAAGT ACGCAAGNGT CAC | 273 |

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

| | |
|--|-----|
| GGCAGAGGCG CCCCCAGCC CTCCTGACG CTCAGCCTCG GGCCTCTCT CCAACTCTCC | 60 |
| CGGCCCACCG TGGCATCGGG AGGCCATGCT CAGGTCTGAA GCAGGTTTGG GGCCTGCTGA | 120 |
| CAGCAATAGC CCGCCTTTGG GAAACCCCTT GCTGTGAAAC TCTCTGCACT GCAGTGAACC | 180 |
| TTCAGTCACG AACCTGCCTC TGCCCCTTCG GGGGACGCCC ACACAAAAGG GNAAGTGCTT | 240 |
| GGCCGTGCTG GTTCTGCCC TGCTGGTGGG CCTGNCCGGG GNTTGGGCGG CCGGTGAAGC | 300 |
| GGGATTGCAA TGGGGATGAG GGTGNACAGG GGCCTGGTTC CTGTTCTCTGA GNGCCNCAGT | 360 |
| NTTGTTCCTT CCTGNCCAGT TCCTGTTCCA AATGCATG | 398 |

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

| | |
|--|-----|
| GGGCACGAGA AAACCTTTTAC AATNAGCATG AAGAGATAAC CAACCTCACT CCACAGCAGT | 60 |
| TAATAGATCT CCGGCATAAG CNCAATCTTC GGGTCTCTGG TGCTGCACCT CCTAGACCAG | 120 |

GAAGTAGCTT TNCTCATTTT GGGTTTGACG AACAACTTNT GCACCAGATT CGGANATCTG 180
GATACACACA GCCCACTCCA ATACAGTGCC AGGGTGTGCC TGTGGCATT AAGTGGTAGNG 240
ACATGATTGG TATTNCCAAA NCAGGTAGTG GGNAAACTNC AGCCTTCATT TGGCCCATGT 300
T 301

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

ATNGTTTGGG AAGCGCATAT TGCTTCNTC TTCCCCGAAT TCTGGCAACT NTTCTCCTG 60
CNATNATGGG CCCTTGGGCA TCATGAACTT NATTAATCCT CACTGGCTGG AATTCAAAT 120
GCCCATCTGT AGTGGTCCCG TCGTTGACC ATGCACCTNA GAATCCACGN GANACGGAGC 180
CCTCCTTGNC GGACGGGCTG GACGNTTTG 209

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GGCAGGAGGA GGAGCAGACA GCGGTGGNCA TCNCCAGCGT CCAGCAGGCG GCGTTCGGCG 60
ACCACAACAT CCAGTACCAG TTCCGCACAG NGACAAATNG AGNACA 106

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TTATGAGCAG GGAGATGAAG AAGCAAATCT TGGTCTGCCC ATCANTCCAT TCATGGATCG 60
TNCTTCTCCT CAACTAGCAA AACTCCAAGA NTCTTTTATC ACCCACATAG TGGGTCCCCT 120

| | |
|---|-----|
| GTNTAACTCC TATGATGCTG CTGGTTTGCT ACCAGGTCAG TGGTTAGAAG CAGAAGAGGA | 180 |
| TAATGATACT GAAAGTGGTG ATGATGAAGA CGGGTGAAGA ATTAGATACA GAAGATGAAG | 240 |
| AAATGGGNAA ACAATCTTAA ATCCAAAACC ACCAAGGAAG GGAAAAGCCA GNCGGGCGNA | 300 |
| TATTTTNGT CCAGCTTAAT GGCACCACCC TTCACTTNGN AAAACCCCCA AGGTTTTT | 358 |

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

| | |
|---|-----|
| GGCACGAGGA CAACCGGGAG CAGCAGCATT TCCTGCAAGA TTGTNACGAG CTGAAGCTCT | 60 |
| GGATCGACGA GAAGATGCTG ACAGCCCAGG ACGTGTCTTA TGACGAGGCC CGCAACCTGC | 120 |
| ATACTAAGTG GCAGAAGCAC CAGGCATTCA TGGCCGAGCT GGCTGCCAAC AAAGACTGGC | 180 |
| TGGACAAGGT GGACAAGGAA GGGCGAGAGC TCACCCTTGA NAAGCCAGAG CTGAAAGCCC | 240 |
| TGGTGTCCGA GAAGCTGAGA GACCTGCACA GGCCTGGGA CGAGCTGGAG ACCACCACCC | 300 |
| AAGCCAAGGC CCGCAGCCTN TTTTATTGCC AACCGAGCTG AGCTNGTTTG NCCCAGAGCT | 360 |
| GTTGTNCCCT GGAGAGCTTG GCTGGAGAGC CTGCAGGCCN CAAGTTGCAC TCCNGTTGAC | 420 |
| TACGGGNAAA GGACCTTACC CAGCGTTNAA CATCCTTNTT CAAGAAGCAG C | 471 |

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

| | |
|---|-----|
| GGCAGANGAT CTA CTGTGTN AGNGAGAGG GCAATTAAAA AGCTGAAGAG AAAGGAGGCC | 60 |
| CTCTNTGTAT TCCGTTCCCT CCTCCTTAAT GCCTCCAAGG GTCCTTGCAT CCCTAGTCTC | 120 |
| CTAAACTCCA GCTCTGAATT CGCCATCAAC CCATGGAGCA ATTCCAAGGC CCCAGTTACC | 180 |
| CATCACCTCC ACACCAGGTG CAAGTTTTGT TTCAGCCCCA AAGGCACTGA GCATTTCTAG | 240 |
| TTTGCCCCCT CTGCCCTGNA ACCCCACAGC ATGCCTGTTT GCAGCTCCCT GTGCCCTCGG | 300 |
| CACCTCCCCA GGCTCATTTG AAGCAGGTGT GCCTTCGGCA GTTCCCCTAA ATTCCCAGGT | 360 |

| | |
|---|-----|
| GCCTCATNCC TNATGNGNTA ATGGCNGTGA GGGGAAAANT TTTCAAGAAG GTGGAAGAGG | 420 |
| CAGCNGGATT NGTTAGGGGT ANCTGTNGTT CANCTTGAGA TGCACAGTGA AGGTTAGGGT | 480 |
| AGNTGGGACA GGCCTACCTG | 500 |

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

| | |
|---|-----|
| TGTATTCACC TATTNATTCT GTGGNTATAC ATAGTGTTNG GGTAGTGGA AACTGGGAA | 60 |
| GCTTGGGCAG TAGTTNCTCA AGGATTGAAG CTTGTTTCTT TAGATCTGNA GGTAGATATG | 120 |
| ACTAGGGGGA AAAACANTGG TNGAGATAAA GGCTACCATT GAAAACCCTG TAGCTCCTAT | 180 |
| CTGTGCAATT ACAATCTGGA TGCTTCAGGN AGCCCTTTTT CTGGGTGCAC ANATGTAANA | 240 |
| TANCCTACAA GTCTTGAGC AANCCTGTTC TCCTTTACGT TCACAGCTGT GTTCC | 295 |

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

| | |
|---|-----|
| GGCAGGAGCN AGTATATGCG GCAGGCGGGA TGGGCCTGGA CCTACGTCNA CACAACCACC | 60 |
| TCCAACACTA TGACATGCTG AAGGACATGT GGGTNTCCCT AGCACCCATG CCCACCNCGA | 120 |
| GATATGCTGC CACCTCCTTC CTCCGAGGNT CCAAGATCTA CGTGCTGGGG GGACGNCAGT | 180 |
| CCAAGTACGC GGTCAACGCT TTCNAGGTCT TTNACATCGA GACTNGNTCC TGGACCAAGT | 240 |
| TTCCCAACAT TCCCTATNAA GCGGGCCTTN TCCAGCTTTG TNACCCTGGA CAANCACTTG | 300 |
| TACAGNCTNA GGAGGCCTGC GGGCAAGGTC GCNTNTTACC GGAAGTCCCA AGTTCCTGAG | 360 |
| GGACGATGGG ACGTTTTTCC GNAATGGNAA ACAGGGGGGG GTTNGCTGAA GATGGAAAGG | 420 |
| TTCGTTNTTT TCCTTNA | 437 |

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

| | |
|---|-----|
| GGCACGAGCC TCAGCCTCGC TCATGCGCAN TNTCTNAGGT GCTTTGGACC ATGGTGATCC | 60 |
| ACATCGGCCT GAGCGTNAAG AGCTTGGCGG GAGGTTTGGT GCTGTTCTTC TTCTTCACTG | 120 |
| CCTTTGCCAC CCTNACCGTG GCCATCCTCC TGATCATGGA GGGCCTCTNG GCCTTTNTCC | 180 |
| ACGCACTGCG CTTACACTGG GTTGAGTTCC AGAATAAATT CTACAGCGGG ACCGGTTTCA | 240 |
| AGTTCTTACC CTTCTCCTTC GAGCATATTC GGGAAAGGGN AAGTTTGAAA GAAGTGAAGN | 300 |
| CCCTTTAAAG GGCCCGTGTG CCCCCAATGT TAACCTTCCC GGCNTTCCTT TCCAAAAGTG | 360 |
| GATTAAAGTN GTGGCNTTTT TTTGCCTTNT G | 391 |

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

| | |
|--|-----|
| GGCACGAGCC ACAGTGCAAG CCCCTGTCCC CTGGAGAGAT CCTGGGCTGC ACATCCCCC | 60 |
| GA CTGTCCAG AGAGGTGGAG GCCGTTNTGT ATCTTGGAGA TGGCCGCTTC CATCTGGAGT | 120 |
| NTGTNATGAT TGCCAACCNC AATGTCCCCG CTTACCGGTA TGACCCATAT AGCAAAGTCC | 180 |
| TATCCAGAGA AACTATGAC CACCAGCGCA TGCAGGCTGC TCGCCAAGAA GCCATAGCCA | 240 |
| CTGCCCGNTC AGCTAAGTCC TGGGGCCTTA TTCTGGGNAC TTTGGGCCGC CAGGGCAGTC | 300 |
| CTNAAGATTC TTGTAGCACC TGGTAATNTN CGATTNCGAA GCCTTGGGCC TTT | 353 |

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

| | |
|---|----|
| GGCACGAGCG GANCCACGGA GCCCACGGAG GAGCCCACGG AGGAGCCCCA GCGTCCGAAC | 60 |
|---|----|

| | |
|--|-----|
| GGGCAGACCC CCTCGAGCCG CGAAGGAGCC CGAGAAGCAG CCACGATGTG CGGAATNTTT | 120 |
| GCCTACATGA ACTACAGAGT CCCCCGGACG AGGAAGGAGA TCTTCGAAAC CCTCATCAAG | 180 |
| GGCCTGCAGC GGCTGGAGTA CAGAGGCTAC GACTCGGCAG GTNTGGCGAT CGATGGGAAT | 240 |
| AATCACGAAG TNAAGAAAG ACACATTTCAG CTTGGTCAAG AAAAGGGGGA AAGTCAAAGG | 300 |
| TTTTTCGATG GAAGGAACTT TTACAAAACA ANGTTTCAGGC ATTGGGCTTA AAAAGTNGGN | 360 |
| GTTTTTNAGN ACCA | 374 |

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

| | |
|---|-----|
| GGCACGAGGC CCCAGGTACT ATGCAGCTGT GGAGGCCAAG AAGGAGAGAA TGAGCAAACA | 60 |
| CGCCCAGACC TTTGGGGCCA AGCAGCCCAC ACATCAGGGG GGCCCTGCAC AGGACCGCGG | 120 |
| AGTGTACCTG TCCCTCCTGG CCTCCCTCCG NACACGTNCC CAGTTNCCCG TGGTGGTGTT | 180 |
| CANCTTCTCC CGGGGCCGCT GTGATGAGCA GGCCTCAGGN CTNACCTCCN TTGACCTCAC | 240 |
| CACCAGTTCG GAGAAGAGCG AGATCCACCT NTTCTGNCA GTGCTGCCTT G | 291 |

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

| | |
|---|-----|
| GGCACGAGCC TGTTTGAACC TCTNCNAGTC CTGGAGACTG GTGCCCTGAG CTCCAACCAG | 60 |
| CGGGCCTCAT CCTACACCCT CACCACCGCA ACTTNTNACC CGAGCAAGAA GCAGCTCCCA | 120 |
| GAGAGAAAGA ACGTTCCCAC CTGCNTAGCC ATGGGAGAGG ACGCTGCACA GGCCGAAAAG | 180 |
| TTCCAGCACC CTGGGTCTGA NATGCGGCAG GAAAAGCCCT CGAGCCCCAG CCCGNTGCCT | 240 |
| TCNTTCACAC NAAGNC | 256 |

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

| | |
|---|-----|
| CCCCCAGAGC TGGACAGCCG GGNTGGAGTG CAGTGGTGTA ACCAAGCTCC CTGACAGCCT | 60 |
| CTNTNTCCCA GCTAAGGTGA TCTTCCTGCC TCGGNCTCCC AGGTAGCTGG NGTTACAGAT | 120 |
| CGAGCGGCAC NTT | 133 |

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

| | |
|---|-----|
| GGCANAGGNA TCCGCAGGGA CTGGCTGACC ATNAACAACA TCAGCCTGNA TGAAAGGCGG | 60 |
| CTCCAAGGAA GTACTGGTTT GTGCCTGACT GCCGAGTNAC TGTCCTGGTT ACAAGGATGA | 120 |
| GGNGGAGAAA GNGAAAGNAG TACATGCTGC CTCTGGGACA ACCTCAAGAT CCGTGATGTG | 180 |
| GAGAAGGGCT TCATGTCCAA CAAGCACGTT TTCGCCATCT TNANCACGGG GCAANGAAAC | 240 |
| GTNCTTNCAA GGG | 253 |

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 424 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

| | |
|---|-----|
| GGCAGAGCCC CTATCAACTC TTTGGTCGAT CGGCTGGCCC TTCTCCAGGT CAGGAGGATT | 60 |
| CTNCAGCAGC TGGGCCTGGA CAGCACGTGT AAGGACAGCA TCGTGGTGAA GGAGGTGTGC | 120 |
| GGANCGTGTC CCGGCGNGCG GCCCAGCTCT GCGNTGCTGG CCTGGCCGCT ATAGTGGA | 180 |
| AAAGGAGAGA AGACCAGGGG CTAGAGCACC TGAAGGATCA CTGTGGGTNT GGACGGCACC | 240 |
| CTGTACAAGC TGCACCCTCA CTTTTCTAGA ATATTGCAGG AAAGTGTGAA AGGAACTAGC | 300 |
| CCCTCGATGT GATGTGGACA TTTCATGCTG TTCAGAAGAT GGCAGTNGNA AAAGGGGCAG | 360 |

CACTGNTTCA TTGTTGTGGG CCAAGAGTTT ACAGNAGCAC AGAGGGGGAA NTAGGAACCC 420
TGGG 424

(2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GGCAGAGCAG GTCTGGGCGG GGCACGTTTC CACGGTCTGA CCCGCCTNTC CCGCTGGTGC 60
CAGGTTGTNT CCAGCGGTTTC AAGTGCTGCC AGGTCAACAT CGAGGNAAGG GCTAGGCAAG 120
TTTTGGTGGA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAACTG GTTTAAGAAC 180
CTTCATCATC TTCATGAATT CTNCTGAGCA GTGGCGCCCT GGTGAGGTCC AGGGGAGAGT 240
NTGAAGGAGG GATTGGCTGG GGAAGGGTGT AGAGAAGCCA GTGGGAAAAG GCTGAGGCCA 300
AAGCCCAGTG GCTCTNAAAA CAGATTGGCT GTGGTNCCAA GAAGAATGAT CTGTTAAAT 360
GCTTTTAGGC TGCTGTTTTG AGCCTNTGGG ATTAGGATTC CNAATTGTTC ACATNGTGAT 420
NCCCTTTAGC ACTGTNCCC 439

(2) INFORMATION FOR SEQ ID NO:248:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

AAATATGCTG CCAAGATGGG GAATCCAGCT GCTGAGCTTT GACAATAAGA TGGAGCTGGC 60
AAAGGTGGTA AAGAGCCACC CCAGTGCCAA GGTTTGTCCA GCAGAGGGGC ACTGCGTGTT 120
TGCATCAGGA TGGTTCTGTG NCATTGCTAC CGATGACTNC CACTCCCTGA AGCTGCCTGA 180
GCCTNAAAGT TTGGGAGTGT CACTGAAATC CTGCAGACAC CTGCTTGAAA ATGCGNAGGA 240
AGCACCATGT GGNAGGTGGT GGGTGTGAGT TTTNACATTG GGCAGTGGCT GTNCTGAACC 300
CTTCAGGCCT ATGGTNCAGT TCCATCGCAA ACGGCCCGGN TTCGTGTTTT GAAAATGGGG 360
CACCCNGGTT GGGGTTTACA AGTTTGCCAC GTTTCTTGGG ACCCTTGGGT GGGTGGGGTT 420
TTCNTGGGC ACCAAAAGGG GGGCCNAAAG TGNAGGTTTT NNAAGGGGTT T 471

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

| | |
|---|-----|
| GGCACGAGAA TGAACCGTGG GGATGACACC CCCCTGCATC TGGCAGCCAG TNATGGACAC | 60 |
| CGTGATATTN TACAGAAGCT ATTGCAGTAC AAGGCAGACA TCAATGCAGT GAATGAAACA | 120 |
| CGGGAATGTG CCCCTGGCAC TGATGCCTGT TTTTGGGGCC AAGATCAAGT GGCAGAGGAC | 180 |
| CTGGTGGCAA ATGGGGCCCT TNTNAGCATC TGTNAACAAG TTATGGAGAG ATGCCTGTGG | 240 |
| ACAANGNCAA GGCACCCCTG AGAAGAGNTT TTTCCGAGAG CGGGCAGNGA AGATGGGNCC | 300 |
| AGAATTTTCA ACCGTATTT | 319 |

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

| | |
|---|----|
| CCAGGAGGTG TTGCAGTNAA CCAAGATCAC ACCACTGCAC TCCAGCCTAG GCAACANAGA | 60 |
| CTCTNTNTCA AAAAAAAAAA AAAAAAAAAA AAAAAAN | 97 |

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

| | |
|---|-----|
| AATTTTCAGTA ACCGAAAAC TAAGCCTTAG TATGAAAAC TGAGGATTTA TAATTGAAAA | 60 |
| TGAAAAAACT ATGTTACTNT CTATCATCAG AATTATAGTC TTTGGTGCTN NGTTTTCAAT | 120 |
| GGGGCATATT ACATAAGGTT GTTCTTTCA CCCCAGAG ACTACTAGGT TACCACTCTG | 180 |
| GGGCATTGNC TTTCCACCTT AACCCCTNAA CCAGTAAGNC TNTTACACCC TTTGTAGGC | 240 |

CCACT

245

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

| | |
|--|-----|
| CTGCTGCCCA ACCGTTTGCT GACCAAGGTG GCCGANATGG CGCACAGCAT CCTGGTCTGC | 60 |
| AGAAGCAAGA CNTGTGCNAN GTGCACCACG AGCCCCCTCAA GCTTTTTTGC CAGANGGACC | 120 |
| AGAGCCCCAT CTNTTTGGTG TNCAGGGAGT CCCGGAGCAC CGNCTNGCAC AGGGTGCTGC | 180 |
| CC | 182 |

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

| | |
|---|-----|
| GGCAGAGGTT CCTTGTCTAT GGCACCCGTA CGTCCAAAGA CAAGAGTGGA GCCTACCTCT | 60 |
| TCCTGCCCCGA TGGCGAGGCC AAGCCCTACG TCCCCAAGGA GCCCCCGTG CTGCGTGTC | 120 |
| CTGAAAGGCC CTTTCTTCTC AGAGGTGGTT GCGTACTATG AAGCACATTC ACCAGGCGGT | 180 |
| CCGGCTTTAC AATCTGCCAG GGGTGGAGGG GCTGTCTCTG GACATATCAT CCCTGGTGGA | 240 |
| CATCCGGGNA CTACGTCAAC AAGGAGCTTG GCCCTGCACA TCCATACAGA CATCGACAGC | 300 |
| CAGGGGTATC TTTTTTCAAA GACCTCAATG GTTTTCAAGG TGGCAAGCCC CGAANGGTTA | 360 |
| TTNTGAAAGG AAGTTNCCNC TTTCCNGGGC C | 391 |

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

| | |
|---|-----|
| TTTNNNCACG GCTCTCTNGT AATGCAGAAT CTGGGTGANA CTTCCACCCC CACACAAGNC | 60 |
| TCGNTGCTCT TCGGCACGGG TCAACGGCAT GATAGGGCTG GTNACCTCAC TTTCAGAGAG | 120 |
| GCTGGTACAA CCTGCCTGCT GGGACATGNC AGAATCGANC TCAATTAANG TCATNCAAAA | 180 |
| GTGTGGGGTA AGATCGAGCA CTGCCTTGCT NG | 212 |

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

| | |
|---|-----|
| GGCAGAGNAT CAAATATGCT GCCAAGATGG NNAATCCAGC TGCTGAGCTT TGACAATGAG | 60 |
| ATGGAGCTGG CAAAGGTGGT AAAGAGCCAC CCCAGTGCCA AGGTTTGTCC AGCAGAGGGG | 120 |
| CACTGCGTGT NTGCATCAGG ATGGTTCTGT GCCATTGCTA CCGATGNACT CCCACTCCCT | 180 |
| GAGCCTGCCT GAGCCTAAAA GTTTGGGAGT GTTCACTGGA AAATCCTGTC AGACACCTGC | 240 |
| TTTNAAAATG CCGAAGGAAG GCACCATGTG GNGGGTGGTG GGTGTGAAGT TTTCACNTTG | 300 |
| GCAGTGGCTG TTCCTGAACC CTCAGGGCCT GATGATNCAG TTCCATNGNC AAACGG | 356 |

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

| | |
|---|-----|
| GACTTTGGAT CCAGCTCAAA ATCTNACCTT NTCCTGAGCC CTTGCCTAGC CCCACCTCC | 60 |
| ATCTTCGCTG CTCTGCTGCC TGTGCCGGGN AGGGGCTCTG TTTTCCCT AGAAATCTAT | 120 |
| GCCTTGCGCT GGGGGCCAGG ACACCACAGG GGTAGGCTCG TNTACAGCCT CACTAGCCCA | 180 |
| AGGGCCTACG AATGCCCTCT TGGGACAGAG AAGCCTGGAA TGGAAGAAAG CTNATGCCAT | 240 |
| TNCCTTGGCT GCTGGTTCTT TTGGCATTGG GAANTCTTCC TTCTCTCTAA TGTCATNCTT | 300 |
| GCTGCTGTNC CGCTGCATTA TTTCCCTTTA AATNTTTCNG GGANTTGGGG GTGAACNGNT | 360 |
| GTTTGCACCN AACCCTGGGG ATGTGCTTGG GGGAGGAAGG GGAGGGGGAA GGTCTGGGAA | 420 |
| NTTTNTNTN TTTGGCCAG TTNAGGTTGN AGGNCAGGGG GGNCCCCGTT CTGGAGGAAG | 480 |

GAGAGCNTCC

490

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

| | |
|---|-----|
| GGNAGAGGTG GCTTGAACCC GGAAGTTTAA GGCTGCAGTA AGCTATCATG GCACCCACTG | 60 |
| CACTCCAGCC TGCNTAACCC AAAGAGACCT TACCTCTAAA AAACAAAAAA ACGGAATCCC | 120 |
| CAAGTAGTTA GTGTTGCATT GTCTGCTGCC GTCCAGAGCC CAGAACGCTT CCTCCAGCTT | 180 |
| GGCGCCAAGG TCCCAAAGGG CGCACTGCTG CTCGGCCCCC CCGGCTGTGG GAAGACGCTG | 240 |
| NTGGCCAAGG CGGTGGCCAC GGAGGCTTCA GGTGCCCTTN CTGGNGATGG CCGGCCCANA | 300 |
| NTTTCGTGGA GGTCAATTGA GGCCTCGG | 328 |

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

| | |
|--|-----|
| NAGAGCACAT CAAGGAAGAN CACAACATGT GGGCACTATC TNTNCTTCAT CGTCCTGGTG | 60 |
| AAAGTNAAAG GAACTCCACC GAATATACTG GGCCTGAGAA GTTACGTGGC AGAAATGAAT | 120 |
| CAAGGAAAGA AACCTTGACT GGTTCCTCCAG GATGAGAAGC CATGTNATTG GTCAGCAGTG | 180 |
| AATTCTGAAA GGAGNACAGT NTGNGCCTGN GGAAACCTG | 219 |

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

| | |
|--|----|
| CAGAGGACCA CCCGACGAG GAGATGGGGT TCACTATCGA CATCAAGAGT TTCCTCAAGC | 60 |
|--|----|

| | |
|---|-----|
| CGGGCGAGAA GACGTACACG CAGCGCTGCC GCCTNTTCGT GGGAAATCTG CCCACCGACA | 120 |
| TCACGGAGGA GGTACTTGAA GAGGCTCTTC GAACGCTATG GNGAGCCCAG CGAAGTCTTT | 180 |
| CATCAACCGG GACCGTGGGT TCGGCTTCAT CCGCTTGGGA ATCCAGAACC CTGGCTGGAA | 240 |
| ATTGGCAAAA GCAGAGCTGG GACGGGCACC ATTTCTTCAA GAGNNAGACC TCTTACGGNA | 300 |
| TTTCGCTTTC GTTAACAACA TGGGNGTNAG | 330 |

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

| | |
|---|-----|
| TGCTGGAGAA CCAGACCCCA GAGTTCTTNC AGGACGTCTG CAAGCCNAAG TACAGCGGCA | 60 |
| CCCTGAACCT GGACAGGGTG ACCCNAGAGG CGTGCCCTGA GCTGGACTAC TTTGTGGTCT | 120 |
| TCTTCTCTGT GAAGCTGCGG GNGTGGCAAT GCGGGACAGA GCAACTACGG CTTTGCCAAT | 180 |
| TCCGNCATGG GAGCGTATCT NTGAAGAAAC GCCGGTACGA AGGCCTCCNA GGCTGGNCCG | 240 |
| TGCAGTNGGG GCGCCATCGG GACGGTGGGG CAATTTTGGG TNGAGACGAT TGAGNAACCA | 300 |
| A | 301 |

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

| | |
|---|-----|
| GGCACGAGCC CAATNGGGNT CCCTNCNCA GCCTCTACCT CTCCTNAANC CTNTGANANC | 60 |
| CNCCTACACA CACACACAGG CATACTCAGN CCCACTCAA GCTGAGAATG ATCCAACCTCA | 120 |
| GCCCTACTTT NCGGATGGAC ATATTAAGGC CANGAGGGG GGNCTTNCC CCAGGTCGTA | 180 |
| TGGCAGNGGG G | 191 |

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

| | |
|---|-----|
| GGCACGAGCA GGTCTGGGCG GGGCACGTTT CCACGGTCTG ACCCGCCTTT CCCGCTGGTG | 60 |
| CCAGGTTGTN TCCAGCGGTT CAAGTGCTGC CAGGTCAACA TCGAGGAAGG GCTAGGCAAG | 120 |
| TNTTGGTGGA TCCTGCGGAA AACCTGCTTC CTCATCGTGG AGCACAACTG GTTTNAGACC | 180 |
| TTCATCATCT TCATGATTTT CTTGAGNANT GGCGCCCTGN TNAGNNCCAG GGTNAGAGTT | 240 |
| TAGAGGAGGG ATTGGCTGGG GAAGGGTGTT AGGAGAAAGC CANTNGGGAA AAGGCTNAGG | 300 |
| CCAAAGCCCA GTGGGCTTNT TNAACACAGA TTTGGCTGTG GGTCCCAAGA AGAATGATCC | 360 |
| TGTTAAAGTG CTTTTAGGCT TGNTTGCTTT GAGCCTTTGG GATTAGAATT CCATACTTTT | 420 |
| TCACATTGTG ATNCCTTTNA GCAATTTNCC NA | 452 |

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

| | |
|---|-----|
| GGCACGAGCC CCTATCAACT CTTTGGTCGA TCGGCTGGCC CTTCTCCAGG TCAGGAGGAT | 60 |
| TCTNCAGCAG CTGGGACTGG ACAGCACGTG TNAGGACAGC ATCGTGGTGA AGGAGGTGTG | 120 |
| CGGACCGTGT CCCGGCGGGC GGCCACGCTC TGNGGTGCTG GCCTGGCCGC TATAGTGGA | 180 |
| AAAAGGAGAG AAGACCAGGG GCTAGAGCAC CTGAGGATCA CTGTGGGTGT GGACGGCACC | 240 |
| CTGTACAAGC TGCACCTCA CTTTCTAGG AATATTGCAG GAACTNTNN AAGGAACTTA | 300 |
| GGCCCTCGNA TGGTGATGTG GACATTTTAT GCTGTCANAA GATGGNCANT GGGAAAAGGG | 360 |
| GCAGCACTGA TTTACTGNTG TGGGCAAGA GGTTTACA | 398 |

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

| | |
|---|-----|
| GGCAGAGGG TAAATCCTAG CTTCTCGGGA AACTAAGGCA AGAGGATCAC TTGAGCCCAG | 60 |
| GAAGGTGGAG GCTNCAGTNA GCTGTGATTG CACCACTGNA CTTTAGCCTG TNTGAACAAA | 120 |
| TTTGTGGGCA TAGGAATTCT TCATAATGTT CCTTTATTAA TCCTTTNTTT TTTTTTTTTT | 180 |
| TNAAAAGGGN GGCCNCTGAC C | 201 |

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

| | |
|---|-----|
| GGCAGAGGTC AATGTACATT TNATATTAAA AAAAGCCAAA ATAACAATGG GGTGAGANCA | 60 |
| GGAGGCCACT ATACCACTGG CCAAGNAGTT CANATCCTTG GAGGCCGTCT TTGGAGAGGC | 120 |
| TCANTGGGAC TCGTATTCTG GGCAGCAGCA CAGCACCGTN TGGGAACAAG GTACACCCTC | 180 |
| CCCACACCTG NGCCTTTTCA CCCACAGGGC AAGGGATGTG GCGAGAACTG NNGGGCACAC | 240 |
| GTGGAAAACA GTTCAGCCCT GCCCGGCGN TCTTTTAAAG GNNGAGCTCT AAGGGATCAC | 300 |
| | 301 |

A

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

| | |
|---|-----|
| GGGAGGCGGG NGGCCATGCG GNTTNCAGCC CTGAAATCTC CCAGCCGCAG AAGGGCCGGA | 60 |
| AGCNCCGGGA ACCTAGAGCT TCCACTCAGT CCGAGCCTGC NAGGTGGGCC GGGAACCCGA | 120 |
| ACGGACCCCA GGATCGGGAA GTGGCTCCGG CCTCCAGGCT CCGGGGCCGG CGNCTGAACC | 180 |
| CCATCCCTGC TTCCTACGGC ATGACATTGA ACCCCGGTGN TTGCTGACAC CCAGCTCGCT | 240 |
| GCCTCCTAAG CATTNCACTT CTGGAGCACC CTGAGTCCCA TTNCGNCCCC GTAGCCCGGC | 300 |
| CAAGTTTTC TTTCCATTTC CATCCAGTGG GCAGNGCCAG GTGCACATNC TTTTNTAAG | 360 |
| GTGGATGGGC TTTTGACCCC GTGGGTGGTT TTNCCCAGGG NNCCAAAANN CTGATTATTA | 420 |
| ANCANCAACA ANAACAACCT TTTNGGGTNA ATTTNNAGCC AGTTTTTTTN CAGCAAGCAT | 480 |

507

TTTAAGGGGG AAANTAGTTN AATTGAA

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

| | |
|---|-----|
| CCACCTGGGA GCAGGTACAG GNTCTCTGAC ATATCTCNAT GGGNTACAAA ATGAAGNTGT | 60 |
| ACTNCCAGAC TAACCCCTAC TTCACAAACA TGGTGATTGT CAAGGGGTTT CAGCGCAACC | 120 |
| GN | 122 |

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

| | |
|---|-----|
| CGGCGGCCAT TGCAGAAAAC TTCCCCACGG CTACTGCGTC CACGTGGNGG TGGCGTGGGG | 60 |
| NACTCCCTGT AAAGNAGAGN GAGCATGGCG CCCGGAANGT CGTGAGTCGA GTCTTTCCCG | 120 |
| GGCTAATCCA TGCCNGNGTG GAGGCTTCTG ACGCAAGTTG GNGCCANGT GCTGGATCGA | 180 |
| C | 181 |

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

| | |
|---|-----|
| GGCACAGGTC TTTTGCCACG GCTCTCTGGT AATGCAGAAT CTGGGTGAGA CTTCCACCNC | 60 |
| CACACAAGGC TCGGTGCTCT TCGGCACGGT CAACGGCATG ATAGGGCTGG TGACCTCACT | 120 |
| GTCAGAGAGC TGGTACAACC TCCTGACTGG ACATGCAGAA TCGACTCAAT AAAGTCATCA | 180 |
| AAAGTGTTGG GAAGATCGAG CACTCCTTCT GGAGATNCTT TCACACCGGA GCGGTAAGAC | 240 |

AGGAACCAGC CACAGGTTTG CATNGACGGT NNACTTTGAT TGNAGAAGTT TCCTGG

296

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GGCANAGGTG GCATATTCCT GTAATCTCAG NCTCCTNGGT AGCTGGGACT ACAGNNACAT

60

62

GC

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GGCAGAGTNT TTTATTTAAC ATGATTTTTTC TATATCGTTA CTGTCGAATG CTAGANGAAG
 GCTCTTTCCG AGGTCGGACA GCAGACTTTG TATTTATGTT CCTTTTGGT GGATTCTTAA
 TGACCCTTTT TGGTCTGTTT GTGAAGCTTA GTTTTCTTGG GCCAGGCCTT TACAATAATG
 CTCGTCTATG TGTGGAGCCG AAGGAACCCC TATGTCCGCA TGGAACTTCT TCGGCCTTCT
 CAACTTCCAG GCCCCCTTTC TGCCCTGGGT GCTCANGGGA TTTNCCCTG TTGTTGGGGA
 ACTCAATCAT TGTGGGACCN TTTTGGGNAA TTGCAATTTG GACAACAAAT AATNTTTCCT
 TGGAGATGT AATTTCCCAA TCAAACCGGG NGGNATAAGA ATNTGAAAA AAACCAATTN
 TTTTGAAAAG G

60

120

180

240

300

360

420

431

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TGAATGGTGG GCATGGNTCA GAAGGATTCC TATNTGGGCG AACGAGGCC AGAGCAAGAG

60

101

AAGGCATCCT TCACCTTGAA GTAACCCNAT NGNAGCACGG T

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

| | |
|--|-----|
| GGCAGAGNCA GGCCTTCTCA GGAAGAAAGT GGAGGTCCTG GCTGAGGCCT GCACAGACCT | 60 |
| GCTTTCGCAC CAGAAGCAGC TCACCGTGGG CCTGCCGCCC GAGCCCCGGG AAGAAGATCA | 120 |
| TCTCTGNGNC CCCTTCCCCC AGAGGAGCTT CANAAAACTN CATCTACGNA GGCCAGTGGG | 180 |
| CAGGACATCA GCATTGCCGT CCTTCACGCA GGAGGATTGT GGTTTACCTG GCCATGTTAT | 240 |
| GTTTCAGGGNC GCACAGACCT NCTTTTNTGG GAGATTGCTT GAGACTNCGG ATTGGGANTG | 300 |
| ATCATTCAAGG TTGTTGGGCC ACGGGAGCNT NGGCACGGAG CCTTGAAANT GNTTCAAGGA | 360 |
| GGAAGAGGNT TTTTNGAAAN TTTTGATGGA ACCTTCAGNC CTTTGGATT ATGNAAAAAT | 420 |
| TTTCCTGNAA CCATATTTTT AAGTGGGGGA AAAAGTTTGG GGGTTTGAAA GAAGTTTNCN | 480 |
| | 480 |

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

| | |
|---|-----|
| TTGGCTGGGA CTGTCTCCAC GCTGGGGTAC AAGTTCTTCA CGCNCATCCT TGAATCAAAA | 60 |
| TTCAAAGTCC AAGACACATG TGGAGTNCAC AACCTCCATG GGATGCCGGG GGTCTGGGG | 120 |
| GGCCTCCTGG GGGTCCTTGT GGCTGGACTT GCCACCCATG AAGCTTACGG AGATGGCCTG | 180 |
| GAGAGTGTGT TTCCACTCAT AGCCGAGGGC CAGCGCATGC CCACGTCACA GGCCATGCAC | 240 |
| CAGCTCTTCG GGCTGTTTGT NAACTGATG TTTGCCTCTG TGGGGCGGGG GGCTTGGAGG | 300 |
| CATCATATTG GTNTTATGCC TCCTAGANCC CTGTGCCCTT TGGGATTGGG TNGGCAACCT | 360 |
| TCTTCCAAGG TGGGGGGGCA AAGAAGNCTT NAAAAATTCT TCCCTTAACC ANCAACCA | 418 |

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

| | |
|---|-----|
| GGCACGAGCC GGTGTTATCC TCCAGTGCTG AGACAGGCCG TCTCCCTGGC CCGGCGCATC | 60 |
| CAGGACCCTC TGATTGAATT TGCCCAGGTG TGCAGTTCCG ATGAAGACAT CCTGTGTCTC | 120 |
| AAGTTTCACC CCTTGCAGGA GCATGTGGTG AAAGAGGAGC TGCTCAACGC CTTGTACTGT | 180 |
| GTAATTTATC AACCGAGTCA ATGAGGTCGG GGTGATGTC AACCGTGCCA TTNGCCCACC | 240 |
| CTTACAGCCA GGCCTTGATC CAGTATGTTT TNTGGCCTNG GACCTTGAA AGGGACCCAC | 300 |
| CTACTGAAGA TCCTGGAAGC AGAACAACAA CCNGGTTNNG | 340 |

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

| | |
|---|-----|
| TACACACTTT TAAACAACCA GCTTTCACAG GAATTCACTC ACTATCATAG GAACAGCACC | 60 |
| AAGGGGGAAG GTGTTAAACC ATTCAGGAGA AACTGCCCCC ATGCATTGGN TAATNATCTT | 120 |
| CCACCAGGCC CTACCTCCAA CGTTGGAGAT TNCAATTCGA CATGAGATTT GGGCAGGGAC | 180 |
| ACAGATCCAA AACATATCAG ACCTAAAAGC AGTTCATGGG AGACCACTGA ACAAGCGCAA | 240 |
| AGTCNCCTGA GAATGTGCGT TCAGGGTGTT NCACANAAGA GGCANAGNGG TCGATGTGGT | 300 |
| TTG | 303 |

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

| | |
|---|----|
| GGCACGAGCT CGTGCNGTTC TAAGTCACTA GGAGATGGTA AAAGCAATAC CATGAGACTT | 60 |
|---|----|

| | |
|---|-----|
| CCGAGGCTAG GGTACGAAAG GATGGCTTCT GCGTGGTGCT CANTCTCTCC CAGATCCCTT | 120 |
| GCTCTGTAGG AAACCAACCC CCTAAGGCCT AAAGATGGAA GTGACCCAGG TGTCTACTGA | 180 |
| TGGATGAACA GATCAACAAA GTGGGATGTA TTCACACAAA GGAATATTAT TCAGGGGGGA | 240 |
| AANGGAAGNA AATTCTTGAC ACATGGNTAC AACATGTAAT GAACCTTNGA AAGACATGAA | 300 |
| TGCTGGAGTG AAAATAAAAC TTAGTCACAA AAAGGACCCA ATTAAGTNGC ATTGAGNATC | 360 |
| CCCANTTTNT TATTGGAA | 378 |

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

| | |
|---|-----|
| GGCAGAGGAT TTTATTTACT ATTATTTTAG AAAAAGTAGG CAGTAATTC GAGTCAACTG | 60 |
| CTTTTTCTAA ATCATTTAAC GTGTAAATG AGGAACCTTA CTGCACAAAT GTAGGGTTAA | 120 |
| GTATCACTTT TGAAGGTTTA CTTCAAAGTA AGTGNAATTA AGGCTATCAA GGGAAGAATG | 180 |
| TTTTTGGCTA TAAACTGGCA TAAAGAAAAN GAAGAACTGG GNGAAATTAC TGAAGTAGAG | 240 |
| GAAGTNCATC GGAAGTAGAG GTGTTGAACT AAATTATTTG TAGACGTGAA TCCGGCTTTC | 300 |
| CATTGTNCCG GGGGAAAATT TCCCATGGTT TTNGTTTGGT CTTCTTCGNC CCAGGTTCCA | 360 |
| TTAATGGGCC ANGNNCCACA CATTTGGGGG TGGGTTTAAG GGNACCGGNN AAATTTAAAC | 420 |
| CCGTTTAAAA AGGGGGGGGG GGGGGGNCCA AGGNTTCCCC CCNTTTGGGG AAAGTGGGTT | 480 |
| | 480 |

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

| | |
|---|-----|
| GGCAGGAGGC AAACANCTCA GCAAGCTCCT TCTGTCCAT GGACACTGGT GTTATACACG | 60 |
| GGTTTCCAAC ATGATTCTCT ATTTTTCCTA TAAGAATGTG GNCTATGTGA AACCNCCTTT | 120 |
| TCTGGTACCA CNNCCTTTTG NGGGATTTTC AGGG | 154 |

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

| | |
|---|-----|
| GGCANAGGGA AAAAGCCATT CTACTAAGTC CTGTCCTTGG ACAATAACAC CAGTAGGNNA | 60 |
| ATGCTGAGTT GGAAAAATTA GCAAATCTAG AGTCTTCTCT GGTTCATTTC TATTNATTTA | 120 |
| AGCTTTATGG GACTTGCTTT NCGATTAGCT GCAGCTCCTG CCCTTAGCTT CTTTNGTTNA | 180 |
| ATTGCCCAAG GGCTAGTGAA GACTTAGGTT CTCCTCCAAG GTTAGAAAAT TNGNTAA | 237 |

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

| | |
|---|-----|
| GGCAGAGCAC AGATGCTGTC CTGAGCAGAT GGCATGTAAT GCGCGCACCA NCCGTTCTGG | 60 |
| GGTCACGTGC AAGAGGCTGG CTGGAAATNA TGCCAGGCAT GCTCTTGCCA CCAGAGAACC | 120 |
| TCTTGCCCTG TTCTNATGTG CCCAGAGCC CAGTNTTGGG CCTCCCCTTG AACGCTCCCC | 180 |
| TTCGTGCCCC CTACCTGTGG GAAGGTCTCT TCTGAACTGC CCCTGTCCTG TTCCCAACAG | 240 |
| GTTCAGGCCA ACAAGGTGAA GAAACTCTCC ATCGTTGTCT CCCTGGGGAC AGGGGGGTTC | 300 |
| CCCACAAGTG CCCTGTGAAC CTGTNTGGGA TGTTTTTCGT TCCCAGNAAA NCCTTGGGGA | 360 |
| GGTTGGGCCA AAATTGTTTT TTGGGGGCCA AGGNAATGGG GGAANATGGT TGGTGGGATT | 420 |
| TTTTNAATTT TGGGG | 435 |

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

| | |
|---|-----|
| GGCAGAGCTT TTGACCCTCA TTTCAAGATC AACAATGCAG TTTCCAATAT CATTTGCTCC | 60 |
| ATCACCTTCG GAGAACGCTT TGAGTACCAG GATAGTTGGT TTCAGCAGCT GCTGAAGTTA | 120 |
| CTAGATGAAG TCACATACTT GGGAGGCTTC AAAGACATGC CAGCTCTACA ATGTCTTTCC | 180 |
| ATGGATAATG AAATTCCTGC CTGGACCCCA CCAAACCTCTC TTCAGCAACT GGGAAAAAAC | 240 |
| TGAAATTGTT TGTTCCTCAT ATGATTGACA AACACAGAAA GGNTTGGGAT CCTGCCAGAA | 300 |
| ACAAGAGACT TTATTGATGC TTACCTTAAG GAATGTNCAA GGCACACAGG CAATCCTACT | 360 |
| TCAAGTTTTC CTGGAGGAAA ACNTCNTTGC GGCACCTGGA CNTTTTTTTTG CCGGANC GGG | 420 |
| ACAATTCCCA ATTGGGGTTG GGTNG | 446 |

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

| | |
|--|-----|
| GAGCCGGCCG TNCTGCCAGC TGCNTGTAAT GCAGGAACCT GGCTGCACCA TGGGTATCTC | 60 |
| CTCCANCTGC AATTTTCCTT TCTNACTTT NTGCAGGTN ACCTACCATG GGGTCTCCCC | 120 |
| ATGTTAAGGT GACTGCAGAG AAAATTAATG GACTTACGAA ATGATTACCT GCANNCGGAT | 180 |
| GAGGCTAATA AAGATTTTTG GTTCAAAGGT ATGGTAAGAG AGTGAATTCA GAAAGGCACT | 240 |
| GGNAAGAGAA TGGNAAAGTT AGGGTGTGGC TAGAGANGGA NCTTCAAAGA GNCTGCCCCAT | 300 |
| GTTGTGGAAC TTCCCATAG | 319 |

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

| | |
|--|-----|
| GGCACGAGGA AAAGAATTAG AGTTCTTGAA AAACTTAAT GATGCTGATC CTGATGACAA | 60 |
| ATTTCAATTGT CTGAGAACTC TTCAGGCACT TCTATCACAA GCAGCATCTT TGTCTGGTAT | 120 |
| TCGAGCCTCT CAGCATGAAC TTACGAGAGG TGTTAAAAA ATATGGTAAA GATGTTGGTC | 180 |
| TTCAATATTAA AGCTGTAAGA TCCTATAGTT CAGCAGTTGT TCCTGGCATT GAAACTCCTT | 240 |

AAAAGATGCA TATNGTACAT GCCGATATCA AGCNAGACAA TATTCTGGGT TAATGGNATN 300
CCAAAACNT 309

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GGCANAGGGC AAAGTCCACA CTGGGGAACG GCCCTATGAA TGTAGCCTGT NTGGGAAAAC 60
CTTCACTACC AGATCCTACC GCAATCGGCA CCAGCAGTTC CACACTGAAG AGAGGTCTTA 120
TGAAATGTAC AGAGTGTGGG AAGGCCTTCA AACATAGTTC CACCCTCCTT CAGCACAAGA 180
AAGTCCATAC TCCAGAAAGG CGTCAGGAGG ACAGGGCACA TGGGGAAGGT CGTTAGCTGC 240
TTAGCACCCT GTTCCATCAG GAAAGGTCTT ATTNCCAGAA AGGNGGTAA GGAGAGTTGG 300
CCCTTNAGAN TTCCCTTCCG AAAGGGGTAA AACCTTGGC AAATTCCCAA CAACCCACCC 360
CCAGGGNG 368

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GGCAGGAGCG GCACGAGGGA AGATCCTAAT GAGGACATTG TGGAGAGAAA CATCCGAATT 60
ATTGTTCCCTC TGAACAACAG GGAGAATATC TCTGAATCCC ACCTCACCAT TGANAACCAG 120
ATTTGTGTAC CATTTGTCTG AACCTCTGTG AAAAAATGTG AATCCTACAG AAGTGGAGCT 180
GGATGAATCA GATAGTTACT GCTTACCCAG AGCAATATCT GTGAATGGAA GNCAGTGCTT 240
ACAGAGACCT GCTTACACTT ATGNACAGAA ACAAGTGCTT ACACAGCTGT GGGTTCCCCA 300
CTTCGTNATT ATGGGTTGGT GAGGACCCAA AATTGGGTGG GGAAAACAGG CCTTTAAANC 360
CCCCAGATTG GCCTTGTTTA TTCCCTG 387

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

| | |
|--|-----|
| TGGGGGCTCT TGGGTTCCCTC GTCTGCTACA CAGAAGTGAG GAGATTCCCC TGACTGATCT | 60 |
| CATGTTGTTA AGTGTTCCTAT CCATCCCCAC CACACCCCAA CTTCTTCATG NAAGCAGGTN | 120 |
| TCCATCCTTA TAACTTGAGA GGCTGTGAAT CATTCCATAG ATGTNGGTCT TCTGCTACCG | 180 |
| NTCTTCACAT TGCCTCTACA TACCAGGTCT TCAGCTGCAT TCTAGGAAAC ATCATATACT | 240 |
| ATTGGATTGC AAATCTATAA ATAATATAAG ACAATGGACT GACAGGGGAA AAAAGTTTTT | 300 |
| TTTTAAGTTT ACAAACNCA ATCCCACTTG TTGGCATTTC NAAGGGGGCN ATACTTTTTC | 360 |
| CTTNATTCCA CCGTTTAAAG AAGTTTNGGA ATT | 393 |

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

| | |
|--|-----|
| GGCACGAGTG GNAATTTTAA GGGAATGAAA ATTAAACCTG GCTCAATGGG NAAACCTTCT | 60 |
| CCTGCTTTTCG ATGTTAAGNT TGTAGATGTA AATGGCAATG TTCTACCTCC TGGACAAGAA | 120 |
| GGTGATATTG GCATTCAAGT TCTACCCAAC CGACCATTG GCCTTTTTTAC TCATTACGTG | 180 |
| GATAATCCTT CAAAAACAGC TTCAACTCTA CGAGGCAATT CTATATCACT GGGGACAGAG | 240 |
| GATATATGGA TAAAGATGGG TATTTCTNGT TTNTTTGCAA GNGCAGATGT TGGCANATAT | 300 |
| NCCCTGGTTN TCGATTGTC CCCTTTGGGT GGNAATCCC CCATTNNCAC CCCTTANTTT | 360 |
| AGAGTNCCCT TTTTCAAANG CCCNACCCT TCAAGGGGGG NGGTNAAAGT TTTNGGNTTT | 420 |
| AAAACCCNTT TCNANGNCCA NTTCAGGGCC CCTTTTAAGG GGTTCGGGG CTTTTAAAAA | 480 |
| CTCCGGGCCT TNAATTCCC CAGGGGGG | 508 |

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

| | |
|---|-----|
| GGCAGAGNCA GAAGCCAAAT CAGGGACTGC TACTCCACAG AGATCGGGAT CAGTTAGCAA | 60 |
| CTATCGATCT TGCCAAAGGA GTGATTCAGA TGCTGAGGCT CAAGGAAAAT CCTCAGAAGT | 120 |
| TTCTCTTACC TCATCTGTGA ACCTCACTTG ACTCTTCTCC TGTGACCTA ACTCCAAGAC | 180 |
| CTGGAAGTCA CACAATAGAA TTTTTTGAGA TGTGTGCAAA TCTAATTAAA ATTCTTGCAC | 240 |
| AATAACAGA AAACCTTGCT TATTTCTTTT GCAGCAATAA GCATGCATAA TAAGTCACAG | 300 |
| CCCAATGCTT CCCATTGTAA TCCAAGTTAT ACCTAATTTT TAACCGGGGG TTNGGGNTTT | 360 |
| NGGATTGCAA TTTGNCACCG GGGTTTGGGA CCAGGTTTTT TN | 402 |

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

| | |
|---|-----|
| GGCANAGCNG AAACCGNGTG CGCANCGATN AAGCAACCTN AAGGACCCCA GGAACCCNGG | 60 |
| NCTGNGANGG AACGTGCTCA GTGGGGCCAT CTCCGCAGGC TTATAGCCAA GATGACGGNA | 120 |
| GAGGAAATGG CCAGTGAATG AACTGAGGGA GTTGAGGAAT GCCATGACCC AGGAGGCCAT | 180 |
| CCGTGAGCAC CAGTGGCCAA GANTGGCGGN ACCACCACTG ACCTNNTCCA TGNAGCAAAT | 240 |
| GCAGGAAGAG GANTGCAC | 258 |

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

| | |
|---|-----|
| GGCAGAGCA GATGTTTACA GCAGCACTAT CCATAATAGC CAGAAAGCAG AAGCAGCCCA | 60 |
| GATGCCCACC AGCAGGTGNA TGGATGGACA GACTGTGGTC TGTCAGTGAA TGGAATATTA | 120 |
| TTCAGCCCTT AAAAGGAATG AGGGACTGAC ACAGCACACA TGAGTNTGGG AAACAGGATG | 180 |
| CTGAGTAAAN GAAGTCAGAC ACAAAGGCC ACACATTGTG TACTGTGTGA TTCCATTTCT | 240 |

| | |
|--|-----|
| GTGNAATGCC CAGATTAGCA ANTCCGTAGA AACAGAAGTA GATGAGTGGT TGCCAGGAGA | 300 |
| TGGGGGAGAA GGAGCGGGGA GTATGTTTCAT TCAGNCTGGA TTCNTTAAAC AAATGCCACA | 360 |
| GANGTTGTTT TAAACAACAG ACATTATTTT TCANGTTTGT GAGGTGGAGT TCTAGGCGNG | 420 |
| GTGCCTTCAA TTTCATTCCC ATGAGGCTTG TTCNTGGTTG CAGAGGCCAC CTTTTATTTG | 480 |
| TTCCACANAN TTTTCC | 496 |

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

| | |
|---|-----|
| ACGNNTNAGT NGCCAACTAC GTGGTCCAGA AGATGATTGA CGTGGCGGAC AGGACCAGCG | 60 |
| GAAGATCGTC ATNGCATAAG ATCCGGCCCC ACATCGCAAC TCTTCGTAAG TACACCTATG | 120 |
| GCAAGCACAT TCTGGCCAAG CTGGAGAAGT ACTACATGAA GAACGGTGTT GACTTAGGGC | 180 |
| CCATCTNTGG CCCCCCTAAA TGGTATCATC TGAGGCAGTG TTCACCCGNT GTTNNCNT | 238 |

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

| | |
|---|-----|
| GGCAGAGGGA AATGGATCAN AGGATTCAGG CTGCAGAACA TAAGACACGG AAAGACGAAA | 60 |
| AACGCAAAGC TGAGGAAGCC CTCAGTGACC TCAGACGTCA TATGAANCTG NAAGTAGGAG | 120 |
| ATCTGCAGGT GAACCATTA AAGCTAAGA AAGCTCGAAG AACAAATCAA ACGCGTAAGT | 180 |
| CCAAAAGGAA GATGTGGCTG CATTGAAAAA ACAAATTTAT GATTTATCCA ATGGGNAAC | 240 |
| CAGAAGTTAA GAAAGACCTT TTAGAAGCAC AGACAAACAT AGCCTTTCTT CAGAGTGAGT | 300 |
| TAGATGCTTT TGAAAAGTGG TTATGCTGAT CCGAGTCTGA TTACTIONAGG GNTCTTGGA | 360 |
| TTATTCCGGG CTTACCCCNAG AGGTTCAAT TNGTNTT | 397 |

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

| | |
|--|-----|
| GGCAGAGTTT CAAACAGGTA TCTAAGAACT TCAGTGAAGT ATTCCAGAAG TTAGTACCTG | 60 |
| GTGGCAAAGC TACTTTGGTG ATGAAGAAAAG GAGATGTGGA GGGCAGTCAG TCTCAAGATG | 120 |
| AAGGAGAAGG GAGTGGTGAG AGTGAAGAGG GGTTCCTGGCT CACAAAGCAG TGTCCCATCA | 180 |
| NTTGACCAGT TTACTIONAGT TGGAATTAGG GTGTCATTTA CAGGAAAACA AGGTGAAATG | 240 |
| AGAGAAATGC AACANCTTTC AGGTGGACAG AAATCCTTGG TAGCCCTTGC TCTGATTTTT | 300 |
| GCCATTNCAG AATGTGACCC GGCTCCTTTT ACTTGTTTGA TGAATTGACC AGGTCTNGGT | 360 |
| GTTCCAGCAC AGAAAGGCTG TTTTCAGTTT GGTTTTGGAA CTTGCTGTAC AGTTCATTTT | 420 |
| TTACACTANT TTTNGGCNGA ACTGTTGGGT CANTGNCATT T | 461 |

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

| | |
|---|-----|
| GGCAGAGCC AGTATTTGGT ATCTNTNTCT AGAGCGAGCA AGAGAGGGAG AGAGGAGGAA | 60 |
| AAAATACACA TANTACAAAC ATACATGCAT GCACACATAC ATACACATGT ATACACACAC | 120 |
| ATAATTTGAA AACTGNNTGG CACTTCAACG NTGCTGAAAT TGTTTTTAAA TTGAAGTTTC | 180 |
| TTTCTTCCAC AAAGCAGCCG TTTCTATTCA AATGGANATT CAGTACCAGA GNNTAAATGT | 240 |
| CTATGTAGTC ATACTGATTT TAGATAGNTA AGGGCTACAG CATACTANNT CGACAACCAA | 300 |
| NTTTGTCATG TGAATAAACC GTTTACTTTC AGTTGGGGCT TACCATTACT GGTTTTCCGC | 360 |
| TTGGGGGNNT TTTT | 374 |

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

| | | | | | | |
|-------------------|---------------|---------------|-----------------|--------------|------|-----|
| GGCANAGCCA GACGGA | ACTG GAAA | ACCAGC TGGAGT | TACAA TAAGAGG | CGA GAAAGAGA | AC | 60 |
| TGCACAGAAA GCATGT | CATG GAACTT | CGGC AACAGC | CAAA AACTTAA | AG GCCATGG | NAA | 120 |
| ATGCAAATTA AAAAAC | AGTT TCAGGA | CACT TGCAAGT | TACA GACCAA | ACAG TATAAAG | CAC | 180 |
| TCAAGANTCA CCAGTT | TGGTA AGTTACT | TCCA AAGATT | GAGC ACAAAC | ANT CTAAAG | AACA | 240 |
| CTGAAGGATG AGGCAG | ACAA GAAAACTT | TGC CATT | TTTGGCA GAGCAGT | TATG AACAGGG | TAT | 300 |
| AATTGNATG ATGGCCT | CTT CAAGCNTT | TAC GGCTAGT | TGA GGCTCCAG | GA GGCAGTT | GCC | 360 |
| CGGGCCTTGN GGNTAC | CG | | | | | 378 |

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

| | | | | | | |
|-------------------|---------------|--------------|---------------|-------------|------|-----|
| GGNAATGGTT ACAAAG | CAAC CATTGATT | AG AAGTATG | CGA ACTGTAAAA | GGGGAAC | TTT | 60 |
| AAAGTTAATA TCTGGT | TGGG TGAGCC | GGTC CANTGAN | CCA CAGATGGT | CG CTGAAA | ATTT | 120 |
| TGTTCCCCCT CTGTTG | GATG CAGTTCT | CAT TGTTTAT | CAG AGAAATNT | CC CAGNTGGT | AG | 180 |
| AGAACCAGGA AGTGNT | NAGT ACTATGG | CCA TAANTTG | TCA | | | 220 |

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

| | | | |
|-----------------------|-----------------------|-----------|----|
| TTTTTTTNTT TTTTTTTTTT | TTTTTTTTTT TTTTTTTTTT | TTTNNTTTN | 50 |
|-----------------------|-----------------------|-----------|----|

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

| | |
|---|-----|
| GTAATGCTCC TTTNNCCCC CGGCAAGNTC TCAACGNCCC TAAACCTCTA TATCCCCACG | 60 |
| ATGGCCTTCA TTA CT TACGT NCTCCTGGCT GGAATGGCAC TGGGCATTCA NAAAAGGTTC | 120 |
| TCCCCTGGNA GGTNNTGGGC CT | 142 |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

| | |
|---|-----|
| GGCANAGTTG GCACCCCTG GCAAGGCNGG TGGGGGCNCC GGGCCCANCC TCCCCAGGC | 60 |
| TTGGTGTACC CATGTGGTGC CTGTCGGAGT AAGGTGAACN ATGATNAGGA ATGCNAGNCT | 120 |
| GTGTAAGGCC TCCTGCCAGA AATGGTTCCA CCGTGAAGTG CCACAGGCAT GGACTAAAAG | 180 |
| CGCCTATGGG CTGCTGNACC ACTGTNAGCT TCTNCCGTCT GGGCCTGCAA TCTCTGCCTC | 240 |
| AAGACCAAGG AGATCCAGTT CTGTCTACAT CCGTNAAGNG GCATGGNGGC AGCTNGTGGC | 300 |
| TNCTAAACGA ATGGG | 315 |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

| | |
|---|-----|
| TGCCCTGGGC CTGNA CTGNG GGTTC TGGTG GGACATNATT TATTGGGAAC CATGTTGCAT | 60 |
| GCATNAAGGG AGTGNCGCAA AAGCAATGCA GCAGAACGCA GGGNGCCTCT GTGAGGNCAC | 120 |
| ATTGTGGNGG ATGGTGTTGT CTTAGNTGAG AAGATCACTG NTGGAAACTT CCTGGCT | 177 |

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

| | |
|--|-----|
| CCAGCTGAAT TTTAAAAAANT ATTTAATAGT GACAGGTCTN ACTGTNTTGC CCAGGCTCGT | 60 |
| TTTGAACCCC TGGGNCCAGG CGCTCCTCCN ACCTTGAACC TCCCAAAGTT CTGGGAGTTA | 120 |
| CACATGTGAG GCCANCACAC CAGGNCCAGA CTGGGTGAAT TTATGAANGA AATTTAACTT | 180 |
| CTGCCCACAC CGNCCNGCCT CCCC GCGAGA | 210 |

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

| | |
|---|-----|
| GGCACAGCGG GCTGAGAGGA GCGTGGCTGT CTCCTCTNTN CGNCATGGNT GTGCTCGGCC | 60 |
| ACNGATATCG GTGTACTCCG AAAAGGGGGG AGTCATTTGG CAAAAATGTC ACTTTGCCTG | 120 |
| GCTGTATTCA AGGCTCCTAT TCGACCAGAT ATNGTGAAC TGTTCATCG CGNACTNTGC | 180 |
| GNCAAAAACA ACAGNCAG | 198 |

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

| | |
|---|-----|
| CACATGAAGT GTTACAAGTG TTGAGGACTG CGGGAAGCCC CTGTNCGNTT GAGGCAGATG | 60 |
| ACAATNGCTG CTTCCCCCTG GGACGNTCAN TGCTGTGTGCG | 100 |

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

| | |
|--|----|
| GGCAGAGCGA AAAAATTCC ACTTCCACGA CTGGAGTGTG TGCCAGCCTG TGGTGAGGGC | 60 |
|--|----|

| | |
|---|-----|
| TTCTACCCAG AAAGAGATGC CGGGCTTGCC CCACAAAGTG TGTTCGAAGG TGTGAACGAG | 120 |
| AACTGCTTGT AGCTGTGCAG GCTCCAGCAG GNAACTGTGA GCAGGTGTGA ANACGGGCTT | 180 |
| CACACAGCTG GGGNACCTNC CTGCATCACC AACCACACGT GNCAGCAACG CTGACGAAGA | 240 |
| ACATTCTGCA AGAATGGTGT AAGTNCCAAC CGGCTGTGCG AAACGNTAAG CTNCTTGCAT | 300 |
| TCCAGTTTCT GGCTGGCCNG CACGTTGACC TCCTGGGNCC GGGGT | 345 |

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

| | |
|---|-----|
| CATGCACTTT GCCTTCGGAA ATGGCTGTAC ATTCAAGATA CTTGTCCAAT GTGCCATCAG | 60 |
| AAAGTATACA TCGAAGANAT NATCAAGGAT AATTCAAATG TATCTAACAA CAATGGATTT | 120 |
| ATTCCACCCA ATGAAACTCC AGAGGAAGCT GTAAGAGAAG CTGCTGCTGA ATCTGACAGG | 180 |
| GAATTGAACG ANGATGACAG TACAGATTGT GAATGATGAT GTTCAAAGAG AAAGAAATGG | 240 |
| GAGTGATTCA GCACACAGGC GCANAGCTGA AGANTTTAAT GATGGATTAC TGACTGATGA | 300 |
| AATTAGCTTT TATTAATGGT TGAGGTATTT GTTTNAATTT CCAGTTCCNT CCAAATGGGG | 360 |
| TAATATCCCT TCACCTTCAT GTGTAACCAG GCACAAAAAC AGTTTCATGT GGATCCGTGG | 420 |
| ATGGGTTTTN CNTTTACNGT NGATGTGNTA C | 451 |

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

| | |
|---|-----|
| GGCACGAGGC CAACGGTACC TGTTTATGCG AGGAGGGCTA CGTTGGTGAG GACTGCGGCC | 60 |
| AGCGGCAGTN TCTGANTGCC TGCAGTGGGC GAGGACAATN TGAGGAGGGG CTCTGCGTCT | 120 |
| NTNAAAGAGG GCTACCAGGG CCCTGACTGC TCAGCATTGC CCCTCCAGAG GACTTGCGAG | 180 |
| TGGCTGGTAT CACGAACAGG TCCATTGAGC TGGAATGGGA CGGGCCGATG GCAGTNACGG | 240 |
| AATATGTGAT CTCTTACCAG CCGACGGCCC TGGGGGGTNT CCCAGNTCCA GCANCGGGTG | 300 |

CCTGGAGATT TGAGTGGTGT CACCATGANG GAGCTGGAGC CAGATCTTTC CATNCTCAAG 360
GGCTACAATT TAAGACGTTC ACAGNGACCA CCTTGGAGTG CAANGGGNGC CTTTT 415

(2) INFORMATION FOR SEQ ID NO:308:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GGCANAGGGT AGACGGAGCC GCCATCCGCA CTGCAGTCCC CTCTCGGCTG CTTGCTCAGC 60
CTGCTCCGGC CCCGGTCTGC CCCCACGGAG CTCCGGGCAC TTGTGGCAGA CGAGCCCGAG 120
GACCTGGACA CGGAGGACGA GGGCCTCATC AGCTTCGAGG AGGAGCGGGC CCAGCTGTCC 180
TTCAACACGG ACACGCTCTG CTGACCACCC AGAGCTGGGC CANGGAGGAC ACGCTCCACT 240
GACCACCCAG AGCTNGGCCA AGGACTTAAC AATGGGGGAC ANAAGTTCCC CANTTGCCTG 300
GCNAAGGGCT GG 312

(2) INFORMATION FOR SEQ ID NO:309:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

ACAGGAACCT NGTGTCTNGT GGCTNGCCCG NGTGCGTGAT NATGAAGGGA GATTCTATG 60
TCATTGAATA TGCTGCCTGT AATGCCACCT ACAATGGAAA TTGTTNACCC TGGGAGCGAC 120
TTCGGCCAGN TAATCCCAAT CCCCTTGGCA ACCAAAGGNC AGCTTCTTGA AGGTTACCAT 180
GGGCTGTGCC CGNGGGATCT NGAGAGNAAG 210

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAAAGNGGAC GCCCAGGGGT GCTGCATNGC ACAACCAAGT TTTTGTGACAG CGGGAGNGGN 60
 CCCGGGNGCA GAGGTAGTAC GCTCAACAAG ATGTGTTAAA GAAATCTTAC TCCAAGGN 118

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

CACCTCCGAG AGCCTGGATG TNATGGCGTC ACAGAAGAGA CCCTTCCCAG NGGCACGGNT 60
 CCAAGTACCT GGNCCACAGC AAGTGACCAT NGGACCATGC CAGG 104

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ACTTTGGACG TTCAATGTCT GTGGAGAAGA TAGACATTAG TCCGGTTTTN CTTCAAAAAG 60
 GAAGCACAAA GATTGCNCTA TATGGTTTAG GATCCATTCC AGATGAAAGG CTCTATCGAA 120
 TGTTTGTNAN TAAAAAAGTA ACAATGTTGA GACCAAAGGN AAGATGAGAA CTCTTGTTT 180
 AACTTNTTTT TGAATTCATC AGAACAGGTG TAAACATGG GAGTACTAAC TTNNTTCCAG 240
 AACAATTTT GGTGANTTC ATTGANTCTT 270

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GGCACGAGGT ATTTTNACT GGATATTGCC TTTNTNCTTT TNCTTGGTGC TGCCTTGTTA 60
 TACTTNCTCT TGTCTGGGT GANAAAATTT ATCTACAGAN NAATCAAAAG TTTGTGGTCT 120
 AGAAATAAGC ATAGCACAGT TAATGGNCAT TACCACAATG GAATCCTCAA TGGCAAGTAC 180

| | |
|--|-----|
| ANAAGAAATG GCCATATTAA ACATGAAAAG AAAGTGAAAT GAGCCAACAG CCCAGGTGAT | 240 |
| AGAAATAAAT TGGTTCACCTC ATTGAATTTT TATTGCTATT ATTTAGTCTA ACAGCTTACT | 300 |
| TAAAAGTAAA ACATCAGTAA ACAATTCTTA ACATGCCCTT ATGAGANCTA CTTAATGAAA | 360 |
| TTCCTGTGGG ATTNAAGGTG GCTGTAAAAA GCACAAACCT AAAATNGCAG AAATGTNNTT | 420 |
| NATTTCAAAT ACTGATGTAG GGGGTTTTTG GCA | 453 |

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

| | |
|---|-----|
| TTACAGAGAA CATATGCACA CTANNNNGAT CTCACAATTA TCAACAATGA AATTNATGAG | 60 |
| ACAATCAGAC ATCTGGNGGA AGCTGTTGAG CTCGTGTGCA CAGCCCCACA GTGGGTCCCT | 120 |
| GTCTCCTGGG NCTATTAGGN CTNTCCCCAG ATATCTGGGG CATAACTGGG AGCACCTCAT | 180 |
| TTGTGGAAAA GCCTCTTTGT TATCGGGCTT GTGTCAGCAG GTCATGGTCC CTAGAGACTA | 240 |
| CCTAGTTGTT AGTGTTGACC TACATTTGAT AATTAATTGT CAGTTNCNAN TAGTTANGGG | 300 |
| GGGGGAAAAA NCATTTACAC ACT | 323 |

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

| | |
|---|-----|
| GGCANGAGGN GCCCGCGGGA TTGTTCAACC GCGCCGTGAG CCGGCTGAGC AGGAAGCGGC | 60 |
| CGCCGTCAGA CATCCACGAC AGCGATGGCA GTTCCAGCAG CAGCCACCAG AGCCTCAAGA | 120 |
| GCACAGCCAA ATGGGCGGNC ATCCCTGGAG AATCTGCTGG AAGACCCAGA AGGCGTGAAA | 180 |
| AGATTTAGGG AATTTTAAA AAAGGAATTC AGTGAAGAAA ATNTTTTGT TTGGCTAGCA | 240 |
| TGTGAAGATT TTAAGGAAAA TNNCAAGGTT AAGACGCNGA TGCAGGAAAA GGCAAAGGNG | 300 |
| GTTCTACATG ACCTTTTNT TCCAGCAAGG GCCTTCNTCA CAGGTCAACG TTGTAGGGGG | 360 |
| CCAATTTTCG GGTTCACNG GAAAGNTTCC T | 391 |

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

| | |
|---|-----|
| AAACAGGCTG AGGAGGTTCC GAGGCTCAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN | 60 |
| ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGGAAGGAG AGAGTAGTGA CACTCAGGAT | 120 |
| CCAAAAGCTA GCCCTGCCCA CCCAGCCCC TGGACCTGCT TACCTGGGTG TGCNACCTGC | 180 |
| TCCGGGGGGT GGAGGTGCTC CCCACAGTCC GGGCCAGGAC AGCCTCAGGG GAGAGTNAAG | 240 |
| GCCTGCAAGA GGGNAAGCGG AGACAAGGAG GGTGTCCAGG GCTAGGGAGT NCCGGTTGAA | 300 |
| ACCAGTTTTG TCCCTGTTGC AAGNTTCCAG GTTNCCGNTN GACAAAACAA GCAGG | 355 |

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

| | |
|--|-----|
| AAACAGGCTG AGGAGGTTCC GAGGCTCAAA GGAGGGGAAG GAGCCCCGAG GAGGCTCTGN | 60 |
| ANTTGATGTC ACTTAGGTCC AGGGCATCCN TGGGAAGGAGA GAGTAGTGAC ACTCAGGATC | 120 |
| CAAAANCTAG CCCTGCCCAC CCCAGCCCCT GGNACCTGCT TACCTGGGTG TGCACCTGCT | 180 |
| CCGGGGGGTG GAGGTGCTCC CCACAGTCCG GGCCAGGACA GCCTCAGGGG AGAGTNAAGG | 240 |
| CCTGCAGNAG GGNAGCGGAG ACAAGGAGGG TGTCCAGGGC TAGGGAGTNC CGGATGAAAC | 300 |
| CAGTTTGTTT CCTGTGCAAG TTCCAGGNTC CCGTTGACAA ACAGCAAGGT GCCACATTCA | 360 |
| GGNCATTAAA AATTNGTGCA TTTGAAGCAG CATTTGACAG TTTNAAATTC TTCCTTTGNT | 420 |
| GNATTCCAGG CCCTTTTTCT TTAAACAAN GGATTGGGG CATT | 465 |

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

| | |
|---|-----|
| TGACCAAGCT TCGGGANGAT GGGCAGGGAG AAATGCCACC ANTACTGGCC AGCAAAGCGC | 60 |
| TTCTGCTCGC TAACCANTAC TTTTGTGTTA ACCCGATGGC TGANTACAAC ATGCCCCATT | 120 |
| ATATCCTGCT TGANTTTCCA AGGTCACGGG ATGCCCCGGA ATGGGCAGTG CAAGGAACAA | 180 |
| TCCGGGCAGT TCCANTTGCA NAGACTGGCC AGAGCAGGGC GTGCCCAAGA ANAGGCGAAG | 240 |
| GGAATTGCAT TGANCTTCAT CGGGGCAGGT GCNATAAGAN CCCAAGGAGC CAGTTTTGGG | 300 |
| ACCAGGATGG GGCCTATNCA CGGGTGGCAC TGCANT | 336 |

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

| | |
|---|-----|
| GGCACGAGGT TATTTTTTAC TGGATATTGC CTTTNTNCTT TTNCTTGGTG CTGCCTTGTT | 60 |
| ATACTTTCTC TTGTCTTGGG TGACAAAATT TATCTACAGA NNAATCAAAA GTTTGTGGTC | 120 |
| TAGAAATAAG CATAGCACAG TTAATGGGAC ATTACCACAA TGAATCCTC AATGGCAAGT | 180 |
| ACANAAGAAA TGGCCATATT AAACATGAAA AGAAAGTGGA AATGAGCCAA CAGCCCAGGT | 240 |
| GATAGNATAA ATTGGTTCAC TCATTGAATT TTTATTGCCC ATTATTNGT CTAACAGCTA | 300 |
| CTTAAAGGTA AAACCATCCG TNAAACCATT CTNACCAGGC CCTTTNGGGG TCCN | 354 |

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

| | |
|--|-----|
| GTGTTTCGANT GGAACATGCT CAAATTTGGT GCCAGCCGGG CCGCCGATGA CGCCGAGCGG | 60 |
| GAAGNCCAGG GACCGAAAGG AGCGGCTGAA AACTCGCGG AACCCGGCTA CCCGNGGCCT | 120 |
| CCCTTCCACA GCCTCCGGCC GCCTGCGGGG GAACGCAGAA GTGGCTCCCC NCANACCCCT | 180 |
| TNACCCCTAC CTTCANACAC GGNTTAACAN CTTCCCCCG GCCCGTTTTT CGGCATNGGA | 240 |

GAGAGAGCGG AAAGTGAAGT TATGCGGGNT GCAACCGGGG GGGGCCCCCG TTAAACATT 300
TTCCTTGGTT NCGAACCTTA ANAGGNCCGA CAAAGATTAN CTTTT 345

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GGCACGAGGG AAGGTGAAGA AAACGGAGAT AATACTATTT CCACTGGTCT GTTGACAGT 60
GAGGCTGACA GATGCCCAAT ATGTCTTAAT TGTCTATTAG AAAAGGAAGT TGGTTTTCCA 120
GAAAGCTGTA ATCATGTCTT CTGTATGACT TGTATTCTTA AATGGGCAGA GACACTGGCT 180
TCATGTCCTA TTGACCGTNA AACCTTTTCA GGCAGTGTTT AAATTCAGTG CATTGGGAAG 240
GTTATGTTAA GGTTCCAAGT AAAAAACAG CTGAGGGGAA ACAAAGNCC AGGAAAAATG 300
GAAACTCCT TTGGGGAAAC AGGTCTCCNG TCCNGGAAAA TTTCTTAAAA GGCTGTTTTA 360
GGGNGGAAAA GNCCCT 376

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATGATGAGT TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGATAA TGTGGAAGCC 60
AGGAGATACG TNGACAGTCG TTGCTTAGCA AATCTAAGGC CTCTTTTAGA TTCTGGAACA 120
ATGGGCACTA AGGGACACAC TGAAGTTATT GTACCGCATT TGAAGTGAAGT CTTACAATAG 180
TCATCGGGAT CCCCCAGAAG AGGAAATACC ATTTGTACTC TAAATCCTT TCCAGCTGCT 240
ATTGAACATA CCATACAGTG GGGCAAGAGA TAAGTTTGA AAGTNCCTT TTCCCACAAA 300
CCTTCATGTT TAACAAATTT TGGGCAANCN NTTTCATCTGC AGGAGGAGTC TTACAGAGGT 360
TCCGGGTGGG NCANATTTGG GANGGNTTTT TCAAGTTTAA AAGGTNCCTT GGCCGGGGCC 420
CGGGAATTGG TCCCCGT 437

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

| | |
|---|-----|
| AATGNTGAGA TCTATACTAA ACAAGATGTA ATTATTACAG CATTAGNTAA TGTGGNAGCC | 60 |
| AGGNGATACG TAGACAGTNG TTGCTTAGCA AATCTAAGGC CTCTTTTAGA ATCTGGANCA | 120 |
| ATGGGCACTA AGGGACACAC TNCAAGTTAT TGTCCCNCA TTNCTGGNG TCTTCNCAAN | 180 |
| AGTCCATCGG GNTCCCCCAG AAGCGGGANA TCACNTTGG GTACTCTAAA AATCCTTTTC | 240 |
| CAGGTGCTTT TNGAACNTGN CCCTAACATG GGGCAAGAGA TAAGTTTNAAGTTCCTTTT | 300 |
| TCCCACAAAC CTTNTTTTTT | 320 |

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

| | |
|---|-----|
| GGCAGGAGCT GTCCTGACCC TNAGGCCTAT GCTCAGTCCA TCGCAGACGN CCGGNTCGTG | 60 |
| TTTGAAATGG GCACCGAGCT GGGTCACAAG ATGCACGTNC TGGGACCTTG GTGGTGGCTT | 120 |
| CCCTGGNCAC AAAAGGGGCC AAAGTGAAGA TTTGAAGAGA TTGCTTCCGT GAATCAACTC | 180 |
| AGCCTTGGAC CTGTACTTCC CAGAGGGCTG TGGCGTGGGA CATCTTTGCT GAGCTGGGGC | 240 |
| GCTTACTACG TGAACCTCGG CCTTCACTGT GGGCAGTCAG CATCATTGCC AAGAAAGGAG | 300 |
| GTTCTGCTTA GACCAGCCTG GGCAGGGAGG AGGNAAAATG GTTCCANCT CCAAGACCAT | 360 |
| CGTGTTACCA CCTTGNATGA GGGCGTGTAT GGGATCTTTC AANTCATNC | 409 |

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

| | |
|---|-----|
| AATGTGATGG TGTATGTTGG GATTCCCATC GGGGAGGGTG CTCATNAATG AAGAGGTACT | 60 |
| CAAGACAATT NACGAGGGAG ATGCCGATGA GGTGACGAAG CAGAGGATTC ATGATGGAAA | 120 |
| AAAGAAGCCA GGTGCTTTNT NGCACATCTT TNCAGCCAAG GATGCAGAGA AGATCCNNGA | 180 |
| GCTGCTCCGA AA | 192 |

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

| | |
|--|-----|
| AGCTCCGCAG GCACTNCANT AAAAGCCTGA CCCAAACATT TGGAGATGAC AAGTACTCAC | 60 |
| TGGCCCGCAA GNGGTGCTCA CCAACATGTG CTCCCGGNCC ATGCAGATGG CACTGTACTT | 120 |
| CTGCTCGGGG CTGCTGCAGG GACCCAGCGC ATTCCGGCAC TACGCGCTCA ATGTGCCCCCT | 180 |
| GTACACACAC TTCACCTCGC CCATCCGCCG CTTTGCCGAC GTCCTGGTGC ACCGCCTCCT | 240 |
| GGCTGCCGCG TTANGCTTTT AGGGGAGCGA TTAGACATGG TCGCCTGGTN ACCCTGCAGA | 300 |
| AACAGGCGGG ACCATGTTAA CGGACCGTCG GCATGGGTNC CCAAGCGNGT GCAGGAGTTT | 360 |
| CAGTTACCAT TTTNTTNTTT GGTGTTTTT GGGTTCAAGG ANGAGTGG | 408 |

(2) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

| | |
|---|-----|
| GGCACCAGTA CATGGCTACA TTTTATGAAT TCTTCAATGA GCAGAAATAT GCTGATGCGG | 60 |
| TGAAGAACTT CTTGGATCTG ATTTCTGCTT CGGGGAGAAG AGACCCCAAG AGTGTTGAGC | 120 |
| AGCCCATCGT GCTTAAAGAA GGGTTCATGA ATCAAGAAGG GCCCAAGGAC GGAAGCGCTT | 180 |
| TGGGATGAAG AATTTTAAAG AAGAGATGGT TTCGCTTGAC CAACCATGGA ATTTACCTAC | 240 |
| CACAAAAGCA AAGGGGACCA GCCTCTCTAC AGCATTCCCA TCGAGGAACA TCCTGGGCAG | 300 |
| TGGAGGAAGC TNGAGGAGGG AGTGTTTTCA AAATGGAAAA ACNTGTTTCC AGGTNCATTC | 360 |
| CAGTCCAGAG CGTTGNNCTG TTACATCCAG GG | 392 |

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

| | |
|--|-----|
| GGCANAGGGG AGCTGCCTGG ACCAGCCCAA TGGTTATAAC TCCCACTGCC CGCATGGTTG | 60 |
| GGTGGGAGCA AACTGTGAGA TCCACCTCCA ATGGAAGTCC GGGCACATGG CGGAGAGCCT | 120 |
| CACCAACATG CCACGGCACT CCCTCTACAT CATCATTGGA GCCCTCTGCG TGGCCTTCAT | 180 |
| CCTTATGCTG ATCATCCTGA TCGTGGGGAT TTGCCGCATC AGCCGCATTG AATACCAGGG | 240 |
| TTTTTCCAGG GCCAGCCTAT AAGGAGTTCT ACAACTGCCG CAGCATTCTGA CAGCGAGTTT | 300 |
| CAGCAATGCC CATTGCATTG CATTCCGGCA TGCCCAGGTT TTGGAAAGAA AATCCCGGGC | 360 |
| CTGCAANTGT ATGATGTTGA GNCCCCATNG GCNTNTNAAG GTTTACAGTN CCTGNTTGAC | 420 |
| AAAANCCTTG GTCANAATGN TTNAAAANTA AAGGTTTGTA AAACTTTTTT TGGGTTATTT | 480 |
| TTTCAAAAGG TGGGGTTTTT CACCC | 505 |

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

| | |
|---|-----|
| GGCAGAGCCA GAACCTACTG GACCGGGATG TTACCTCCAA GTCCGACCCC TTCTGTGTCC | 60 |
| TCTTTACAGA GAACAATGGC AGATGGNTCG AGTACGACAG GACAGAAACC GCGATCAACA | 120 |
| ACCTCAACCC CGCCTTCTCC AAGAAGTTCG TGCTTGACTA CCACTTCGAG GAGGTACAGA | 180 |
| AGCTCAAGTT CGCGCTCTTT GACCAGGACA AGTCCAGTAT GCGGCTGGAC GAGCATGAAC | 240 |
| TTCTTGGGCC AGTTCTCCTG CAGCCTGGGN ACGATTGCTT TCCAGCAAGA AGATCANTAG | 300 |
| GCCTCTGCTG CTGCTGAATG ACAAGCCTGC GGGGAAGGG CTTTGATTAA GATTGCTTGC | 360 |
| CCCAGGAGTT GTTCCGACAA ACCGGGTTC AATCATTAAG NCTGGGGGGG CAAGAAGGTT | 420 |
| TGNNCAAGNA AGGGACCCTT TTTGGGAAGT TCANA | 455 |

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

| | |
|---|-----|
| CCTTTNAGGA TGCTCCTACA GCAGCTGCCT AATACTTTNA GTTGCAGTNA GATGTTGGCT | 60 |
| GGGACCACAG TCATCTAAGG NTACTGCTCA AGATGGCTGT TGTNTNGNAA ACTCAGCTGG | 120 |
| GGCTACTGAT CAGAGCACCT GNCATGTGGC TGTCNAGCAA GGCAATGTTA AGGAACATGG | 180 |
| GTGACATTTG GAGGTCAAAT TTCAGATGAG GTTGCTGAAC GGCTGATGAC CATCGCCTAT | 240 |
| GAAAGTGGTG TTAACCTCTT TGAATACTGC CGAAGTNTTA TGCTGCTGGG AAAGGCTGAA | 300 |
| GTGATTTCTG GGGAGCCATC CTTCAGGAGG AAAGGCTGGA GGAGGTTCCA TTTGGTTCAT | 360 |
| AAACAACCAA ACTTTACTGG GGTGGNAAA GCNTGNAACC NGAAGAGGGG TTNTTAAGAA | 420 |
| AGCCTTTTTT TTGA | 434 |

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

| | |
|--|-----|
| GANAGACCCT TTAAGTNTCC TGANTNTGGA AAAGNCTTCA AAGAAAAGTC AACTGTCATC | 60 |
| ATACATTACA GGA CTCACAC AGGTGAAAAA CCTTATGAAT GTAATGATTG TGGAAAAGCC | 120 |
| TTCAC TCAGT AAGTCCAACC TCATTGGTCC ATCCAGAAAA CCCACACTGG TGAGAAAACC | 180 |
| TATGGTTGCN CTTAAATNTG GAGTNTCTTT ACATTACAGA AGCTTGATCC TTAGTTGATN | 240 |
| NC | 242 |

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

| | |
|---|-----|
| TTATTGAGAA TCTCTTTGCA TTAGCTGGTG ATGAAGAACC AGAGGTACGG AAAAATGTGT | 60 |
| GCCGAGCACT TGTAATGTTG CTCGAAGTTC GAATGGATNG CCTGCTTCCT CACATGACAT | 120 |
| AATATAGTTG AGTACATGCT ACAGAGGACT GAAGATCAAG ATGAAAATGT GGCTTTAGNA | 180 |
| GNCTGTGAAA TTTTGGCTAA CTTTAGCTGA ACAGCCANTA TGCAAAGATG TACTAGTAAG | 240 |
| GCATCTTCCT AAGTTTGATT CCTGTGTTNA GTGAATGGGC ATGAAGTAAC TTNGGACATN | 300 |
| GATATTTATC CCTACTTAAA GGGTNGATGT TTNGAAGGAA GTCGGAAACG G | 351 |

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

| | |
|--|-----|
| GGCACGAGCT ATGCCTTAAA ACTNCCGAGC CCCACTCCAT GTAATAGGAT TCCTGGGCTT | 60 |
| CCTCAATGGG GGTTTCATGTN CTTGGACTGC GGGCCCTCAG TCCTTAACTG GAAAGTGAAC | 120 |
| CGTCCACTGC CCCATGGAGC CCATCTGGAC ACAGCACAGC CCCAAAACCG TTAGCAGCTG | 180 |
| GCTCTGTTTC CAAGCCTGGG GAGGGGTTCC TCAGTGCCAG GAGTTGGGGA CAGGCTGGGG | 240 |
| ATCCAAGCTG CTTGAGGGGG TCAACCTTGG GACCAAATTG CCTTAAAGCC TGTGGTTAAA | 300 |
| AGGGCTTNAG GGAAGGTTA ATGGGGCCAC NTGCTGGGAA GTTGGCCAGT TGCCCCGGTTG | 360 |
| GCAATGGTGT GAATNTTTTG GGCCNTGTTC CCTGCCCTGG GGTTCANCA AGTTNATCCC | 420 |
| TCCTTNTTNT NTNTNCTTTG GGGTTTGTTC CNGTNGTCAT NGGTTAATNT CCCCTAGTTT | 480 |
| CAAGTTTAC ATAGGCCTC C | 501 |

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

| | |
|---|-----|
| GGCACAGTAG AAATGGAAAG AAGGNGGGGA TTGTGGTGGC TTGTGCCAG ACTGGAGCCT | 60 |
| GGANTAATGG CAGCTCAGTC AAGGAGCAGA CCTGGNACTG GAACAGNTTG AAAACCAGNG | 120 |
| TTTTGTACTT TGAGAGGAGA GATTCCANGC TGCTTCTTGA ATCAATCCAA NTTTCATTTA | 180 |

CAGCTCTNGG AACACTTTGG GNGCTGATTT GTCTCTTTAG GGGGNCATCC CCAACATGGT
TGAATTCCAA CTNCTTCAGA TCTTGNGGCT T

240

271

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

TGTAAATTTA TTGTGATATT TTANGGTTTT CCCCCCTTA TTNCCGTAG TTGTATTTTA 60
AAAGATTCCG CTCTGTATTA TTTGAATCAG TCTGCCGAGA ATCCATGTAT ATATTTGNAA 120
CTAATATCAT CCTTATGAAC AGGTACANTT TCAACTTAAG TTTNNACTCC ATTATGNCAC 180
AGTTTGAGGA TAAATGAAAT TTT 203

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GGCAGGAGNG CAGACTATTG CCTCAAGGAA CAGTCATTTT TGNAGATATC AGCATTGGAC 60
ATTTTGAAGG AACTNGAACC AAAGTTATCC CAAAAGTACC CAGTAAAAAC CAGAATGAAC 120
CCATTGGGCA GGACGCATCA AAGTTGACTT TGTGAATCCC TAAAGAACTT CCCTTTGGAG 180
ACAAAGATGA CGAAATCCAA GGTGGACCTT GCTGGGAAGG TGACCATGTT AGGTTTAAAT 240
NATTTNCAAC AGACCGACGT GGNCAAATTT AGGAGCGGGG CANCCCAATA TAGNAAGTTT 300
CTGT 304

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

| | |
|---|-----|
| GGCACGAGCT GGGGCCACGC TGGTCTGGGA ATAGTTGGGC AGGGAGGCTG TCTACCTGGT | 60 |
| CTCCAGAATG GACGGCCCTG TGGCAGAGCA TGCNANGCAG GAGCCCTTTN ACGTGGTNAC | 120 |
| ACCTCTTTTG GAGAGNTGGG CGCTGTCCCA GGTGGCGGGC ATGCCTGTTT TCCTCAAGTN | 180 |
| TGAAGAATGT GCAGCCCAGC GGCTCCTTCA AGATTGCGGG CATTGGGCAT TTCTGCCAGG | 240 |
| AGATGGCCAA GAAGGGATGC AGACACCTGG TGTGCCTTCT TNAGGGGGTA ATGCGGGCAT | 300 |
| CGCTGCTGCC TATGCNTGCT AGGAAGTTGG GCATTCTCTG CACCATCGTG CTTCCCCGAA | 360 |
| AGCACCTTCC CTGCCANGTG GGTGCCAGAG GCTTGCAAGG GGGAGGGGN CCNAGGGTTC | 420 |
| CAGTTGACTG GNAAAGGTTT TTGGAACGAG GNCCATTTT | 459 |

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

| | |
|---|-----|
| GGCACGAGNA AAATTGGAAG AGAAAATACT ATTCTGGGTT GGGTATCCTT AAGGATTAGA | 60 |
| ACCGCAGGAC TCCTCCAAGT CTGTAGGCCT ACTTTCTCTA TGAGAATCGT NATGTTAGTC | 120 |
| CATCTAACTG AACCTCATCT CTCTTTCAAT GCAGGTATCA CTACCATTAA AGTTAACATT | 180 |
| CGTAAATGCC AATTCCCTGG GNNGAGGCTT CCATTGCTGG ACCTGCGATG TCCGGTGNTG | 240 |
| NGGCACCCTA CAGTCCTANT TGGACTGAAC AGGCCTGATG GAGGTTGTGG CTGGNCTCAG | 300 |
| TTACACCTAA GAAGNTTTGG GGCAAGGTTT ATTCTNNTGC TTTTAAAAAG TGGCATGGAA | 360 |
| CTGTAGTGGT TTNAACATT CATNTNGTTT AACAGGGGTC GTAAGCCTGG TTTGG | 415 |

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

| | |
|---|-----|
| TGGNCTNATT CCCCAGCATG AAGGCCCTGA GCCCGGTNCC CGGNTGCAAC NAAGGCGGTG | 60 |
| TCCTGCCTGT GGGAAAGCAT CTGGCCATCG CCCGGGGCCG AGGGAAAGGG CCCGGNAAGC | 120 |
| TNAGGAGCCG CTGAANCTTG CTGGGACGAN ATGNAACCAC TG | 162 |

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

| | |
|---|-----|
| CGGCATTGCG NCANAANGNC CNAAGGAGGA GTCCTTCGGG CCTGTAATGA TCATCTCTCG | 60 |
| GTTTGCTGAT GGGGACTTGG AATGCCGTGC TGTTTCGGGC CAATGCCACG GAANTTTGGC | 120 |
| CTGGNTTNTG GTGTCTTCAC NAGGAACATT NNCAAGGCC TGTANTNAGT GAACAAGCTC | 180 |
| CAGGNAGGCA CTGTGTTTGT NAAACACGTA CAACAAGACC GACGTNGCCG NTTCCCTTTC | 240 |
| GGAAGGGATT CAAACAGTCT GGGATTTGGG CAAAGATTCT TAGGGAGAGG CGGGNTCTGA | 300 |
| AACGAGTNAC CTGNNGGGTT AAAGACCAGT GAACCTTTCG GAATACTTNA AGNAAAGGTC | 360 |
| TTTGTGAAGG AAG | 373 |

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

| | |
|---|-----|
| GGCAGGAGCA ACCCGGGNGG TCGCCACGCA CCGCATGCNA CCTNANCCCC AGCCCCGATG | 60 |
| GTNAGGCCTA CACACTGGCT TCGAGACCAC CCGTCCGCCT CAATNATGTC ATGCTCAGGC | 120 |
| TGGTGACGGA GCTGCGCTGG CAGAAGTNCG TNATNTTCTA CGACAGCAAG TATGGTGAGT | 180 |
| TGTCCGGCAG GCGAAGCTGG GGCTGCTTGG GGACAGGGAT GGCCAGATGC TGGGAGACCT | 240 |
| GAGAAGTGGG TGGGGCCCTG GACCGGTNGG GGGTGGTCTG TGCTGAGTGG GCCTCCAG | 298 |

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

| | |
|--|-----|
| TTAAGTGTAG AATCAATGAA AAGACTTAAC AGCCTTCTCA ATATCCCAGA AAAGTGTCCCT | 60 |
| GAACAGGGAG GGATGATTTG GAAGATATCT GAAGATAAAC AGCTAGCAGT TTGCCTGAAA | 120 |
| TATGCTGGAG TATTTNNAGA AAATGCAGAA GATGCTGATG GAAAAGATGT ATTTANTACC | 180 |
| AAATCTGTTG GGCTTTCTAT TAAAGAGGCA ATGACTTATC ACCCCAACCA GGTAGTAGAA | 240 |
| GGCTGTTGTT CAGATATGGC TGTTACTTTT AATGGACTGA CTCCAAATCA GATGCATGTG | 300 |
| CTTGATGTAT GGGGTATACC GCCTTAGGGC ATTTGGGNCA TATTTTCCAN TGATGCATTG | 360 |
| GTTTTCTTAC CTCCAANGGT TCNGCACATG NANTGAGANT GGTAGAAAGC GTGATATGAN | 420 |
| NTTGTNTAGG ACTGTGTTGT NCATANTTGT GGTAGTAACC ACANNTCCAT TACAGCTGTA | 480 |
| NGTTTCTCTT CCTTTCNAAT TTGGTG | 506 |

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

| | |
|---|-----|
| GGCAGAGTNG AAGATGGGGA CCACGGTCTC ATTCAGGGGA TCCTTGTTTT TTTCCAGCCA | 60 |
| GCCCACAATG CTGTANGGCA CCTGGAGAGA CAAGTCAGGT GCTGAGCCCG NGTGGGAGAC | 120 |
| CTGGAGCAGG GCGNGAGGAG ACNGGCCGAG GGCTGGGGTT CNAGNAAGCA CCTACCACGC | 180 |
| CTGCTTAGTG GACCACCTCG AAAGTGGGCC TGGTACTTGC GCCTTCTTGT CAGGCCGAGG | 240 |
| CTGCTGGAAT TTGGGTGACT TCCCCGCGTG GTTNTGCGTA GAGCTTGGCC CGGAAAGCTG | 300 |
| GCGTCTGAGG CCTTNGGGAA CATGCATTCC TNCTACCAGG TTGGACAGGT TGCCAGTGG | 360 |
| CTGGGCAACA GAACGAGCTT GAAAACCACC ATTCAAGCCA TNCCATNGTA AAGTACTGT | 420 |
| AACCCTGGTT CCCCAGTCCA ANTTNCTTTT GGGAGCNTNC CNAAATCCC CAGTTTCAGC | 480 |
| ANTNTCCCCG GNTGGTTCAG ACAACACAAC CATTC | 515 |

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

| | |
|---|-----|
| AGAACTAGTG GATCCCCCGG NCTGCAGGAA TTCGGCANAG GGNAGCGTGC NGNATTCAAA | 60 |
| GCTTACCGAG ATGCTGATGG CCTGGTTATT GACCAGCATG AAATATTTTT GGACTIONAG | 120 |
| CTGGAAAGGA CTCTCAAAGG GTGGATCCCT TGGNCGACTT GGAGGCGGTC TTGGGGGAAA | 180 |
| AAAGGAGTGC TGGGNCAACT GAAAATTTGG GGGACGGGAC CGGCCTTTTC GAAAACCTAT | 240 |
| TAAACTTGCC CGTTGTTNAN AAACGACCTC TATAGAGAGG GAAAACGGNG NAAGGCGGGN | 300 |
| | 300 |

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

| | |
|---|-----|
| AGGGAGCACC GGAATGCCC AAGGGGATCG TCCATACCCA GGCAGGCTAC CTGCTCTATG | 60 |
| CCGCCCTGAC TCACAAGCTT GTGTTTAANC ACCAGCCAGG TGACATCTTT GGCTGTNTGG | 120 |
| CNGGACATCG GNTGGATTAC AGGGACACAG CTNACGTGGT GTATGGGCCT CTCTGCAATG | 180 |
| GTGCCACCAG CGTCCTTTTT GAAAAGCACC CCAGTTTATC CCAATGACTG GTNCGGTACT | 240 |
| GGGAAGACAG TAGAGAAGGT TGGAAGATCC ANTCNAGTTT CTGATGNGGC GGNCGCAACG | 300 |
| GTCTGTTCCG GGCTGGTTG | 319 |

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

| | |
|---|-----|
| GGCAGGAGCT CGTCCTTGNA AACTNATCCA ACAGCCTCAA AATGCGAGCN TGTTTGTNAA | 60 |
| CAGACCCGCC CTCGGAATCC TGCCTCCGGA GAACTTTGTG GNAGAAGCTC CGGCAGTCCT | 120 |
| TGCTCTCGGT GGCTCCCAA GGGATGTTCC CAGCTCATCA CCATGGCCTG CGGCTCCTGC | 180 |
| TCCAATGAAA ACGCCTTAAA GACCATCTTC ATGTGGTACC GGAGNAAGGA AAGAGGGCAG | 240 |
| AGGGGCTTTT TCCCAGGAGG NGCTGGAGAC GTGCATGNTT AAACCAGGCC CCTGGNTGCC | 300 |
| CCGATTACAG TATCCTTTNC TTCATGGGGG GGNTTNCCTT GGGAGGACCC TGGGTTTGTT | 360 |

TAGNGGCCCA GGAAATTTTA AAGCCCTTCA AAAGGTTGGG NAATCCCTTT CC

412

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

| | |
|---|-----|
| GGCACGAGNA CACCCTGGGC CTCACACCCC TGCATCACGC CTCTCGGGAA GGCCACGTGG | 60 |
| AGGTTGCCGG CTGCCTGCTG GACAGGGGTG CCCAGGTGGA TGCTACCGGC TGGCTCCGAA | 120 |
| AGACCCCCCT ACACCTGGCT GCAGAGCGAG GGCATGGGCC TACCGTGGGG CTTCTGCTGA | 180 |
| GCCGAGGGGC CAGCCCCACT CTGCGGACGC ATGGNGCCGA GGTGGCCCAA ATGCCTGAGG | 240 |
| GGGACCTGCC CCAAGCGGTT GCCTGAACTT GGAGGGGGGG AGAAGGAGTT TNAAGGCATA | 300 |
| GAGTNCAAGG GGGTTTTAGC CAAACAAGCA AGGTTTCCAA GGTTTCCAAC NGGCCCAATT | 360 |
| GANTTTTCCA AGGTTTTTTT GGGTTTNAAG GTTNNCCTTG CNTTGAAGG GGGACAATTA | 420 |
| AAGGNAAGAG GGTTTTCCG GAGGAAGGGG NTTGGGGGAA AATTAAAGGG GTTTTTGGGT | 480 |
| TTNACTTTN AATTAAAAA NGGCTT | 506 |

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

| | |
|---|-----|
| GAAATACGTN TTGCTTTNAT AACTCTNATT GCTTCTTGC TGTTGGGGTG TGTAAGTAA | 60 |
| GCATTGATTT NAGTGCTGAG NAATGTGAAA CGGGACTTAC AGGNATGCTT GGATTAGTNC | 120 |
| ATCACAGGTT CTNATGAACT TTNCCTACCA CAGTTGANTA ATATTTNTCC TCAAACCTGT | 180 |
| GTGCCCTAAG GANTNTGTTA NAATAATTGT TGGATAATTT CTAGGTGGGT GTTTATCCAA | 240 |
| GGCGCNAGAA ATTCCCTGCC CTTGGACCAG ATGTGTGGGG GCCNTCTGAC AAAATGGTAT | 300 |
| GNTNTGGTTT ANTTTACCAC AC | 322 |

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

| | |
|---|-----|
| GTCTGGTCGC NAGCAACCTA ANTCTAAAAC CTGGAGAGTC CCTTCAANTG CAAGGCGNGG | 60 |
| TGGCTCCTAA CGCTAAGAGC TTCGTCCTGN AACCTGGGCA AAGACAGCAA CANCCTGTGC | 120 |
| CCTGCCCTTN | 130 |

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

| | |
|--|-----|
| GGCAGGAGCC TCANTCCTTA ACTGAAAAGT AACCGTCCAC TGCCCCATGG AGCCCATCTG | 60 |
| GACACAGCAC AGCCCCAAAA CCGTTAGCAG CTGGCTCTGT TTCCAAGCCT GGGGAGGGGT | 120 |
| TCCTCAGTGN CAGGAGTTGG GGACAGGCTG GGGATCCAAG CTGCTTGAGG GGGTCAACCT | 180 |
| TGGGACCAAA GTTGCCCTTNA AGCCTGTGGT AAAAGGGCTT CAGGGGAAGG TAAGTGGGCC | 240 |
| ACCTGCTGGA AAGTTGCCAG CTGCCCCGTT GGCAATGGTG TGAAGTTTTT TGGGCCCTGT | 300 |
| TCCCTGGCCC TGGGGGTTCC AGCAGGTGCA NTCCCTTCCC TTGCTTACTN TNCTNCTTTT | 360 |
| GGGGGTTTTG TTCCCTGTNA GTTCACTGGG GGTAA | 396 |

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

| | |
|---|-----|
| GGCTATTGTA GGGCACCTNA CATTGCACAA GAAATGCCCC TTGCACTGGT GAATNTGTGC | 60 |
| CATTTCGTAG GGTCCGNATC CTCTGNTNAG CGTGGTTTAC CA | 102 |

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

| | |
|---|-----|
| GGCATNGTGN CAGGTNTGCA GCAAGTTGTT TCTTAGTGTC CCAACGGAGG AACCACTGAA | 60 |
| GCAAAGCTTT ACCTGTGCTC TACAGAANGA AATACTATAC CAAGGAAAGC TGTTTGTATC | 120 |
| AGAAAACCTGG ATTTNTTTTC ATTCCAAAGT CTTTGAAAA GACACAAAGA TCTCTATTCC | 180 |
| AGCTTTCTCG GTAACCCTAA TAAAGAAANC CAAACTGCT CTTCTAGTGC CAAACGCCCT | 240 |
| GATCATAGCA NCAGTCACAG ACAGGTACAT ATTTGTTCTN CCTTNACTTT TCCAGAGATT | 300 |
| NCAACTT | 307 |

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

| | |
|--|-----|
| GGCACGAGGN AATCATCTTT AANATCACTT TCTNCTTCTT TGTNATTGTN ATTCTCTTGG | 60 |
| CCATAATACA AGGTCTAATT ATTGATGCTT TTGGAGAACT AAGAGACCAA CAGGAACAAG | 120 |
| TCAAAGAAGA CATGGAGACC AAATGCTTCA TCTGTGGGAT AGGCAATGAA TTA CTTCGAT | 180 |
| NACAGTGCCA CATGGCTTTG AAAACCCACA CTTTACAGGA GCACAACTTG GCTAAATTAC | 240 |
| TTGTTTTTTC CTGGATGTAT CTTATNGACA AAGNTGGAAA CAGNNCACAC AGGGNCAGGA | 300 |
| ATCTTATGTT CTGGGAGGAT GTTATT | 326 |

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

| | |
|---|-----|
| TAGGAGGATA TNACGGCTTG AATATCTNAA ATNCAGTTGA GAAATACGAC CCNCATACAG | 60 |
| GACATTGGAC TAATGTNACA CCAATGGCCA CCAAGCGTTC TGGTGCAGGA GTAGCCCTGN | 120 |

TGAATGACCA TATTTATGTG GTGGGGGGAT TTGAATGGTG ACAGCCCACC TTTNTTCCGT 180

TGGAAGCATA CACCATTCGN ACTGN TTCCT GGGACAACTG TN 222

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

TGATATTCAC CTTCTGGTC TGTNGGNTTG CCTTATATCG TNATCTNCTT CTNGGTGGTT 60

AATGGTCATG GTCACCTGGT CACTCCAACA ATATCTGTTG TTTCGTACCT CTTTNNTAAA 120

TNGAACACTG TNTACAATCC GGTGATTTAT GNCTTC 156

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GGCAGGAGCA ACATATTAAG ACTCTGTCTC TACCAAAAAT ACAAATAAGT NAGCTGGGCA 60

TGGTGATGCA CTCCTATAAT CCCAGCTACT CAGGAGGCTG AGGTGGGAGG ATCACTTGAG 120

CTCTAGAGGC CAAGGCTGCA GTNAGCCGTG ATCATGCCTC TNCACCCTAG TCTGGGTGAC 180

AGAAGGAGAC CCTGTCTCAA AAAAAAAAAA AAAAAAAAAA AACNNNGGGG GGGGCCCCG 239

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AATCAAAATT GAATATCATT ACTTTTATA GATCTATTCA GATTTATTCT TTGTNCTTGA 60

GTCAACTTTG TTGGATTGT ATGTTTCTAG GAATTTGTCT GTTTCATCTA GGTTATCCAA 120

TTTTTTGAAC ATATAGCTCT TATACTAATT CTCTTACAAT CCTTTTATT CCTATAAATC 180

AGTAGTAGTG TCTTTCATTT CTGAATTTTA GTAGTTGAGT ATTCTTTTNC CNTAATCTAG 240
TTAAAGCTTT GTTCAACTTT GTGGANCTCT TNCAAAGAAC TAAATTTTNG GTT 293

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CGCACTCAAG GTCGACACTA GTGGNTCCAA AGANTTCGGN AGAGGAAACA GCGGTTAACN 60
CCCGGTCCCC AGGGCCAGTC CCTCACCNGG CCCAGAGCAA GGCCACTAAG GATGGGCCGT 120
GGAAACCAAA GTGGTCATCT ATTNANNCAT CATNNNCNGC AATTTNCCTN TTATCGGNGT 180
NGAAAGNGNA AGACATTCGA GCCAACTTCA CAAGAAATGT CTAGANAAGA AAGTNCTTTA 240
TGTGGACCNT GAGTTCCAC NGGATGAGAC CTGTCTCTTT TATAGCNAG 289

(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

CTANTCCNAG CACTTGGAAG GCNAAGGNAG GAGGATTNCT TGAGGCCAAG AATTTAAAC 60
CAGCCTGGGC AACATAGCAA GATCCCGTCT CTATAGAAAA NCTGTNAANT TAGCTGGGCA 120
TGGNGCCATA TGCCTNAC 138

(2) INFORMATION FOR SEQ ID NO:360:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GGCACGAGTG GTGGCTCATG NATGTAATCC CAGCACCTTG GGAGGCTGAG ACAGAAGGAT 60
TGCTTCAGCC CAGGAGTTCC TGA CTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAANNCN 120

GGGGGANTTT TTNGGGGG

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

| | |
|---|-----|
| GGCACGAGGT GGCGAGCNCC TGTAGTCCCA GCTGCTGGGG AGGCTGAGGC ACGAAAATCA | 60 |
| CCTGANCCCC GGAAGCGGAG GTTGCAGTAA GCCGAGATTN CCCCACGGCA CTTNAGCCTG | 120 |
| GGTGACAGAG CGAGAACTCT GTCTCAAAAA AAAAAAAAAA AAAAAACNN GGGGGN | 176 |

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

| | |
|--|-----|
| ATTA AAAACT CCTCTGGTTG CCGTATTTNA TGATCTGGAT ATAGAAGCGG ATGAAGAAGA | 60 |
| TGAACTTAGG GCAAGAGGTC TTACAGGTTT GAAAAATATT GGAAATACTT GTNACATGAN | 120 |
| TGCAGCTTTG CAGGCTCTTT CTAATTGCCC ACCTTTGAAC ACAGTTTTTN CTTGATTGTG | 180 |
| GGAGGGACTT AGCTCGNAAC AGGATTAAGN AAACCTGGCC ATTTGTGAAA AGTTAATCTN | 240 |
| CAAACCTAAT GGACAGNGCC TGTGGGCATT AAAAGCCAGG GCCAGGTTTC TGTTTGTGGC | 300 |
| CTACTTACTC TGTTTTCAAG GGATTTAAAA ACTGTTAAAT CCCAACATTT CGGGGGGGTT | 360 |
| TTTCTNCAGC CAGGGTGGNT CCAGGAATTN CCNTTCGGTG TTTAATGGG NTTTGNCTTC | 420 |
| CAGGAGGGAT TTGAAAGGGG CCAGTTCCTG GGAGTTGGAA GGAGGNTCCC CGNAANCCTT | 480 |
| AACCCTTGGG GGGGG | 495 |

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

| | |
|---|-----|
| GGCAGAGGAG NATGACCTTG TGCCACAGC ACCTTCTCTG GGCACCAAAG AAGGTTACCT | 60 |
| CACCAAACAG GGAGGCCTGG TCAAGACCTG GAAAACAAGA TGGTTTACTC TGCACAGGAA | 120 |
| TGAACTGAAA TACTTCAAAG ACCAGATGTC ACCAGAACCA ATTCGGATCC TAGACCTAAC | 180 |
| AGAATGTTCA GCTGTACAAT TCGGATTATT TCACAAGAAA GGGTAACTG TTTTGTGTTG | 240 |
| GTATTTCCAT TNCAGGACAT TTTATCTCTG TGCAAAGGAC CGGAGTAGAA GCTGTTGAGT | 300 |
| GGGNTCAAGG TATTTACGGN TGGGNAAATT TGTTCACCAN ATTAAGGAAA AACCAGGTTT | 360 |
| CCAAACCCAG GGGGGN | 376 |

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

| | |
|---|-----|
| GGCAGAGGGG TAAATTAAGT ATTGAAAAAA TGCTATGGGG CAGAGGAAGA AATGCTAAGC | 60 |
| TTCTGTGAGA AGAGAAGACA GCTTGTTACA CAGGTGAAAA GAACAAGCTG CAGCTGAGAG | 120 |
| AAGAAAAGTA TAAGAGTTGC TAGGTGTGAC AATCTCAAGA CTTTTCACC ACTACAAATT | 180 |
| TAAACAGCCA CCCTAAATCA CCCC | 204 |

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

| | |
|--|-----|
| GGCAGAGNAT TTAGACATTA TTA CTCAAAA TATTCCAGAA AAGGTAAGTT TGTTTGTAAG | 60 |
| ANTTTAAACT TGACTGTAAA AAAAGAATTG TATGTATTTG TACCAATTTT TTATATGTNG | 120 |
| AGCATTCCTG TGAAATGTTT GCAATTTTNC CCTTTCCTTT CCACTGCCCT GCTAAATGTG | 180 |
| CACATGTATT AGNACACAAA TACCCAGTAA ATGGGGAATT ACCCATTTAC ATGGCATACA | 240 |
| CACTGAGGTG GGCTTGNGGT ACATACCAA TTTT TAGGAC AACTTACTG GGGTAAGTTT | 300 |
| TTGTGGGATA CTTGTNTNAN AANTGATTAA TT | 332 |

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GGCANAGNAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANAAN

56

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

AGACCTTAAN CCCAGGAGGC GGAGGTTNCA GTAAACCNAN ATTAACCCAC TACTCTCCAG

60

CCTGGGCCAA CAAGAGCAAA ACTCNGTCTC AAAAAAAAAA AAAAAAAAAA AANC

114

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GGCANAGCGG CCACNCCAAA GTTTTGGGAA TTACAGGCAT GACCCACCGC CCCTGGNTGG

60

ATTTCCTTTG AAAAAGNNAA AAGAAAAAAA AAA

93

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GGTGAACCCT GGCCGCCAC CTCCCCGCGC AAGTTCACCC CTGNGATGCA CGNTTCCNTG

60

GAACAAGTTC CTGGTTTCTN TGANGCACCG TGCTGACCTC CAAATACCGT T

111

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

| | |
|---|-----|
| TGTAATCAGC ATCANTAATA ACTGTGAAGT CCTTCATTGG CTTAGGTTGC ACTTNTNGGT | 60 |
| AGAGGCTGGG GCAAGGNTTT NTTGGGATCA GGGACACTAG GCAGCCACTC CTCAGGCACC | 120 |
| AGTAGTGGTG GGCANTGAAG TCAAATGTGC CAGTNTTCAC ATGCCTGGNT AGCATACACA | 180 |
| GATTACCACT GGTGGCTGGT NTGGNTGGGC TGGTCCTTGA ANCCTNCAGG TGGGCATGGC | 240 |
| TCCAGGTGCC TGGTGGTGGC CAGTGGTAGG CTTAGGGCAG GTGAGGTGCC TTGGGCCCNT | 300 |
| TGGAACAGTG TGGCATGGAA TTGGTGTTG ACAGGNTTGG NAACTNTGCC TTGGCAAAAT | 360 |
| TN | 362 |

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

| | |
|---|-----|
| AGAAGCAAGT TNCTTAGCTG GGTGAAGTGG CTCATGCCTA TAATCCGGCA CTTTGGGAGC | 60 |
| CTGNGACAGG TGGCATTGNT TGAAGCCAGG AGTTCAAGGC CAGCCTGGGC AATAAAGTGA | 120 |
| GAACCTGTCN GTNATAGACA AAAAAAAAAA AAAAAAACAA AAAANCNGGG GGG | 173 |

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

| | |
|---|----|
| GGCAGAGCTG GCGCATCGGT TCATTTCCTA CCTCAACGGC CAGATCATGG CGTGCNACAA | 60 |
|---|----|

| | |
|--|-----|
| GCGGTGCAGA TCTTCGACAC CTGGGGTGGC AACCTGTCGT CGGCGGCGTA CCAGGAGTTC | 120 |
| TCCCTGGGCC TACATGCGCA ANATCGTCAG CGGCCTGATC CGTGAACAGA AGGGCGCAAA | 180 |
| GTGCCGGTGA TCATGTTTAC CAAGGGCGGC GGCCTTTGGC TGGNAGAGCA TTNCCGACGC | 240 |
| CGGCGCAGAN CGCTNGGGCC TGGATTGGAC CTGCGACCTG GGCGAGGCCG GTCAGCGCGT | 300 |
| GGGTAACCGG TTGGGCTGCA AGGTTNACAT GGACCCAACGT GTGCTTTACG NCAAGCCGGA | 360 |
| AGCGATTTGC AACGAATTTG GGCCGNATNC TTGGCCAGTT NTGGCAAGGG CAAGGGGCNT | 420 |
| TTTTTTTCAA CTTGGG | 436 |

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

| | |
|---|-----|
| GGCAGAGGNA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT | 60 |
| GTACCGCACT GTGCATCGAA ACCGGTGAAG TGTTTATTT CAAAGCCCGC GCTACCGTGC | 120 |
| TGGCGACTGG TGGACAGGGN CGTNATTTAT CAGTCCACCA CCAACGCCCA CATTAACACC | 180 |
| GGCGACGTTT GNGNCATGGN TATCCGTGCC GNCGTACCGT GCAGGATATG GAAATNTGGC | 240 |
| AGTTCCNNCC GACCGGGCAT TGGNTGACGG GNNATACTGG TCCACCGAAN TTGNCCGTGG | 300 |
| TGAAGGCGGT TATCTGCTTG AACAAACATG GGCGAACGTT TTTTATGGGA GCGTTAATTT | 360 |
| TTTTNT | 366 |

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

| | |
|--|----|
| GGCAGAGTNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAAT NNNGGGG | 57 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

| | |
|---|----|
| AGGTAGAACC CACCATGGTG CTGTCTCCTG CCGACAAGAC CAACGTTAAG GGGGGGNTTT | 60 |
| TNTAAGGTCG GTGNAC | 78 |

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

| | |
|--|-----|
| AGGGTACCGT ACGTCGTCGC TGNTGAGTGG GCGAAAAGCT GCAAATGAAA CAGCACTGCC | 60 |
| CACATCCGGA TCTGTTACAG GTCGATCCGT TCGAAGCCAT CATCGATGAA GAGCTGGAGC | 120 |
| CTGGTGATAT TCTTTATATT GGGNTGGGAT TCCCGGCATG AAGGCTACGC GCTGGGAAAA | 180 |
| TGCGATGGAA CTATTCCGTG GGCTTTCGCG CGCCAAATAC GCGGGAAC TG ATTAGTGGAT | 240 |
| TTGCCGATTA TGTGCTGCAA CGTGAAC TNG GCGGCAACTA CTACAGCGGA TCCGGATGTT | 300 |
| TCCACCTCGC GNTTCATCCT GCGGGATGTT TCTGNCCGCA AGNGAATGGN TNAACTGCG | 360 |
| TGAGAATGGA TGCNTCGGAA TTGNTTCANC CAGCCNGTNA CAATTTTAAG CAATGGTTTT | 420 |
| GGCGAGTTTT ATNTCCAGT CAAGTCATGG AANNTGGGTT ATTGGGGCNG CCAANGCCGG | 480 |
| CTTTTCAGCC GGTGNAATTT ACGGTG | 506 |

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

| | |
|---|-----|
| GGCAGAGCAT GNTTATGGGN TACAAAGNGA TGTTATATTT TATGAATATT TAGCTGGGCA | 60 |
| TGGAAGCTCA TGCCTGTAAT CCCAGCACTT TGAGAGGCTG NGGCAGGTGG AGTGCTNGAA | 120 |
| GCTCAGGGGT TNAAGATTAG CCTGGGCAAC ATGGTGGGAA CCTATCTCTA CAAAAAAN | 180 |
| AAAAAANC TGGGGGGGAA TTTTGNAGT GTTCNGGGN CCTATGGGTT TTACCC | 236 |

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

| | |
|---|-----|
| TTGGCTATGG GACTATATGT NATCTANTGA CTTTTTAAAA ACAGATTACA AACTGTAGGC | 60 |
| CTTAGATNGG TAAGTAATTT TTCAGCTGGG CATGGTGGCT NATGCCNGTG GTCCCGGGGC | 120 |
| TTTGGGAAGG CCGAGGCAGG CGGATCACGA GGTCGGGGGT TCGGGAACCA TNCTGGTCGA | 180 |
| TGTGGCGGGN CCNCGTGTTT TGACTGAAAA AAGTGCAGAA ATTGGGCTGG GACATGGTGG | 240 |
| CGTGACNTG TGGTNCCGN TGCTTGGGGG TGCTTGGGGG CGGGGGGGGT CGCTTTGGGC | 300 |
| CTNNGGAAGG AGGAGG | 316 |

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

| | |
|---|-----|
| GGCAGAGCNG AAAGCGGGCT GCACTACAAC CGACATCGNT ACTACAATCC GGATGTTGGT | 60 |
| CGCTATCTGA CGCCTGATCC GGTGAAGCTG GNNGGTGGGC TGAACGGATA CCAATACGTG | 120 |
| CCCAACCCGA CGGGTGGNTG GTATCCGTTG GGATTAGTTT GTACACCTGG GGCAGTGCCG | 180 |
| GGNCTTCANC AAATAACACA GCAGTTAGCA AAGTCCCTGG AGGGGGATTA GCCGCGCATG | 240 |
| AAGCAGCTGG GGGTCATCTA ATTGAAAGGC ACGTTCGGTC AGACAACGGC GCAGTAAGCT | 300 |
| TTNAAGGCTT GTAGGCAGAG CCAANTATT TCCAGNNGCA TCCACGGTTT CAGANT | 356 |

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

| | |
|---|-----|
| GGCAGAGCTG NTTGACCGAA CCGTTGAAGC GGTTCGAT ACGACGCAGC TNACCGTAGC | 60 |
| GCTCGCCCGG GGAGATGTTG CAACCGCTGG AGCAGNCATG GCAGATGCTC GGCGCAAATT | 120 |
| GCATGTCCCA CTTACGGTTG TAGCGCTCGG TAGTGGGTCT TGTCGGTGAA CACACCGATC | 180 |
| GGGTCAGACC TTCGGNGAAG GTTNCCGGAG AACTCGCTT CTCCAGCACG CCGTACTTTC | 240 |
| AACGCGAACC GAAGTACACG TTGTCGTGGG ACGCCGAACA CGCCGAGGTC GGTGCCGNCG | 300 |
| GGNTAAGTCT TTATAGAAGC GCACGNANCG GTAGCAGGCC GATGNCAGCG GTTTCATTTT | 360 |
| CGTGGGGAAA TGAACGGGGC CCNAGGTTCC NGGTTTCTGG TTGGT | 405 |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

| | |
|---|-----|
| GGCAGAGNGT TTTNCGGGCT CAGTTCGTGG TGCCAGCTGC CGTGGGTGCG GTCAATGAAA | 60 |
| CGAGTTTCAC AGAACTCCCA GANGCGCCGG TACCAGGTTT CGTAATGCAG CTCCCCGTC | 120 |
| CTTTTNANCA GCGCCTGGGC CAGCGGGCAC TGGCTTCGCA ATGGGTCCAG TGCAGGCGCC | 180 |
| TCGCGCCACC ACGGGGCGCT GGCTTCCANT CGAGGGTTTA GACAATNCCN GGGGGGGCCN | 240 |
| TTGAAGGGCC N | 251 |

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

| | |
|---|-----|
| CCCTGGCTCT CTTGATAGAG GCGNGAGAGT NNGNTTCCAG ACCAGAATTT ATCTTCAAAC | 60 |
| GCTTCGGCTT CGCGCGCCGC TGCGTTAAGA ATACGGGTCC GCTGGATAAT AATGGCCCAA | 120 |
| GATGCGATTG AAAAACCAAT CAAAATCAAC ATGATAAGTT TAACCAGAAG GCTAGCCTTC | 180 |
| AGG | 183 |

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

| | |
|---|-----|
| GAGTTGGCGG TCAGGTCACC GCGGCTTCC AGGGGCGAAA TCAGGAAGAT CACCGCCACC | 60 |
| GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCGG TAGGCTGATC | 120 |
| AGTGGCAGCT GGGGCAGGGC GCCCAGGTTT GACGCGGCCC ATCCACCAAG CCACCACAAA | 180 |
| ACCCAGGGTC AGGCCGATCA CGATCGAACC CAGGCGCAGG NAACGCGTTG TTGAAGCGGT | 240 |
| TGAGCACCAC GNATGGTCAG CAGCACCAGG GCCGCCACAT GGTTTGTCCG GNGGNGTCCA | 300 |
| GGTCGTTGGT GNCATTAAC CGCNGGT | 327 |

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

| | |
|--|-----|
| GGCAGAAAAT AAAACCACCG GGGCCTCCCT TTAAACTTTN GTTCTCAAAG GGCCCCCTCCA | 60 |
| CCTGGCCCTG TTCTGGCCCC CAAGGATTCT ATGGGAAGCA GTGGAGTCCC ACAGATCTCG | 120 |
| CTCCANACTC TGCTCCCTGA ATCCCGGGGC TCCTCCTAACT CCCCCTGGCC TCTAANACTC | 180 |
| CTTCCCATCC TCCCCTCCCA CTCAGAAAAC TCTTTGTGGT CCCC GCGGAT GAGGCCCAGG | 240 |
| CTCGAATCCC ATATGCCCGT GTNAACCACA ACAAGTACAT GGTGACTGAA CGCGCCACCT | 300 |
| ACATCGGTGA GTGTTTTGAG GCACCACGGG GCGCTTGAAG AAGAGGGGGT TTCAGACACC | 360 |
| AGGGCGGNCC CCCGAGGGTG NCCTTATGTT NCACCCCTTN CTTTTAGGA ACTTCCAATG | 420 |
| GTTTGATNGA | 430 |

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

| | |
|---|-----|
| GCTTCGCTGG TTTTCGGCTG TTCCAGNATG GTGCTGACCT TGTGTAGGT NAGGCGGGCC | 60 |
| TGGGAGTGNA TCACCGCTTC GTAGAACTGG TAGTCGGTCA TTTCGNCGGT TTTCGAGATG | 120 |
| GTCATCTCGC ACACCATGGC CAAACGGTCG ACTTTTCGGGT TCAGGGAGCA CAAGCCGTTG | 180 |
| GACAGNTGCT CAGGCAGCAT AGGGATGACG CGCTCGGGGA AGTACACCGN GTTGCCGCGC | 240 |
| ACCTGGGCTT CGTTGTCCAG GGCCGAACCG ATCTTNACGT AGCTGGGACA CGTCGGCAAT | 300 |
| CGCGAACGNA ACAANTTTCC AGCCGCCGGA GGAACAGGCG CATTTGCCAG GCTTGGNTTT | 360 |
| CGCATTAGNC CGCATNTNNC GAATTCGCGG GCANTTTTCGG CTTTCATGGTG ACGAACGNCA | 420 |
| GTNNANGCAG TTCGATGNGG TTNTNTTTGT NNTTTTNTTC GATTTCCGNT TGAGTTGGGG | 480 |
| GTTTTTTGAG CACAGNNTGA G | 501 |

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

| | |
|--|-----|
| GGCANAGGNC TGTACGTGCG CCATTGCTCG TGCATGGGGT TTTTANTGAT TAAGCCTGNG | 60 |
| TATGCAACAT CAGCATTAAG NAGCTCGTGT AAANCAGAAT AAACGGCATT TGCGAGCATG | 120 |
| ATTGGCTTCT GTCTGCTTGG ATCAGTTGTA TAAATTGGAG TTTTTCAGCTC GAAAAATGCA | 180 |
| TGTAATCGTC CGTTTTGAGG ATTTTCAGCA ACAAATTCG GCATTGGTAC GCCATCAAGT | 240 |
| GGAATATAAA ATTTCACTTC AGGGCTGGAT TTCATNAGTC GAGTTTCAAG CACAAAGTAA | 300 |
| TACTGGATAA AACGGACTAT TTTGGGCTGA ATGTACTTGA ATGCCAGTGC TGGTATTCTC | 360 |
| TCGGGACGTA TTTTTCAGAC CCGTGNTCAG NTCCNTCCGT ACATTNGGNT TTGGGTCCGT | 420 |
| TAAGTTA | 427 |

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

| | |
|---|----|
| GGCANAGGTC TCTGTNGCTG TAATTAAGGA TCTTGAGATG AGGAGGCAAT CCTGAATTAT | 60 |
|---|----|

| | |
|---|-----|
| CCGGGTGGGA CCTGTACCCA GTGACACATC AGGAGAAATT TTTTATATG AGAAAATGTG | 120 |
| GAAGGGGAAT TTGAGACAGA CAGAGGAGGA GCAGCCCGAG GGGAGGCGTT GTGTGCAGGC | 180 |
| GGAGGCAGGG ACGGGGCGAT GCACCACCGG CTGAGGAAGG ACCGCGGCCA CCGGGTAGCT | 240 |
| GGAAGACGCA GNTGGAGCCT CCCCTAGAGC TTTTGGNAAG GGACACAGCC CTGCCAGCAT | 300 |
| CTTCGTTTTN GTCTTTGGGC CTNCAAAGAC NAAAATCAAG GCTTTTTNGA ACAAAT | 356 |

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

| | |
|--|-----|
| NGCAGAGCGC GAAGTGGTGT GCGGTACTCC TTGAGCGAGC TGCCTTCCGG CGCCACATCG | 60 |
| GTGTCGTGGA AGCTGTAGTA GTCGATGCCC AGCTTGGAGA AAAACTCAAA GGCCGCGTCA | 120 |
| NCTTGACCGA TGGCCACTTC CATCGCTTTA CCGCTGCGTT GCCACGGGCG CTTGAAGGTG | 180 |
| CCCATGCCAA ACATATCCGC CCCC GGCCAC ACAAAGGTGT GCCAGTAACA GGCGGNCATG | 240 |
| CGCAGGTGCT CGCGCATCGG TTNCCGAGG ATCAGCTTGT TTGCGTCGTA ATGGCGGAAG | 300 |
| NCGAGTGNTA GAGTCGCTNG TCAAGG | 326 |

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

| | |
|---|-----|
| GGCAGAGCCA CGGTCAGGCC GNCATCGGTA CCGTTCTTGA AACCCACGGC CGAGGACAGG | 60 |
| CCGAAGCCAT TTCGCGGTGA GTCTGGGATT CCGTGGTGCG TGCACAATNT GCCGACCAGN | 120 |
| TGGTCAGGTC TTGCAGGTAC TGGNGGGAAA TCGTGTCCAG GGTTCGGTT GNCGTNGNAG | 180 |
| GCCCATTTC GNCAAGTCCA GNAGTAATTG NACGACCGAT GTGCAGGCCG TCCTGGATCT | 240 |
| TGAACGAGTC GTCCAGNTAC GGGTCGTTGA TCANGNCTTT NNAGCCGACG GTGGTACGCG | 300 |
| GCTTGTTTCA AATAGACACG GATCACCAGG TTTTNAAGGT GTTCGGACAT TTTNGTNGGT | 360 |
| CAGCACTTTT CAGGTGGTTN GG | 382 |

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

| | |
|--|-----|
| GGCANAGGCT GATCGGNACC CAGNTCGAGC ACGTTCCGGC CATGCTGGAA ACCATCTTCA | 60 |
| AGAGCGCCTT CGGCCTCGAC CCGGTATTTG GCGGCCTGNT CGGCAGCGCC ATTGTNATGG | 120 |
| GTGTGAANGA GGTGTGTTTCG CCAACGANGC TGGCCTGGGC AGTGCGCCCA ACGTCGCCGC | 180 |
| CGTAGGGCGN TTNAACACC CCGGTGCNCA AGGCGTGGTC CAGGCCTTCA GCGTGTTCCT | 240 |
| CGATACCTTC GTGGATTNNN CACCTGCACC GCGTTGCGNN TTNCTGCTGT CGGGCTTTTT | 300 |
| ACACCCCAGG NTTTGAAGG TGAATNGAT CGGGCCTGNA CCCAGAACTT CGGTGGGCC | 360 |
| GCCCTGGGTT CGGTGAANT GGGGGNCCG | 389 |

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

| | |
|---|-----|
| GGCAGAGCTT NGCTTCGCTG GTTTTCGGCT GTTCCAGGCA TGGTGCTGAC CTTGTTGTAG | 60 |
| GTNAGGCGGG CCTGGGAGNG NATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTGNCNG | 120 |
| GTTTTCGAGA TGGTCATCTN GCACACCATG GCCAAACGGT CGACTTTCGG GTTCAGGGAG | 180 |
| CACAAGCCGT TGGACAGNTG CTCAGGCACA TTAGGGATGA CGCGCTCGGG GAAGTACACC | 240 |
| CNGTTGCCGC GCACCTGGGC TTCGTTGTCC CAGGGCCGAA CCGATTCTTC ACGTAGCTGG | 300 |
| ACACGTCGGC AATCGCGAAG GAACAACTTT CCAGCCGCCG GAGNAACAGG CGCATTTTGC | 360 |
| CAGGCTTGGT TTCGCATTAG ACCGCATCGT CGAAGTCGCG GGCATTTTGC CTCATGGTGA | 420 |
| CGAACGGCAA TGACGCAGTC GATGGGTTCC TTTGGNCTTT TTTTNGATTT CCGGTTTNN | 480 |
| TTTGGGGTTT TTTTtagGCN A | 501 |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

| | |
|---|-----|
| GGCAGAGNAA GACATCCCAT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT | 60 |
| CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC | 120 |
| TATCAAAATC TCAGCTGGCT TCTTTGTAGA AACTGACAAA TTGATTCCAA AATTCATATG | 180 |
| AAATTGCAAG GGATGCAGAA CATCAGAACA ATCTTGTAAG AGANCAAAAC TGGAGTACTC | 240 |
| CCACTTCTCA AAAACTTACT GCAANGCAAA AGTAATCAAG ATAGGTTGGG CATGGTGGCT | 300 |
| CATGGACTGT NAATNCCAGC ACTTTTGAAA GTTCCGAGGC GAGTGGGTTT ACTTGAGGGT | 360 |
| CCGGGGTTTC AAANCCAGCC TNGGCCAACT TGGTGGAAAC CCCTTTTTTA TTAAACTTTT | 420 |
| AAANAATTTG GNTGGGCTGG TGGGCGGGN CCTNAATCCC GGTTTTTCGG GGGTTTGGGC | 480 |
| NGGGCATTCTG | 490 |

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

| | |
|---|-----|
| GGCNCTAGAT GTNGTTAAG GTGTAAAACA GACCAACCCA CAGCGCCCGT ACCTTAACTT | 60 |
| CANTCGTCAG GAAGAGGCTC AGCGTCGGGG CCAATAGCGC TCCGGCAATG CCAGAAAGGT | 120 |
| AACGCAATCA GCAGGTAAAG CGGTCAAAAA TGGGGATTAA AGCGGCGTGG TNAACCCGTA | 180 |
| CAGACGTTTC ATATTGTTN TCCCTGTNCC CTNAACGTNT GAAGTGAGGA | 230 |

(2) INFORMATION FOR SEQ ID NO:394:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

| | |
|--|----|
| GGCANAGTGA ACAGCGTAGG NACTGTAAAG CATGTNTTGG GGTAAACTT TCCTTTGATA | 60 |
|--|----|

| | |
|---|-----|
| AAGAGAAACA GGTTCCTTG GATGAATAGA AGGNACAGAG AAGGCAGATC CAGGCTTATC | 120 |
| CTTCTCGTGT AAGGGTATAG TAAAGAAAGG TCTATGCCGG GCGCAATGGC TCACGGCTGT | 180 |
| GAATCCCAGC ACTTTGGGAG GCCGAGGTGG GTGGGATTCA TGAGGTGCAG GNGATCAAGA | 240 |
| CCATCCTGCC TAACATGGTG AAACCCGTCT TTNACTAAAA NTGACAAAAT NNA | 293 |

(2) INFORMATION FOR SEQ ID NO:395:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

| | |
|---|-----|
| GGCACAGNAG AAAACAGGCA AAAGAGACAC TTCAGGTGGC ATTGATCTGG GAGAAGAGCA | 60 |
| GCATCCCTTG GGCACACCCA CTCCAGGACG CAAGCGANNA AGGAAGGGAG GAGACAGTGN | 120 |
| ATTATGAACG ATGATGATGA CGGATGACAG TGAATGGACC AAGGGGATGA AGATGATGGA | 180 |
| GGATGAAGNA AGGATAAAGT AAGGACAAAA AAAAAAAAAA AAACCNCGG GGGTNNCTTT | 240 |
| TGGGAGCGCC CGTG | 254 |

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

| | |
|---|-----|
| GGCANAGNAG AAAACTGAGC TCGTTGGCTG GTTCTCAAA AATCCACTCA TTTGATGATT | 60 |
| GTGGTGGTGT TCACTGACTT TATCCCAAAC CTACATGGAA GGGTGTCCG GACAGACAGC | 120 |
| TCTTCCCCAA AGAAAATGTC CTCTTAGCTA AGAGTCCATG TTTCTTTTC TAAGTAAGAT | 180 |
| TTTGACAGAG AATGGCATAT GTATATGTGN AGGGCTGGGT CGTGTCGTTT CAAATGGAAG | 240 |
| CAACAGAAAA GCAGAGCAGG TGTGTCTGGG GAGTATAGAG ACTGAAGGCT GAANGGTGGT | 300 |
| TGAGTTTCTG GGTAAATTGG TGGATGGTTA GTATGTATTG ACTTTGAACT TNCCNTTCTG | 360 |
| GAGCATTTGT TAGAAGGCAG NNAATCCACA ANGACAGGGA G | 401 |

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

| | |
|---|-----|
| GGNAGAGNCG TTGAGGNGCG CGGNGCCGAG GCATAGAGCG TGTCGATCGT GTNGCTCGAT | 60 |
| TTGCCACTGC CGCTGACCCC GGTGTATGCA GGTGAAGGTG CCGAGCGGCA GGCTGGCCGT | 120 |
| CACGCCCTTC AGATTGTTGG CGGTGGCGTT GTGGACGGTC AGTTTCTTGC CATTGCCCTT | 180 |
| GCGATGGGTG GTNGGTACCG CGAACTGCCN NCCTGTNCCG ACAGATAATC GGTGGTTGAT | 240 |
| GCTGTTGGGG TTGGTCGAAG TGACTTNCCT TCGTAACGTG GCCCTNCGCG ATNGGATTCG | 300 |
| GCCCCACCCA TGGGAACGGC GGGNAACCCG GACCCATGTT CGATGNACAT GAA | 353 |

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

| | |
|---|-----|
| GGCANAGCTG GNAATGGTTC GCTGAAGAGC CTGGCTGGCA ACTNTTCGCG AAATGGCGAG | 60 |
| AGCTGGCAGC CACTCGCTGC CTTCCGGTAT GCCGACCGCG GCGGAATTCG CTGTTGGGGT | 120 |
| AGTAGCTTTC GCTGCGCTGG NTAGGCGGTG TAGGAACAAT GCCCGGTTGG TCCATTCGAA | 180 |
| ATCGAACAGC ATGCCCAATG CTTACGCAC GCGCCTGGTC GGCGGAACGC NGNCGCCGGT | 240 |
| TNATTCATGG AACAGCGCCT GGGTGTGCT GGGGAATCCG GTGNAGGTAT CTCGGNCCGG | 300 |
| GATG | 304 |

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

| | |
|--|-----|
| GGCAGAGTGA ATTTTNGCCA GTGAACACTT CAGCCACCAC GGTGTATTTCG CTAAAGGTTG | 60 |
| AACAGCCCAT GTAGTGGAAG ATTGGCTGGC CGTTGTAAGA AAAACGCGTT GTCCTATCAG | 120 |

GCATAACCCC TTTGACCCTG CGTGGCGCGA ACGGCGACAA ACAGATTGGT TTTACCTGGA 180
TTTACAGAAC AGGCATTTCG CACATTCTGC AGTGTAAGC GGAATTAACG TGATCGCCTG 240
GCACAACGCT GGTCACAACT TTGGCCCACT TNTACCACTA TGNCCGGNAC CTTTNGTGTT 300
CCCAGCAAGG TTTTGTN 317

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGCANAGGGA GTGGTATGNG CTGGATCTGG TGAAAAACCA GGATGGCGCG GTGGTGGGTT 60
GTACCGCACT GTGCATCGAA ACCGGTGAAG TGGTTTATTT CAAAGCCCGN GCTACCGTGC 120
TGGCGACTGG CGGACAGGGG CGTTATTTAT CAGTCCACCA CCAACGNCCA CATTAAACCC 180
GGCGACGTTT CNGGCATGGN TATCCGTNCC NG 212

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GGCANAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTTA GCCCGCCGCT GCACGCTAAG 60
CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ANTNCCGTTG 120
CGCACCACTG CATGAAGAAT GGTTCACCA ACGAAGATGC GGTTCCTATGC CGCGGCGGCT 180
GGTTTCAACT TCGGGGTAAT TCAGGCATAG CATCTCCAGG TAATGGAACA GAATGACAGT 240
CAATATGGGG GTCAGGCAGA TNNTCCAAAA AACCCCGGCG GAGGCGAGGT TTTTTTTTNA 300
ACATCAAAGG CGAGGANTTN TTTGATT 327

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

| | |
|---|-----|
| TGCACGTTNN TTGATCATGA CGTGCATGNT GTGTCTTGGG CATTGACANC AACCATGAGG | 60 |
| TTGCCACACG GTGCTTGTTG GACAATNGCC ATGTAGGAGT CCACAAGGTT CTGGGTGGTT | 120 |
| TCCATTTGCC GNTCCAGCTA TGGGTCCATG GAGTTTTATN AAGCTGTCNN TGCCAT | 176 |

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

| | |
|---|-----|
| ACAGAGTTTG TCAACCTCAN NNCTACTGAC ATTTGNGCT GTGGTGTGGG GCCGCCCTGT | 60 |
| CCCTGGGNAG GAGGTTGAAA AGCATCCATC GTCTTCACCC ACTTGGTGNC AGGAGCGCCC | 120 |
| TCTAGCTATG AATGGACCAA GTTGCCACGT GTGCCTCTAG TGGCAGGGTA GGGAATGCAG | 180 |
| TCACCCCCAG GTGAGGGACC ACGGCTTCC CTCAAGTGT CAGGGATAGC CTCTNCCGAA | 240 |
| TTGGTGACAT TGGGAATCCA GATGTGGAGG AGGTGGGGAA AAGGGNCCTG TGGGATAAGG | 300 |
| TTAGGGGAAG AGTTTTTTCC AGGTTCGTTA GGTGGGGAAA GGTTTNCCAA GGGCANGGAA | 360 |
| TNTNCCCCC CGGGGCAANC AGAAAAGGGC CATT | 394 |

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

| | |
|---|-----|
| GGCAGAGCAG GTCCAAGGCC TCGCAGAACC GCAACATACC TGTAAGCACC TGGGCGCCTT | 60 |
| TAGGGTCATG CTGGGCAACC ACAAACCTGC GGTCGATCTT GATGAAATCC ACAGGAAACT | 120 |
| GGTGACATA GCTCAACGCA GAAAACCCAG TGCCAAAATC ATCCAGATAG ACCTTGGCGC | 180 |
| CCATGGCCTG CAACTTCTGG ATGGTCTGGC GGGTGGCCGG GATGTCGCTG ACCAGGGCGT | 240 |
| CTTCGGTAAT TTCCACTGAA ACTTGCCCAC GGGCCTGGCG AAGAATTTNC ACCAGGCGGT | 300 |
| CGCCATAGGG GCGTCCTTTG NAGCGTGGTG CTGGAAATNT TGATGGGTCA TCGGCAGTTT | 360 |

CAAAACCCAN CTTTTGNCCA TTTCTGATAA TTGGNGGCAA CAACCTGGGG ATTGCCACCC 420

ACAAGTTTAN GTNCCGGGA 439

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GGCAGAGACT TGAACCAGGG AGGTGGAGGT TGTAAGTAAGC CGAGGTCGTG TNACCACACT 60

CCAGCCTGGG CGACGGAGTG NGGACTTTGT CTAAAAA AAAAANNTC 120

GGGNGAA 127

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

AAGACTGNAN CANCCNAACA GGNCCAGGAA GTACACGAGA AGCTCTGTAG GATGGCTTAA 60

GTCCAACGTC TCTGAATGCG GTGGCTCAGA GCACCCGTAT CATTTATGGA GGCTCTGTGN 120

ACTNGGGCAA CCTGGAAGNA GCTGGCCAGC CACCTNNTGT GGATGGCTTC CTTGTGGGT 179

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

GGCACAGCGA ATACGTACAC CGTATCGGTC GTACCGGGNG GGCCGGCAAC GATGGCCTGG 60

CGATCTCGNT GATCTGCCAT GGCGACTGGN ACCTGATGTC GAGCATCGAG CGCTACTTGA 120

AGCAGTCGTT CGAGCGCCGC ACCATCAAGG AAGTCAAAGG CACCTACGGC GGGCCGAAGA 180

AAGGTCAAGG CGTCGGGCAA GGCTGTTGGC GTGAAGAAGA AAAAGGTCGA CGCCAAGGGG 240

| | |
|---|-----|
| GACAAGAAGA AGGCCGGTGC CAAGTCGCCG ACCAAACGCA AGATTGCCAA CCGTCCGTAG | 300 |
| ACCGACAACC TGTCGTTGG TTCAGCAAGG TTGGGCATGG GGNCTTTGAA AGCGNCGNAA | 360 |
| AGCCNGNAAG CA | 372 |

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

| | |
|--|-----|
| GGTCACGAGG TACCCAGTGT GGTCCCTGCC TGGACCCAGC CTCTNCTGTT GTCCCCAGAC | 60 |
| CACAACGAGT NTNCCACCAG CACCATGTCTG TNCTAACGGC GTGTGTCTCA ACGAGGATGG | 120 |
| CAGCTNCTCC TGCCTCTGCA AACCCGGCTT NCTGTTNGCG CCTGGCGGCC ACTAACTGCA | 180 |
| TGGGTAAGCC TGGAGCCAGA NTGGCCAGCG GTNG | 214 |

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

| | |
|---|-----|
| GGCAGGAGCG GAGATGCCGG TGGTCAGCC GGTGGNGCTT TCGATGGACA CGGTAAACGC | 60 |
| GGTGCTGAAC ACGCTGCCAT TGCTCGGCAC CATCTGCTGC AGGCCGAGGC GCTGGCAGTG | 120 |
| TTCGTCGGTG AGGGTCAGGC AAATCAGGCC ACGCGCTTCC CGGGCCATGA AGCTGATAGT | 180 |
| CTCGGCGGTG CAGCACACCC GGGNCAGCAA CAGGTCGCCT TCGTTCTCCC GATCCTCGTC | 240 |
| GTCCACCAGG AGCACCATTT TGCCCTTGGC GGTAGTCTTC GATGGTGTCT GCGANTGTTG | 300 |
| TTGAAAGACA TGGTGGNTGN TCCGATTTAT TGTTGTNAT GTATTNTGGT NTTACCACAA | 360 |
| AACCAAGCAA GAGGATGTTT ACGATGGAAG GTTTNANTGG GTTTNCCCNT GTGAANGTGT | 420 |
| TCCGTTGNCA GAGCAGTAAC ACGCATTACA CCCAGCGNG GGCCTGGGGC CTTTCGGGAA | 480 |
| TTTTGGCGGG CGTTTCCTGG GCCANGGGN TN | 512 |

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

```
GGCACGAGGT AAGCCCCCCC GTCGNTGTAG TGGAACAGAA ACGGCGGAAG TTTACTTTTT 60
GCCGCCGTCC GGTAGTCCGT TGAAGCAGAA ATAATCATCG TAGTTTCTCG TNATTNTTGT 120
TTTGGTAAAC GGTGTAGTGG TAAAGGTTGT CCCCAGCAAG TGTAGTTTAG ATAAATCAAG 180
GTGATGGAAA TTAAACCAAC GAGATCGCCA TAAACAGACT AAGCTCCAGA AGAGACGCTC 240
GCTTCAGGTG TCCTGCGCGN AATGCCTNCG NNGCCTTGGA CCN 283
```

(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
GGCACAGGCC GGTGCGGNT AATCCGCAGC NACTGGTGCG CGGCACTGCT TTACCGCCTG 60
CGAGGCACCC TGCGGAAAAC AACCTGNACG GCAAGACCGG CTCCATGAGC GGCGTGTCGT 120
CNTTAACTGG GTATGTNACC GATGCCAATG GGCGCAACTG GTGTTTTCAA TGGTGACCAA 180
CANTTACGTG GTCGCAGGCG CGCGGNTCAA GGCGCTGGGA AAACCGCCTG GCCACGGCAC 240
TGGGCCAACA GCACGGACTT ATTGAGCACC GAAGATCAAA TTGTACGNGG GGCTTGCTCC 300
GGAATGGGGT NGTGACANTC CAACACNTGT TACTGATTGG NTCCCA 346
```

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```
GAGTGCAGTG GTCTGATCAT GGCTCACTAT AGCTTCANTN TCTAATCCTC CCGCCTCANC 60
CTTCCGGTAG CTGGAACCTAC AGGCGGACAC GCATGCGCAT ATTTTAAGTA GAGACGGGTT 120
TCGCCATGTT GCCCAGGCTA GTCTCTCCAA CTCCTGGCCT CAAGCGAATC CTGCCGCTTT 180
```

GGCCTCCTAA AGTGCTTGGC TTACAGGCGA GCCACCACGC CTGGCTCCAG ACTTTTTTTTTT 240
TTTTTTTTTT TTTTTTTNAA AAAAGGGNTT TTTTNTAANN AG 282

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GGCAGAGCGC CNATCCAGCT ATTCATNGGG TGCGGTGTCN CCGGGTTTCG ATNATGTTTCG 60
GCAACTGGGA AATCCGCCCC AGCAACCGTC CCANTGCGTC CAACCCCGGA ATCTCGATGG 120
TCAGGGACAT CAACGCATTN TGNTCTTCCT TGTTCAACG GGTGTTGACC GNCAGCACGT 180
TGATCCGCTN GTTGAGCAGG CACTTGTGAA GAACGTCACG CAGCAAGCCG GGAACGTTTCG 240
TTAGGCACGG TTGGATAATG TGCCACCGGG ATACGTGAGT NACCGGCANC GGCCCCCAGC 300
TGNACCTGNG NTG 313

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GGCANAGTTG GAAACTTACT TGAAAATCGG NCAAGGCAAA ANTTTTTTTTT GTTTTGTTTT 60
GTTTTGT TTTT TAGTTCCATG TATACTTCAA AAAGAACTT GTNTTCGGAA GTTGAGAATG 120
CCACTGGGCG CGGTGGCTCA TCCCTATAAT TCCAACACTT TGGGAAGGCT GGAGTGGGCG 180
GATCACTGGG AGCCCAGGAG TTCCAGATCA GCTTGGGCAA CATAGTGAAA ACTCCTCTCT 240
ACAAAAAAT TAGCCGGGTA TGGTGGCAGG CGCCTGTNTT CCCAGCTACT CCGGAGGCTG 300
AGGCGGGGAG GATCACTTGA GCCCCGGGGA GGTGAGGCT GCCATNCAGC CATGATTCCC 360
ACCATTACAT TCCANNCCGG GGNAACAGGT TTAAAAAAA AAAACNCGG GGGTATTTTT 420
AGGGGGCCCCG GGGGCCCCCTG CGTTTTNCCC CCCGG 455

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

| | |
|---|-----|
| ACTTTTNAAA CCCGAAACTG AAGACACTCA TCATCAACCG AAATGTCGAC TGNCGTTCCG | 60 |
| TCTCTCGGGG AAATCAACGC CCTCAACGTG CCCTCCCTTC CGGGCAACCT GAACAAGCCC | 120 |
| AATCAGACCC CCGCCTGGAC CAGCAACCCT CTGTTTGTNT ATNTNACCGA GACGTACAAC | 180 |
| ACCATTGCNT CGAAGCGNAG TGGNCCTGAA CCTCCTTAAA CCCCGBAACC CTGGAGAACC | 240 |
| TCAACAAGGA GGTGTNCAAG GACGTGTTCC TCACCAACTA CTTCTTTTAC CGGTTTGCGG | 300 |
| GCCGAGATCT TCCAAGACAT TTCAGCATGA ACCCNGNCTT TCCAGTGTTT CCATTCTTTT | 360 |
| TTTTGGGGGT TCCAAGGTGT TNCCCCCTTA GGGNTTTN | 398 |

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

| | |
|---|-----|
| TCANCATATG CATTTTTTGG TGCAACTTTN CGGGAGGNGC ATAAGAAGGA AGTCACCCCG | 60 |
| ATGCTTCANT CAACTTGCTC ANAGGTTTCT AAGAAGTGGC TCAGAGNGGT T | 111 |

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

| | |
|---|-----|
| GGCACAGGTG ATCGGNACCC AGNTCGAGCA CGTNCCGGCC ATGCTGGAAA CCATCTTCAA | 60 |
| GAGCGCCTTC GGCCTCGACC CGGCATTCCG CGGCCTGGTC GGCACNCCAT TGTNATGGGT | 120 |
| GTAAANGAGG TGTGTTGCGC AACGANNCAG GCCTGGGGCA GTGCGCCCAA CGTCGCCGCC | 180 |
| GTANGCCGAT TNAAACACCC CGGTGCNCAA GGCCTGGTCC AGGCCTTCAG CGTGTTCCTC | 240 |
| GATACCTTCG TGNATCGGCA CCTGCACCGC GTTGNCTGAT CCTGNTGTCG GGGTTCTAAC | 300 |

ACCNCAGGNT TTCGAAGGTG AATGGGNATC GTGCTGGACC CAGAATTGGG TGG

353

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

| | |
|---|-----|
| CGGGAACAGG TTGGNATCAA TATTCTCCNC TGGCGTNAAG ATCANCCCGT NATCCGNCGC | 60 |
| AAACTNTTAT TACAAACCAC GCAGGAATCG ATTGAGAACC ATTGGCCGTT TCGTCGGCTA | 120 |
| TGAANGATCA GCTGTATTTT TGGCGGGTAT TCCGCAAGCG GGTGGAGTG AAGCCCGANT | 180 |
| AATTTTGGTC GCCGCACGTG GNAGATTAAT TATCCTGCTA AACCGTATAA AGCGCCGGCG | 240 |
| GGATAAATGC GAATTGCATA CCATTTTAA GGCTTTGTTA AGCCTGAGAG TTTTTTTTGC | 300 |
| AAGGGAACCG CTTGCTAAGG GCGGTTTNC CACCTTTTCC CTCGNGTGG ATTTTTTGAA | 360 |
| ACGGGAACCA CAGGNTTTTT AAGGGTCCAC AAATTTNCCC CGGGTTCAGG GTTCCTTTTT | 420 |
| AAAAAAGGC GAGATTGGTG CGNATCCAAA AATTNCNCTT GAACGGATTG GNCAGGGTTT | 480 |
| | 481 |

T

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

| | |
|---|-----|
| TCGAATTCCT GGACTCAAGC AATCCTCCCG TNTNAGCCTC CCAAATTGCT AGGGTTNTAG | 60 |
| GTGTAAGCCA GCCCTGGCAA CAAAGTGTA AGACCCTGNT TCTGACCAAA AAAAAAAAAA | 120 |
| AAATTNAAAN CA | 132 |

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

| | |
|---|-----|
| CNGNGCTTCC ATCGGNTNAC CGCTGCGTTG CCACGGGCGC TTGAAGGTGC CCATGCCAAA | 60 |
| CATATCCGNC CCCGGCCACA CAAAGGTGTG CCACTGAACA GGCGGCCATG CGCAGGTGCT | 120 |
| CGNGCCATCG GTTTGCCGAG GGATCAGCTT GTTTGCNTCG TAAATGGCGG AAGGCGAGGG | 180 |
| GAGAGTCGCT GGCAAGGCCT TCGAAGCGCA CCTGATTCTA CAACGGGGAN NTTACGGGCA | 240 |
| TGGGNGTTTT CTTATTGTT CTTGGGCGAT GTTTGGGTTA TTAGCAAAGG NACCTGGGGT | 300 |
| TGCTGNTTTT TGGAAATTAA CCAAGGTGTA NTNGCGGTTT TGAGTTGGNG AGGGTTA | 357 |

(2) INFORMATION FOR SEQ ID NO:421:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

| | |
|--|-----|
| GGCACAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTTA GCCCGCCGCT GCACGCTAAG | 60 |
| CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG | 120 |
| CGCACCACTG CATGAAGAAT GGTTCACCA ACNAGNATGC GGTCTATGC CGCGGCGGCT | 180 |
| GGTTTCAACT TCGGGTAATT CAGGCATAGC ATCTCCAGGG ATGAACAGAT GGAGTCAATA | 240 |
| TGGGGGCAAG CAGNTATCAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATGCAAAG | 300 |
| CGGAGAATTA TTTGATTTTG CGCTTCTTTG TAGATNCACG TGGCTGGGCG GAACA ACTGG | 360 |
| GNCCGAATTT TTTNANTTNC CAATTTTTTC CGGCTTNANN ACGTTTGTTN CCTTCGTAGT | 420 |
| GGNTNTAGAA GNGNCCANT ACCNGNAGGA GGAACCCACT TTGNTTTTTT CAAGGATAAC | 480 |
| CTTTAGNCCA GGNTTTTTTC CCNTAAGNAT TNAGACT | 517 |

(2) INFORMATION FOR SEQ ID NO:422:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

| | |
|---|-----|
| GGCAGAGCAG CCCTCAGGCA GCTCCAGCAG CAGATATTTA GCCCGCCGCT GCACGCTAAG | 60 |
| CNCTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTTNCGTT | 120 |

| | |
|--|-----|
| GCGCACCACT GCATGAAGAA TGGTTGCACC AACGAGATGC GGTCTATGC CGCGCGGCT | 180 |
| GGTTTCAACT TCGGGTAATT CAGGCATAGC ATCTCCAGGA ATGAACAGAT GCAGTCAATA | 240 |
| TGGGGGCAAG CATNTAACAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATCAAAGC | 300 |
| GAGATTATTT GATTTTCCGC TTCTTTGTAG ATCACGTGCT NGCGAACAAAC TGGATCGATT | 360 |
| TTTTTCAGTT CCCATTTTTC CGGTTTAGTA CGTTTTNCCN TCGTAGTGGT ATAGAAGTGA | 420 |
| CCCATTANCC GCAGAGGAAA CCATTTGATT TTNTCANGG | 459 |

(2) INFORMATION FOR SEQ ID NO:423:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

| | |
|---|-----|
| GGCACAGGTT TTTNGGGCTC AGTTCGTGGT GCCAGCTGCC GTGGGTGCGG TGAATGAAAC | 60 |
| GAGTTTCACA GAACTCCCAG AAGCGCCGGT ACCAGGTTTC GTAATGCAGC TCCCCCGTGC | 120 |
| NTTTGAGCAG CGCCTGGGCA GCGGCACTGG CTTCGCAATG GGTCCAGTGC AGGCGCTCGC | 180 |
| GCACNANGGG GCCTGGCTCC AGTCGAGGGT GTAGACAATG CCGGGGGCGC CGTCGACGGC | 240 |
| CCAGGCGTAT TCACAGGCGC TGGCGAACAG GCCCTTGGCG TCGGTCACTA ACCACTCAGG | 300 |
| GGTGACGAGC CCGGCATCCA GCGCGCACT TCAGGGTGCA AACCANTCGN GCCCATTGAA | 360 |
| ACCNTGGCCC GGGGGTGATN CCNTAGGGAC G | 391 |

(2) INFORMATION FOR SEQ ID NO:424:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

| | |
|---|-----|
| GANTTGGCGG TCAGGTCACC GCGGCTTCC ANGGGCGAAA TCAGGAAGAT CACCGCCACC | 60 |
| GGGATAAACG CCACCCAGTC GAACGAAAAA CCGTACTTGA ACGGCACCGG TACGCTGATC | 120 |
| AGTGGCAGCT GGGGCAAGGC GCCCAGGTCG ACGCGGCCCA TCCACCAAGC CACCACAAAA | 180 |
| CCCAGGGTCA GGCCGATCAC GATCGAACCC AGGCGCAGGA ACGCTTTGTT GGAAGCGGTT | 240 |
| GAGCACCACG ATGGTCAGCA GCACCAGGNT CGCCACCATN NTTTTNCCGG CGGNGCCAG | 300 |

| | |
|---|-----|
| GTCGTTGGCG CCATNAACCG CCGGNCATGT TCGGTGACGG NCACTTGNTC AGGGACAAAC | 360 |
| CCTTCAAGGT AATGATGGTG CCCGTGAACC ACCGGGGTGT TTAATTTGGC CATTTNCCCG | 420 |
| TTGAAATGTT TGNGNACCNT TTGNTTAAAA GC | 452 |

(2) INFORMATION FOR SEQ ID NO:425:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

| | |
|---|-----|
| ACACCAACTA CCAGTATCAC CGGCAGTTGT NCCTGTNTTA CCCANTCTGC ANAAGTGAAA | 60 |
| GTNTCAGAAA GCGGCGTAAA CCAGCCGCCA GCACCTTCCA CTAACACCCA GTCAGCCTGT | 120 |
| TGTNCAAGCG CCGCGTAAAT CCGGCGCTCA TTACCAATGA ATTCTATCGG TCTGCCCTCT | 180 |
| TGCGCCGCTG GATGATGTGC GGCGNAGTGG GTTCTGCGAA NGTGTGAAGG NTTTACTGTT | 240 |
| GCGTAATCCA GCTGCAGGCT GCTGTTGCCC TGTGAACGCC AGGCGTCGCT ATTGCGTGAA | 300 |
| CCCTTCCGGG GTNTTTTCCG NTGNCANTGG NGACCGGTTT TT | 342 |

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

| | |
|---|-----|
| GGCACGAGGN CAGCCAGACC TTGCCGGTTC CCGACGGCCT GGACTGGATT CAGGCGGCAC | 60 |
| GAATCCCGGA AACCTTCTTC ACCGTATGGG CCAACCTGTT CGGCATCGGC GGTGCGCATA | 120 |
| AAGGCCAGCG CGTNTTGATC CATGGCGGCA CCAGCGGCAT CGGCACGACC GCGCCTGATG | 180 |
| CTCTGCCGCG AAGTTCCATA TCGAAGCGTT CGCCACCGCC GGCAGCNTGG NAAAAATGCG | 240 |
| CCGNCATCCG CGAAGCTGGN TNCCGAGCCG ATCAACTACC GGGAACAGAA TTTCGCCGAG | 300 |
| GTCATCGCTG ACAAGACCGC AGCGANAGGN TGTCAATGTN GGTCTTCGA AATCATGGGT | 360 |
| GGCTNCTACC TGANCGG | 377 |

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GGCACGAGGG AAGCACGGCC CANCCNTCCG GAATTCAACA TTGGCTCAGC AGGGAATTCA 60
GCCCANCCCCA CGGNACCTGN 80

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CNNCTGCAGG TCGACACTAG TGGATCCAAA GAATACAGCC GAGTTTCACA CCAACTACCA 60
GTATCACC GG CAGTTGTNCC TGTNTNACCC AATCTGCAAA AGTNAAAGTN TCAGAAAGCG 120
GCGTAAACCA GCCGCCAGCA CCTTCCACTA ACACCCAGTC AGCCTGTTGT NCAAGCGCGC 180
GTAATCCGGC GCTCATTACC AATNATTCTA TCGGTCTGCC CTCTTGCGCG CTGATGATGT 240
GCGGCGAAGT GGGTTCTGCG AAGGTGTAAG GATTTACTGT TCGGTAATCC AGCTTGCAGG 300
CTGCTGTTGC NCTGTAACGN CAGCNCGTCTG CTATTGCGTA AAACCTTCCG GGGTCTTTTC 360
GGTTGCCAGA GGCGANCCGG TTTATAAAAC CTGCCGTNCC GGTAGCCTGT NGGCTTTTTC 420
NGGGTTGGTA AAAAGTNGCA CAATTGGGGG AACAATTTTT CCCCCANTTT GGGGTATCCC 480
GTTTCCGGTG 490

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GCTGAATATN ATCGAGTGCT GGGGCGATGA TGTACCTCAG GGGCAGGTNA CCTCNTTTC 60
CATGGCGGTC AAGCTCAAGG AGGATGAAAC CNTGGTGTTT TCCTGGATCG TNTGGCCGTC 120
GCGGCAGGTG CGTNTCGNCG GGAATGAGCA AGGTGAATGG NAAGACCCGC GCCCTGAAAG 180

GCAGACGTCA ATCCGATGCC GTTTGATGGG CAACGGGATG GATCTATGGC GGATTTAAGA 240
TGATCCTCAA CACCTGAGGC CAGGCGTTCA TGGGACGGCG GCTTTANTCC CGATTCGTCT 300
NTTCGCANGG TTAGGACCGA CGATAAATTC TGGGTTGCAA GACCANTGNC GAAAAAAGT 359

(2) INFORMATION FOR SEQ ID NO:430:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GGCACGAGCA AAACTCTGCT AAGGACCATA AGCATATTTN ATCACTTGCA GAGAGGCATC 60
ACTGTCACCC CAATTTACAG ATGGGAAACT GAGCAGAAAG TTGTTAAAAC ACCCAGCACT 120
TTGGGAGGCC GAGGTGGATG GATCACTTGG ATCTCTGGAG GTTGAAGCC AGCCTGGGGA 180
AACATAGCAA AACCCCATCT CTACAAAAA AATCCAGAAA TTAGTTGGGT GTGGTGGCGC 240
ACGCTGTGAG CCCAGCTGC TTCAGAAGGC TGAGGCTTGC AGTAAAGCTG AGGTTTGCCA 300
CCCACTGGCA CTTCGNGGCC TGGGGGCAAC AGGNGACCCT GTTTTCAAAA AAAANN 357

(2) INFORMATION FOR SEQ ID NO:431:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

NCGATATCGC CACGNTCGTT CAAATACTTG AAGTCGACGT TCTGTGAACC GCTGCCATGC 60
AGATGAATTT NTCCTGTNCG GCCGGCAGTN CGTTGAACGG CACTTCCAGG GCTGAACTTG 120
TAGTGCGAAA NCAGACGAAA CCCAGCATCT GGAAGTAATA GACGTTACGC CTGTCCCCAG 180
NCACGTATCG CACCCTTCCG NCAGTNTGNA GGTCACCGTT GAACCAGGCG CTTGATTGTT 240
CGAAGAATTG CTTTAACCN CAGGNCATCA CAGGTTCGGG CAAGTGNCCG GCCGGGGTTG 300
TTTNAAGGG AAAACAAGT TTCGGTTTCC AANTTCGCT 339

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GGCAGAGGNC GNCGGCGGNG GCGGCGGGGN ACTCGGACTC CTGGGACGCC GACGCTTN

58

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GGCANAGTTT GCATTAGGA GAAGGGCAGA TGGTGTGTGG TCGAAAGCTC ATGGGACTGT
AAATTGGTAG ACTTTTTTAA AAATCCAGCT TTTGCCCTA ACTTTTGGTC TCGGAGACCT
CTGTCCTTTA ATAAC TAGAA CTGTAGGCCG GCGTGGCGG CTTCATGCCT GTAAATCCCA
GCACTTTGGT AGGGTGAGGC GGGCGGATCA CAAGGTCAGG AGTTTCGAGN ACCAGCCTGG
CCCAGCATAG TGGAACCCTG TCTCTAGTAA AATTACAAAA TTTAGCCAGG CATGGTGACG
TGCGCCTGTA GTCTTCAGCT ACTTGTTAAG GGNTGGGGGC AGGNGNTTTG CTTTGNAACC
CGGGGNG

60

120

180

240

300

360

367

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

AGCTTCCAGG TTGAAGCCGG NGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG
ACCACCCTGC TGCGTACCCT GGTCAACGAA CTGACTCCGG ATGCCGGTAC GTGCAAGTGG
TACCGACGCG GCTGAAACTG GGCTATTAAC GCCCAGAACC ATGCTTCGGA ACTTCAAGGA
CGAAGTCCAA CCTGTTNCGA CTGGGTTGGG CCGCTGGACC AAGGGAAGGG CGAGCAAGTG
NGTTCGCGGT ACCCTGNNGC CGCAAAC TGG TTCTTCCAAC GANGNGG

60

120

180

240

287

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

| | |
|---|-----|
| GGCACAGTAA AAAGGTTGAA AATGGCTTTT TTCCACTAGG AAGGCTGTGG GGACATAAGC | 60 |
| TGACAACTAC CCTACATGGA ACAGGCAACC CCGTCATGCA AGTAGGCCTC TCTCCCAAAG | 120 |
| GCACCTCCAT CCCTGCTGTC ATGTGGCACA GATGAGCACA CCTACTACGT CACAATGCAG | 180 |
| TGTAGCCACG CCAGACTGGA CCAAGGACAC ACTCTTAGCC TTCTCTTCTC TCCAAATTCA | 240 |
| CTTTATTAAT CTTTAANCCC ACACATCCGT GGTGCGGAAA GGTGTCCTTT GATTCTTCCA | 300 |
| AAATTCAAAA GGGCNTTCCC TGNTATGGNT GTCTGGGATT TATNTT | 346 |

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

| | |
|---|-----|
| GGCANAGCTA GTNCTTTNTT CCATAAAAAA AAGTCGTGCC TGTGGTTATG AAAAAATGTT | 60 |
| CAACTAACCT AGAAGAGTTC AGCTACCAAG TGAAGGATTA TGGGAAAGCA GTATTTTTTC | 120 |
| AGACCTGGGT ATGCATGAGT GAATACCCAT GAAAGCTTTA TGAAAAATAT ACATCTCCTG | 180 |
| GGCCCCATT AATCAGAATT TCTGTGGGTG TGGCCTCCAA GTTCATACTT TAAATGGGA | 240 |
| TCTCCACATA ATTCCATGTA CACCCAGGCT GGGTAAACA CTGAGTTTCA TGTATTTATT | 300 |
| ACTATTCCAG AAACAAACAC AAATCTTGG GGTGGGATTT TAAAGGGNGC AAGGTTTTTN | 360 |
| GGNTGGTGTT AAGCAAAGCC ATTTTNAAG TTGGTCTNTT GGCAACTCCA AGG | 413 |

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

| | |
|--|----|
| AANCTANCGC NANGNGCGCC TGCAGGTCGT AACTAGTGG ATCCAAAGAA TTCGGCACGA | 60 |
|--|----|

| | |
|---|-----|
| GCGTGACCT GCGATTCCG AAAAGCTCGG TGTTCGTGCG TNATGAACGC AAGCCCAGCG | 120 |
| CCTCGGTCCT GGTGGAACCT TTTGCCGGCC GCTCCCTGGA GCCTGGCCAG GTATTGGCGA | 180 |
| TCATCAACCT GGTGGTCCAC CNACNTTCCT GAATTGAGCA AGTGCGCAGA TCACCGTAGT | 240 |
| CGACCAGAAG GGCAACCTGC TGTNCGGNAC CTTGCGGAGG AACTNTTTNG CTGACCATGG | 300 |
| CCGGNCAAGC AGTTCGGACT GACAG | 325 |

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

| | |
|--|-----|
| GGCACGAGGN AGAAAAGGAA GGGTGAAGG AAAAGAAAAG AAAAAAAGGA AAGGAAAGAA | 60 |
| AGGGAAAGAC AGGAAAAAAA AAAAAAAAAA NCNCGGGGGN NCTT | 104 |

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

| | |
|---|-----|
| GGCACGAGGC CATGGTGTCTG ACCAGGNGGC TCGGTTTCATC AATGCTGTTG AGCGAAGACA | 60 |
| GGACTTCAGC CGGGACTTTN TTGCCCAACT GCACATATTG CTCGAACTGC GACANAGCTT | 120 |
| GCGCACGNAC AACTNGGATT NATGATCCCG GGCTTCGA | 158 |

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

| | |
|---|-----|
| NNGTANNGCG CCTGCAGGTC GACACTAGTG GATCCAAAGA ATTCGGCAGC AGCCGNCACC | 60 |
| CAGCGTGGCA TGACCTTGGA ACTCAGAGGT CGGCTTTTTG CGTACCAGGT TGATAGTGGC | 120 |

CCCCAGTGAA CCAGCACCGG TCAGCAGGNC ANTCGCGCCC TTGAAGTACT TCAACACGGT 180
CGTAGATCGC CATGTCGCTC AGCGTGTTC CCGTCGAGTA AGCCACGTTG CGTGCGGTGG 240
AAGGGNATCC CGTNATATTN GGAAGTTGTT GATAGAGAAA CCACGAGCGT AGTAGTTGCT 300
GCCTCAGTA TCGAAGGCTT GAAACGGNAA TGCCCGGCGT NTGGNGCATC AAGTTNGNCG 360
ACACTGGTCA GG 372

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAGTAGGNGC CCATNCATCT TTGCTGTGGA GCATTNGCTC CTTTTTNGGG GTGGGAATNT 60
GCCTTGCCCG GTCTGCCGGA AACCAGCAGG AGCAACCTGC GGTNCCCACA AAATTTNGGG 120
TGTA CTGGAC CCACTNGCA 139

(2) INFORMATION FOR SEQ ID NO:442:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GGCAGAGTGN CATNCAGNTC GGACCGAAAA AAGTGGTTTA ATTCGGGCTG GCTTGTGCG 60
GTGTGAGCGG TCTGTTTTAT GCCATGGCTT TTTGGTTCAC TGGTCTGCCG TTGCTGAGTT 120
TAATTCTGCT GTGCATTGGC AGGGTGTTC TCGGCGTCGG CNAAGCTTT GCCAGTACGG 180
GGTCTACCT ATGGGGGATT GGCCTGGTGG GGCCGTGCA TACCGCCCGG GTTATCTCAT 240
GGGAATGGGG TGGCGACTTA CGGTGCGATG GCTGCCGGGG CACCGCTTCG GTGTTTTACC 300
TCAATCAGCA CTGGGGGGTT GGGCTGGGGG TGGCGGCGTT GATCGTGTTG GNCGGTGGNC 360
GGTTTCGCTG TGGGNTGTG GAATTNCAA CCAACGTGA ACGATTCNNC GNCGTTAANG 420
GTAATTGCCC TTANCGCAAT TTTNGGGGGC TTATTTGGAC TTAAGGTTTT GGGACTTGCA 480
ATGGGTACCT GGGTTTTGCC GGNANCGNA 509

(2) INFORMATION FOR SEQ ID NO:443:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

| | |
|--|-----|
| GGCAGAGCTT GGCTTCGCTG GTTTTCGGCT GTTCCAGGAT GGTGCTGACC TTGTTGTAGG | 60 |
| TCANGCGGGC CTGGGAAGTN AATCACCGCT TCGTAGAACT GGTAGTCGGT CATTTGCGCCG | 120 |
| GTTTTTCGAGA TGGTCATCTC GCACACCATG GCCAAACGGT CGACTTTCGG GTTCAGGGAG | 180 |
| CACAAGCCGT TGGGACAGCT GCTCAGGCAC ATAGGGGATG ACGCGCTTCG GGGAAGTACA | 240 |
| CCGGGTGTC GGGCAACTGG GGCTTCGTTT NTCCAAGGCC CGNACCNGTT CTTTAAGGTA | 300 |
| GCTTTGGACA AGTTGGGCAA TCGGGGACGA AACNAATTTT TCCAAGCCNG CNGGAGGAAC | 360 |
| AAAGGGGCAA NTTTNCCAA GGTTTTGGGT TTCGCAATTA AAACCCCAT TGTTCGAAA | 420 |
| TTCNCGGGG NAATTTTNGG CCNGAANTGG GGGACGGAAC CGGAAATTTT ACCGCAAATT | 480 |
| | 480 |

(2) INFORMATION FOR SEQ ID NO:444:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

| | |
|---|-----|
| GGCAGAGGAA GACATCCCAT GTTTATGAGT CTGAAGACTT AACATTGTTA AGATAATACT | 60 |
| CTCCAAATTG ATTAAGAGGA TAATACTCTC CAAATTGATC TACAGATTCA ACATGATCCC | 120 |
| TATCAAAATC TCAGCTGGCT TCTTTGTAGA AACTGACAAA TTGATTCCAA AATTCATATG | 180 |
| AAATTGCAAG GGATGCAGAA CATCAGAACA ATCTTGTAAG AGANCAAAAC TGGAGTACTC | 240 |
| CCACTTCTCA AAAACTTACT GCAANGCAA AGTAATCAAG ATAGGTTGGG GCATGGTGGC | 300 |
| TCCTGGACTG TAATCCCAGC ACTTTGGAAG GTCCGGGGCG AGTGGGGTTC ATTTGAGGTT | 360 |
| CAGGGGTTC AAAACCAGNC TGGGCCACCT GGGTGAACC CCCTTTNTA CTAAACTTT | 420 |
| TAAAAAATTT GGNTGGGGCT TGGTGGGCGG GGNCGTAAT TCCCGGTAC TCNGGGGGT | 480 |
| TT | 482 |

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

| | |
|---|-----|
| GGCAGAGGGC TTCCAGGCAC ACCAGCGCCA GGNAGTAGCG CAATTCGTCA TCGTCCGGGT | 60 |
| ATTGCNGCAC GAGGTTGGCG AACTGNACCT TGGCGTCTTC CATGCGGTCC TGTTCGACCA | 120 |
| GCATGCGGGC ATAGGTCAGC AGCAGGCGTT TGTCGCCCCT GTACTTCTTG ATGCTTTTTT | 180 |
| CCCAGCAACG GGAATCGTTT NCTTGCCNGG GTTTGAGGTT TTNCAACAAG CGGGCGCGCA | 240 |
| NANGGATTCG GGG | 253 |

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

| | |
|---|-----|
| GGCACAGGAA GGAAGAAGAA GAAGGAGGAG GAGGAGGAGA AGGAGGAAGA NGAAAGAAGA | 60 |
| AGAAAGAAGA GGAAGAAGAA GAAAGGAAGA AGGAAGAAGG AGAAGGNGGA GAAGGNGAAA | 120 |
| AAGCGNANAG AGGGAAGGAA GANGAAGGGA AAAAAAAAAA AAAAAACC | 168 |

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

| | |
|---|-----|
| GGCAGAGGNA AAAAGGGAGA TACTATTTTN AGTAAATTTG AGGGCAAGGA ATATACAAAG | 60 |
| GAGTTAGGTG GCTTGGAAGA AGATTTTTC TATATATGTA AACTAAGCTG TGTGTGGGTG | 120 |
| GGTATTTTGC TTGTTGGTTT TTGAGACAGG CTCTCACTGT AGTCCAGGCT GGAGTGCAGT | 180 |
| GTGGCAGTCA TAGCTCACTG TAACCTTGAA CTCCTGCACT CAAGCCATCC TCCCACTTCA | 240 |
| GCCTCCTGAG TAGTTAGGAC TACAGGTGCG TGCTACCACA CCCTGCTCAC TTTGGCATTT | 300 |

TTTTNTNTTT TNTGTTTNTT TGATTTTTTTT GGGACATAGT

340

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

| | |
|---|-----|
| GGCAGAGTCT GGACCGGNCT GGCCAATATG GTGAAGCCCC CCTCTCTACT GAAAATGCAA | 60 |
| AAGTTAGTCG AGTGTGGTGG TGGGCACCTG NTAATCCCGG CTATTTGGAA GGCTGAGGCA | 120 |
| GGAGAATTAC TTGACGCTGG GAGGTGGAGG TTGCAGTGAG CCAGGGTCGT GCCGCTGCAT | 180 |
| NCCAGCCTGG GNAGACAAGA GTGAGACATT ATCTCAAAAA AAAAAAAAAA AAAAAANAAA | 240 |
| AAAAACCCCG GGGGGTTTTT TTTGGGGGGC CCGGGGCCNN TGNTTTTCCC CCCGGGGGGG | 300 |
| GTGNCCCCG | 309 |

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

| | |
|---|-----|
| AGCTTCCAGG TTGAAGCCGG TGAGCGCGTG GCGATCATCG GCCCGAACGG TATCGGCAAG | 60 |
| ACCACCCTGC TGCGTACCCT GGTCAACGAA CTGACNCCGG ATNNCGGTAC GTNCAAGTGG | 120 |
| ACNGACGCGG NTGAACTGG GCTATTACGC CCAGGACCAT GNTTCGGAAC TTCGAAGACG | 180 |
| GAGTCCAACC TGTTGACTG GATGGGCCGC TGGACCAAGG NAAGGCGAGC AAGTGGTTTCG | 240 |
| CGGTTACCCT GGGCCGCATN GTTGTCTTN CAACGNCAG NTCCTTTAAT TCGGTTGTAG | 300 |
| GTGAATTTCC CCGTTGG | 317 |

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

| | |
|--|-----|
| GGNACAGCTC GCGGGAGCGA TATCGCCACG GTCGTTCAAN TACTTGNAGT CGACGTTGTG | 60 |
| TGAACCGCTG CCATGCAGGA TGGAATTTCT GCTGTTTCGGC CGGCAGTTCG TTGAACGGNC | 120 |
| ACTTCCAGGN TGAAC TTGTA GTGCGANNCA ACGAAACCCA GCATCTGGGA GTGAATAGAC | 180 |
| GTTACGCCTN TCCCAGCCAC GTNATCGCAC CCTNNGGTCA GTNTGTAGGT NANNNTGTGA | 240 |
| CCANGCGCTT GGATGTT CNT AGAATTGCTT AACCCCCAGG CCATCACANG TCGGGCAAGC | 300 |
| GCCGGCCGGG TTGTTGAAGG AAAACANCTT CNGTTNCCAG CTCGTGAATG GNATGGCCTC | 360 |
| AGATTCGTGC A | 371 |

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

| | |
|---|-----|
| GGCAGAGCAG CNCTCAGGCA GCTCCAGCAG CAGATATTTA GCGCGCGCT GCACGCTAAG | 60 |
| CACTGGTTGG TCGCTTAAAC GGTAGATCTC TTCTGAAACC GGCCAGCGCA ATTGCCGTTG | 120 |
| CGCACCCTG CATGAAGAAT GGTGTCACCA ACGAGATGCG GTTCTATGCC GCGGCGGCTG | 180 |
| GTTTCAACTT CGGGTAATTC AGGCATAGCA TCTCCAGGGA ATGAACAGAT GNAGTCAATA | 240 |
| TGGGGGCAAG CAGATANCAA AAAACCCCGC CGGAGCGAGG TTTTTTTTTT ACATCCAAAG | 300 |
| CGGGNATTNT TTGATTTTCG CTTCTTTGTA GATCACGTGC TTGGNGAACA ACTGGTTCNN | 360 |
| ATTTTTTT | 368 |

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

| | |
|---|-----|
| GGCAGAGGNA TGGGTGCCTG TGGTCCCCAG CTGCTCGGNA GGCTGAGGCA GGACAGTCGC | 60 |
| TTGAACCCGG GCAGCAGAGG TCGNGGTGAG NCNAGAATTG TGTCGCTGNA CTCCAGCCTG | 120 |
| GGCGACAAAG GAAGACTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAC N | 171 |

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

| | |
|---|-----|
| GGCACGAGGC GCTGAATATC ATCGAGTGCT GGGGCGATGA TGTACCTCAG GGGCAGGTGA | 60 |
| CCTCGTTTCC CATGGCGGTC AAGCTCAAGG AGGATGAAAC CGTGGTGTTT TCCTGGATCG | 120 |
| TCTGGCCGTC GCGGCAGGTG CGTGAACGCC GGTNATGAAG ACAAGGTGAT GGAAGACCCG | 180 |
| CGNCCTGAAG GCAGACGTCC AATTCCGATG CCGTTTGATG GGCAACGGGA TGGATTCTTA | 240 |
| TGGGCGGATT TGAAGNATGG ATCCCTCCAA CACCTGAGGG CCCAGGCGTT TCATGGGACG | 300 |
| GGCGGGTTGT TAGTTCCGAT TCGNCTGTTC GCCAGGGTTA GGGACCCGAC GGATTAAACT | 360 |
| TCTGGGTGGC AAAGACCCAT TGCCGNAAAG ANTANNTTCT TAGAGCGGCC CNGGGNCCCA | 420 |
| TTCGTTTTTT TCCANCCCGG GTTGGGGTTA CCAGTTAAGT NTTACCCATT TCGGCCTTTT | 480 |
| AGTGATCGAA TTTTACAATT TCATTGGC | 508 |

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

| | |
|--|-----|
| GGCACGAGGC CATGCGCAAG GACGTGCTGG CTAAGTGCTA CGGCGGCGAT ATCTCCCGTA | 60 |
| AGCGCAACTG CTTGGAAAAG CAGAAGGCCG GCAAGAAGCG CATGAAGACG CTGGGCTCCG | 120 |
| TCTCGGTGCC GCAGGAGGCN CTTCGTGGCC GCGCCTGTCT ACCGACGCCG ATGATTAACC | 180 |
| CACCCAAGCA CGCCGAACCC TTCTCGCAGC CGGCCTTGG TTGCGAAGGT TGTCAGCTGC | 240 |
| CGGATTCCAC GGCANGCTTG AGCGNCCCG TCCGCGCAAG AGGGGTTGGG GCTGGGGCTT | 300 |
| TAGGCGAGTA NTTAGGTTGA ATCGGCCCAG GGTNGGACCC AGACTATTTCG GTNCTGGTGT | 360 |
| TCGTTTCGAGA GTTATTTTTA NAGCGGNCCG GGGGCCCAT TCGATTTTCC ATCCGGGTGG | 420 |
| GGGTACCAGG TNAAGNTTAC CCAATTGGNC CTTTAGTGGA TCGTTTTACA AATTNATTGG | 480 |
| CCTNGTTT | 488 |

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

| | |
|--|-----|
| GGCAGCAGNA CTGCGGCGTG CTTCTGTCTG CGTTTCGCCA AGANCTTCAA TTGGGCCCCAC | 60 |
| CTGGACATCG CCGGNACCGC CTGGTANCAG CGGCGGCAAG GACAAGGGCG CCACTGGCCG | 120 |
| TCNGGTTCCA TTGCTGACCC AGTACCTGCT GGAACCGCGC CAAAGCCTGA AAATNAAGAT | 180 |
| TNCCGGGCGC TTGTAAACC GCCCGNGCT GCAGGGAACC GCAATGTACC CAAGTNGACT | 240 |
| TCTTATATAT TGCCCAGCGC CGATTCTTC CGCGGGCCTG GNACTTTGCC TGCAAGCTTC | 300 |
| ACCGNAAAAA GCCTGGCGCA TGGGCCACCG TATCTNACCT GGCATTNGCA ACGGTTGCCG | 360 |
| NCCAGNTTNA CGGACCTTGG ACGGNCCGTC TGTGGGGGTT TTCAAGGGGC GAAAGTTTTC | 420 |
| GTGMNCCCAG GGTGNCCGCC GAATTCAGAA CCGGAAGGGC TGGTTGGTAC TNGGGTTTTG | 480 |
| GGGCGACAAT TGN | 493 |

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

| | |
|--|-----|
| GGCAGGAGCG CGAAGTGGTT GCGGTACTCC TTGAGCGAGC TGCCTTCCGG CGCCACATCG | 60 |
| GTGTCGTGGA AGCTGTAGTA GTCGATGCCC AGCTTGAGAGA AAAACTCAAA GGCCGCGTCA | 120 |
| CCTTGCCGAT GGCCACTTCC ATCGGCTTNA CCGCTGCGTT GCCACGGGCG CTTGAAGGTG | 180 |
| CCCATGCCAA ACATATCCGC CCCC GGCCAC ACAAAGGTGT GCCAGTAACA GGCGGCCATG | 240 |
| CGCAGGTGCT CGCGCATCGG TTTGCCGAGG ATCAGNTTGT TTGCGTCGTA AATGGCCGGA | 300 |
| AGGCGAGGGG AGAGTCGCTG GCAGGGGCTT CGAAGCGCAN CTNATCGACA ACGGGGGAAG | 360 |
| TACGGCATGG GGC GTTTTTTC CTNATTGTTC NTNGGG | 396 |

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

| | |
|---|-----|
| GGCAGAGGCC GGTTCGCGNT AATCCGCAGC GACTGGTGGG CGGCACTGCN TTACCGCCTG | 60 |
| CGNGGCACCN TGCGGNAAAA CAACCTGCAC GGCAAGACCG GCTCCATGAG CGGCGTGTCG | 120 |
| TCGTTGAACT GGGTATGTCA CCGATGCCAA TGGGCGCAAC TGGTGTTTTC GATGGTGACC | 180 |
| AACAATTACG TGGTCGCAGG CGCGCGGGTC AAGGCGCTGG GAAAACCGCC TGGCCACGGC | 240 |
| ACTGGCCAAC AGCACGGACT ATTGAGCACC GAAGATCAAA TTTTNGACGN GGTTCGCTCC | 300 |
| GGAAATGGGG TTGTTGACAT TCAACACATG TAANTGATTG ATCCCAGCGT TTTTCGGGGN | 360 |
| AAAANCCC | 368 |

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

| | |
|---|-----|
| GGCANAGGCC AGGCCATCGC CCTCAAATAC GACGGGCAAC AAGCGCCGAC CCTNNNCGCC | 60 |
| AAGGGGAGCG NATGCCCTGG CCGAAGCCAT GCCTCAAGCT GGCCCGGGAA GAACGANTCC | 120 |
| CGATTTACGA AAATGCCGAG CTGGTCAAAT TACTGGCAGC CATGTNGTTG GGCGACACAT | 180 |
| NCCCGGAAGA NTTGTACCGC ACCGTCGCCG AGATCCATCG CGTTTGCNTG GGACGCTGAA | 240 |
| GGGCAATTCC CGGTGGGCTA CGACCCGGAA CGCGGGGCCG GTGGAGCGTT TTTTGACGGG | 300 |
| AAAGAGGGCG ACGATTTATT AAGGTNGGGA GCCGGTTGAN NTTTCCCAAG TTTTGGGGG | 360 |
| CCNCCGN | 367 |

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

| | |
|---|-----|
| GAGCAGACAC CAAGAAGTCC CAGGCCAAAA TTTTAATTGG NCTAGANAAT GTGGCTGGGG | 60 |
| TGTNAGTNAC CAGCCTCAAG GATGGGCTCT TNAGCTTGCA TCTAAGTNAG AATGTCATCG | 120 |
| GTGGGCTCCA AGGGGGACTT CCTGCTGGTN AGCGAAGCCA TGTGAATTGA CCTGCTGACC | 180 |
| AAAATGTACC GGGCTGTGCT GGATGCNACG CNAGGCAGCT TACAGTCACC GTGAACTAAG | 240 |
| AAAGTTCTCC AGTGAAGGTT CCAAGGAGAA CAGTGTGGCT GTCNAGGTTT GTNCCAGGGC | 300 |
| CCTGCAGTGG TGNACCAGN AAGGTTACGT TACAAAAAAA GGGGGNGTCC TTG | 353 |

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

| | |
|---|-----|
| TNCNTNTTTT TATTTAGTNC TACATAGTTT TATTGCATGG TTGGGTAAAA CTAACACCAC | 60 |
| AGGNAAGCAA TGTAAGATTG TCATGACCAC CATGGTCCCT GGTGCTNNAT TTTAAATTTT | 120 |
| TTTGGGGGAT GCGTCTNAC TTTNTTGCCC AGGGTAGAGT GCAGTGGTGC NATCTCTG | 178 |

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

| | |
|---|-----|
| GGTGGTGAAT TTCCCCAACT ATNACCAGAC CTNAAAAATC GTGGGTAANA AGCTGGTGGG | 60 |
| GGTNTCCACC ATCGNAGGCG TGACCTATGA GCGCNTAANA AGAGAANTGG CCTAAGCAGC | 120 |
| CAGGCCCCGGC CCAGGGAAGC TACAAACCCA CCANTAAAC TGAATATAAG GACAAAAAAA | 180 |
| AAAAAAANTT TTGGGGGGGG GNCCGGNTCC CN | 212 |

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

| | |
|---|-----|
| CAAGGATTAC AGAGCTAGTA AGTGGCAGAN CTGGGCTTTA AACCCAGGGA AGCTAGATTC | 60 |
| CAAAGTTTTG TTTCTTAAC TACTAAGCTA CACTGTTGAT CACCCTTGGN GTCGTGGGTT | 120 |
| AGGAAGAAAA GGAAGGGGAA ACAATGAAGG TGGGAGAAGA TGAAGGACTT AGGGCTCAAA | 180 |
| GCTGATGCTT CANTGAAGGT GGGAAAACCT GTGCCTGTGG GGTTCCTC AGATTACACA | 240 |
| CACGTGGCAC AGTTTTNCAT NATNCAGGTT GCTGAAAAAN AGGT | 284 |

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

| | |
|---|-----|
| GGCACGAGGC TCTGTGGAAG ACGACCACAT CCCCTTCCTC CGCAGAGGGG TACCCGTGNC | 60 |
| TCCATCTCAT CTCCACGCCC TTCCCTGCTG TGTGGCACAC CCCTGCGGAC ACCGAGGTCA | 120 |
| ATCTCCACCC ACCCACGGTA CAAACTTGT GCCGCATTCT CGCTGTGTTC CTGGCTGAAT | 180 |
| ACCTGGGGCT CTAGCGTGCT TGGCCAATGA ACTGTGGAGA GGACTGTGAA GAGAGAAGGT | 240 |
| CCCAGCGGGG GCCAGTGAAA GCTCAGGCAG GTTACTGCCT AGGGTGTGCT GGTTCCTC | 300 |
| TTTCANACCT TTGTTTCCN AATTGTGCTA CANTGGAAGA CNTGTTTGNT TTG | 353 |

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

| | |
|---|-----|
| GGCACGAGCT CACTTCTGGA GAAATTGTTT ATCTTCTGGA GAAGATAGAT ACAGATTGGT | 60 |
| ACAGAGGGAA CTGTAGAAAC CAGATTGGCA TATTCCTGC CAACTATGTC AAAGTGAATT | 120 |
| GTAAGTGGGT TGTGTTTGT TTAATTGGT CATATACTCA GTGGGTTCTA TGTGACTTGT | 180 |
| AGGTTGGAAA AAATAACTAG AAACCCAGAT TCTAGTTCTC TTTCATTGAT TCATTTGGCA | 240 |
| TTTGAAAAT TCAAAAATAA NGTTTGGTCA ACTAGGTGGT GGTTAATTAT TATNTTATGG | 300 |
| GGTGTTAGGA ACTTAATGCC NANANGCTGT TCTGAA | 336 |

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

| | |
|---|-----|
| GGCACGAGCC AGGCTGGTCT CGAACTCTTG GCCTCAGGTG ATCCTCCCGC CTCAACCTCC | 60 |
| CAAAGTNTTA GGATTACAGG CGTGAGTCAC TGCATCTGGC CAATTGGATA CATTCTGCA | 120 |
| GCCAAATTTT AAATTCTTCC TATTGTGCTA TAGTATGGAT GTGCCTTAAT GTATTTAACC | 180 |
| CACCCCTTAT TATTGGGCTT ATTATTGAAC TTATTTCCAG CTTAAGTGAT AGAAACAGTG | 240 |
| CTGTACATCC TCCTAGCTAA ATCTGTGTAT ACACCCCTAG TGATTTCTT AGCTTCAACT | 300 |
| CTTAGAAGTG GGATTTNTGG GTCAAAGGGC ATGCATCTTT TAAAGTNNTT GATGTTTATT | 360 |
| GCCAANN | 367 |

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

| | |
|---|-----|
| GGCANAGTGG TAGCACCTTC AAAGAAATCC CCGTGAAGTG TCTATAGACC CACACTAACA | 60 |
| AAAGTNAAAA TTAAAGGTGA ACCTGAAATT CAAACTGATT AAAGAAGGTG NTACCAATGA | 120 |
| ACTNGAAGTG GTCCATGGAG AGCCAATTAT TAAAAAATAC ACCAAAATNC ATTGATGGAG | 180 |
| TGCCTGTGGA AATANCTGAA AAAGAAGACA CGTGAAGAAC GGNTNCATTA CAGGTCCTGA | 240 |
| AATAAATNAC ACT | 253 |

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

| | |
|---|-----|
| GGCAGAGCA GATTTGGAAA AGCAAGGGAT AACATATGCA GTACAAAATA AGTGGTGAGA | 60 |
| TGAAAGCTAA AATGAACATC TGGAAGAAAA AAGCATGGCC AGATGGGGTA AAGTCCAGAA | 120 |
| AGAAGAGTGA ACAGAGCTGG AGGTACAATG GTAAACTGTG TCTCACTAAA ATCTTCCAGC | 180 |
| TCCATGAAAA GGGCTGTGGC TTGACGTTTA TAAATGTNTG GAAGGAAAGA GAAGTCTATA | 240 |
| ATAATCTACC TGTTGACACA ATATACATTG GGGAAGTTAC ANCTTAAACA ATTATTTTNA | 300 |
| TATCACTTCA TTTTACCCAG GTATTTTCAG GGAAATTTTT AAAACGGTTA CNCTTTTTCC | 360 |
| ATGTACCCCN AAAGTTCNTG GGCAGTNTCA TCTTNGGGCC | 400 |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

| | |
|---|-----|
| GGCAGAGNCT AACCTCATTA AACACCTGAA AGTTNACACT GGAGAAAGGC CTTATNAGTG | 60 |
| CAGTGAAATG TGGGAAATCC TTTAGCCAAA GTTCTAGCCT CATTCAACAC CGCAGAGTTC | 120 |
| NCACGGGNAA AAAGGCCTTA TCAGTGCCAG TCAATGTGGG AAATCCTTTG GGCTGCAAAT | 180 |
| CTGTCCTCAT TGCAACACCA GAGAGTTNCA CATTGGAGAA AAGCCTTAGC TGTACTGNNG | 240 |
| AATATGCAAT TTCCCTTTTA GTGTAATTAT ACTGAAGNG TAACANCTNT GAAGNGNGGA | 300 |
| CAAGTTACCT GATTTGGGAA GCCCCAACAT NTAGGGTTAT ACAGTGGGGC GGTTTTCCCC | 360 |
| TTTAAGTTCC CGGTTATGTG NTTAACATTT TTTNNAACAT GGCCTTTTAG GAAGGGTTAN | 420 |
| GACTTTTTTT NAATTG | 436 |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

| | |
|---|-----|
| GGCAGAGTTA CAGTGGATGA TCTGAAGAAC CTTTTCATAG AAGCTGGATG TTCAGTGAAG | 60 |
| GCTTTTAAAT TCTTTCAGAA AGATCGCAAA ATGGCGCTCA TTCAATTGGG ATCTGTGGAA | 120 |
| GAAGCAATTC AGGCCCTCAT TGAGCTTCNT GAACCATGNA CCTTGGAGAA AATCACCACC | 180 |

| | |
|--|-----|
| TCAGAGTTTC CTTCTCAAAA TCTTACAATC TGNACTTTNC TGTGAATTTT TCTCCTAAAA | 240 |
| CTGGGACCAT AATTTCNCAGT AAAAACCTTC AGACATNGGA CTGAAGCAGC TTCAAGACCC | 300 |
| AATTTTGCCC TCTTTNCACA AAATAAACTC TTTNCTGAGT TTGATATTNC AAGTATATTT | 360 |
| NNAAAAATCA AGGGGTTTTT TTTTTTGGA ATTCCCCC | 398 |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

| | |
|--|-----|
| CCCAGAGGAC AGATTATCTA CACGTGGAAA GGAGCAAATG CCACACGAGA TGAGCTGACA | 60 |
| ACATCTGCGT TCCTGACTGT TCAGTTGGAT CGGTCCCTTG GAGGACAGGC TGTGCAGATC | 120 |
| CGAGTCTCCC AAGGmAAAGA GCCTGTTTAC CTA CTGAGTT TGTTCAAAGA CAAACCGCTC | 180 |
| ATTATTTACA AGAATGGAAC ATCAAAGAAA GGAGGTCAGG CACCTGCTCC CCCTACACGC | 240 |
| CTCTTTCAAG TCCGGAGAAA CCTGGyATCT ATCACCAGAA TTGTGGAGGT TGATGTTGAT | 300 |
| GCAAATTCAC TGAWTTCTAA CGATGTTTtk GGTCTGAAA CTGCCACAAA AATAGTGGCT | 360 |
| ACATCTGGGG TAGGAAAAGG TGCTTAGCCC AGGAGGAGGA GGAAAGGAGC AGAGTATTGT | 420 |
| AGCAAAGTTG TCCCTAAAGG TGCAAAAACC TTAGGGATCC CAAGAAGGcG AGGAGCCAGA | 480 |
| GGGAGTTCTT GGAATTCCCC CTTGGAGGG | 509 |

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

| | |
|---|-----|
| TTATCATAGA TTTNCCNGGT TTAGTTCACA TCTATCTCGA TGAGTGCTCT TGCCTGCGCC | 60 |
| AGTCTTAAGC CTCCTTGCTT GTTACATTCG TTCAATAGAG CAGATTTGTA TTCTAAATAG | 120 |
| GCTCCAGGGA CCAACCTCAC CATCTGACAG AGCTCCTTTT CTTTTTCATT CAGCTTCTCT | 180 |
| GTGCCAGGGA GGCCAGTGAG GTTCAAGGGT GGTGCACTCC GTCTACCTGA ATTCGAAGCC | 240 |
| ATTGGAATGG AAGGACTCAG GCCGGAATCA ATGTCAGCTT GCCGGCGGAG CCACTGCTGG | 300 |

| | |
|---|-----|
| CAAGCACTAC TGNNTGGAT ATACTGGAGA ACTTCTGAGA GCATAGTGCG TTTAAGGCGC | 360 |
| TCTTCCTCCC GTGTCTTCTT GAGGTGATCG TAGGTCTTGG CACTACAAAA ATTGGTAATG | 420 |
| CCTGCTGTCC TGTATTCTTG GAGCCTCTTG ATTTCCCTTC GGAGTTCAAA TTCCAATGCA | 480 |
| TGGNTTTCAA TGAATTTGGC ATGTTCCACT GGCCCCACAA TTCTTGCAAA TCGNCTCATT | 540 |
| GTTTCATACA GGTCCCTGGAC CTCCTTGGGA TACCGCCGNT CCATTAATTG AACTTTCTA | 600 |
| | 600 |

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

| | |
|--|-----|
| GGCANAGACC TGNATGTAGA TGCCCATCCC AAAAGGAGCA AGATCTGCTC TTGCAGTGGG | 60 |
| TGTTGAGAGG GGCTGGGAAG GCTTTTTTCAG TCAAATATGG AGCTGAAAAN NTTCAGAATG | 120 |
| TGCNTATGTT GTACATTATC ANTAAGAATC CTAACAGGAG CACAGTGTGA TTTCTCTTCG | 180 |
| TAGTGGGCGT ACATGGTCTT GGGTTTCCAT GTGCAGCAGT GAGAGTTGGT CTCCAAAGCA | 240 |
| GAACGGTCAG CATTAACTTC AGCCAAGCAA GCATTCTGTA TGGGGTGCTC CCTTTAAAGC | 300 |
| CCAAGGGAAG GCAGGCTCTG CTGCTTTTGC CCACCTTTTC AGAGGGAGAG GTGTTGCCCC | 360 |
| ACCANGGGTG CCAGGTGTGC TGGGGGCCCTG AAGNTAAAT TAAGTTGTTT TGGGAAAAAA | 420 |
| TAATGTCTTT AAGTTTCTGC CAGAGNGAAT NNGTANCCAT TTAAATCCA TTTCATCAGG | 480 |
| GGGTTTTTTT AGTCAGT | 497 |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

| | |
|---|-----|
| GGCAGAGCTG GTGAAGACCC AGAGGAAAGG GGAGTAAAC TTGGATTGGG AGATTTTCATT | 60 |
| TTCTACAGTG TTCTGGTTGG TAAAGCCTCA GCAACAGCCA GTGGAGACTG GGAACACAAC | 120 |
| CATAGCCTGT TTCGTAGCCA TATTAATTGG TTTGTGCCTT ACATTATTAC TCCTTGCCAT | 180 |

| | |
|---|-----|
| TTTCAAGAAA GCATTGCCAG CTCTTCCAAT CTCCATCACC TTTGGGCTTG TTTTCTACTT | 240 |
| TGCCACAGAT TATCTTGAC AGCCTTTTNA TGGGACCAAT TAGCATTCCA TCAATTTTAT | 300 |
| ATCTAGCATN NTTGCGGTTA GAATCCCAGG GATGTTTCTT NTTTGACTNT AACAAATCTG | 360 |
| GGGAGGACAA GGTGGTTTNC CGTGTNCCAC ATTNACAAGT CAAGNTCCCG TTGGACTTTG | 420 |
| CAGTTCCTGC CAGTTTCCGA CCANCTGCAN TTTNGGACTT GGAGGGGGNC CTAGGNAACG | 480 |
| GTTTTGACCA A | 491 |

(2) INFORMATION FOR SEQ ID NO:474:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

| | |
|--|-----|
| GGCAGAGNCA GTGTATAACA TATTACATGG TATGCCATGG AATACTATGC AACAAATAAAA | 60 |
| AGGAATAAAC TATTGATACA CACAACAAC TAGATGGATC TCAGGGGAAC TATGCTGAAT | 120 |
| GAAAAAGTCC AACAGAAGAA GTTACATAAA TATGAATTCC AGTTAGAAGA CATCTTGAA | 180 |
| ATGGCAAAAT TATAGAGATG GAGAATAGAT TATTGATTG ACAAGTCTCA AGGATGGAGT | 240 |
| GGGGAGAGGG GTTGTGTAAG CCAAAGAGAG GTAGCAAGAG GGATCCTTAT GGTTGATGGA | 300 |
| TCAGTTCTGT ATTTTAACTG TGGTGGTGGC CNCTATATCT ACACNNTGGN TAAACTACC | 360 |
| CTAACTTTAC AAACACACAA TGGGTACTTT NAANCCGTTG AGTCGGATTA TCTCTNGACC | 420 |
| AAGTCATTTT CCATTTNGTA TTNACCTTGG TTGACCGGTT TTTCTGTAA GNATTGCCGT | 480 |
| CTGGGGGGTC CACCG | 495 |

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

| | |
|---|-----|
| ATTTTATGTT TTCTTTTAT TAATTTTCT TCTTAAATAC CATGTCTTTC TGGCTGAAAT | 60 |
| CCTTGCCAAA ACCAGGAAGG GCCAGTGAC TGTGGGTGAA TTTTNCTAAT TCATTTCTTT | 120 |
| GTCATTTGAA GCCTTCTGTG GCTTCATGCT GCTTTATGTG TGTGTAAATA TTCAGTATCT | 180 |

| | |
|---|-----|
| TTTCCTAGTT TGCACCTTTG TCACAACTGC TAATTAAGCC ACCTATGGAC ACATTGTAAT | 240 |
| ATAAATTATT TTGGGCCACG GTGGAGTGGG AGGGAAAAGAA TCCAGTTTCA CAGGGGTAA | 300 |
| ANTNTGGCAT GTNGTGGAGG TTAATATTTN ANTAAGTTTG CAAAACCAC TTC | 353 |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

| | |
|---|-----|
| NTTGCTGCCG TCTGCACACG GTCCGCGCGT CGNTGGAAGA CCTGGGNTGG GCCGATTGGN | 60 |
| TGCTGTGCC ACCGGAGGTG CAAGTNAACC ATGTGCATCG GCGCGTGCCC GAGCCAGTTT | 120 |
| CCGGGCGGCA AACATGCACG CNCNGATCAA GACGAGCCTG CACCGNCTGA AAGCCCGANA | 180 |
| CGGTGCCAGG GCCCTGTN | 198 |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

| | |
|---|-----|
| GGCAGNNGTG GAACAGGACA TCCAGCCTGA TGGGCAGATG CCAAGTGACA AGACCATTGG | 60 |
| GGNGAGGAGA TGATTCCTTC AACACCTTCT TCAGTGAAGA CGGGGGCTGG NNNCATGTGC | 120 |
| CGAAGGCAGT GTTTGTGGGA CTTGGAACCC ACAGTNCATT GATGGAAGTT CGCACTGGGN | 180 |
| ACCTACCGCC AGCTCTTCCA CCCTGGAGGC ANCTTNATNC ACAGGCAAAG GAAGATGCTG | 240 |
| NCAATAAACT TATTGNCCCG AGGGGNACTT ACACCATTG GNCAAGGGAG GATTCATTGG | 300 |
| AGCTGGTGGT TTGGGANCCG AA | 322 |

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

| | |
|---|-----|
| AGCGCAAAGA CAACTTCCAG ACCATCCTCA GCCTCCAGCA GTTCCAAGGG NCGGGCGCAC | 60 |
| AGGGACATCC TGGTATGCAT GACCTCGTGT TCTGGTTCGG GGACCTGGAA CTTACCGCAT | 120 |
| TGGAGAAGCT NATGAACCTG NCACTTTGGT TCAAGTTTGG NCATGCGTAC AGTNAGTGCA | 180 |
| GNT | 183 |

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

| | |
|---|-----|
| GAAGACCCCA GACATCAAGC TCTTTGGGAA GTGGAGCACC GATGAATGTG CAGATCAATG | 60 |
| AACATTTCCC TGACAGGATT ACATTGCAGT GAAAGGAGTN AGTGATGNCC AAGTACCTGC | 120 |
| CTCTGCACAG TGCCAGGGNC GGTNATGGCG CATATACGCC TTGCCGCCAA AGTTTCAGTT | 180 |
| GTGCCCATTA GTGGTGGCGN CCTGCACTTA ACTACCATGN NTGAATGGCA CGG | 233 |

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

| | |
|---|-----|
| CACCCTGCAG GTGGACAGCT GGCCGGTCAA CGAGCGGTAC CCGGCAGGCC GCCAGCTGAC | 60 |
| CATCTTGAAC AGCCAGGCTG CCATCAAGAT CGGGGGCCGG GAATCAGGGC CGCCCCTTCC | 120 |
| AGGGCCAGGT NTCCGGCCTC TACTAACAAT GGGCTCAAGG TGCTGGCGCT GGCCGCCGAA | 180 |
| GAAGCAACCC CAATGTGNCG GNACTGAGGG TCACCTGCGN CCTGGTGGGG GAGGNGCCGT | 240 |
| CCGTGNTGGC TNCAGTGCGN GGAACCACGG CCACCACNT GGCTGGTTGT ACATGGGCCA | 300 |
| CCACNTTCT GGGAGGACTA CCACCACCAT GGGCCACTTA | 340 |

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

| | |
|---|-----|
| GGCACGAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAANANANAA AAAAAAAAAA AAAAAAAAAA NAGN | 104 |

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

| | |
|---|-----|
| GGCACGAGAA GAATTGAATT TACATGAGCT CTGTGCAGTG TGCCTAGAAG ACTTCAAGCC | 60 |
| TCGAAATGAG TTGGGGATTT GCCCATGTAA GCACGCCTTC CACAGAAAGT GCCTTATTAA | 120 |
| GTGGCTGGAG GTTCGTAAAG TGTGTCCCCT GTGCCAACAT GCCAGTTCTA CAGCTGGCCC | 180 |
| AGTTGCACAG TAAGCAGGAC CGTGGACCCC CTNCAGGGAC CCCTTCCTGG GGCAGAGAAC | 240 |
| ATTGTATAGC TTACCGCAAG GATNCAGACT GTTGCTGGAC ACGAACGTCT GTTTGGAGCC | 300 |
| AGGAGGAACA CATGTGGTGT TTGTTTGGTT GCTNTNTNAC CTNGGGACAC CA | 352 |

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

| | |
|---|-----|
| GCNTCGNTGT CCAGCNTGGT NTCCAGTCGG TTNTTTCCTC ACATGGTGGC TCCTGNCCAC | 60 |
| CCTGGCCTGC CCACCTNAGG GATCCCCCAC CCTGCCATCG TTTCCCCCAT CGTNAAGCAG | 120 |
| GAACCGGCAC CCCCCAGCNT GAGCCCTGCA GTGAAGCGTG AAAATCACCA GTTNACCGTG | 180 |
| AAAAAAGGAG GAGGAAAAGA AAGCCCCACG TGAAAGAAGC CTCTGATTGC TTTCATGTTG | 240 |
| TATTATGAAN GGAGATGAGG GCCAAGGTGG TGGCTGAGTG CACCCTGAAG GGAAAGTGCC | 300 |
| AGCCATTTAA CCAGATACCT TGGTAAGNAA AGTGGGCACA ACCTGTTTTC GNGNAGGANC | 360 |
| AGGTCCAAGT TATTAGGAGN TTGG | 384 |

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GGCAGAGCTC CGTCCCNNGA GATTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTT 53

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GGCAGAGGAC CGTCGCAGTC GGACCAACTG CTGGCAGAAT CTTCTGCCGC ACGGCCCCAG 60
CTGGAGTTGC ACTTGCGGCC GCAACNNCNA GGGGGCGCCG CAGAGNGTGN GNCAAACGGG 120
GACGACTGTC GCTCGGGNCC GGGCGNTGCT GCCGTCTGCA CACGGTCCGC NCNTCGNTGG 180
AAGACCTGGG NTGGGCCGAT TGGGTGCTGT CGCCACGGGA GGTGCAAGTN AACCATGTGC 240
ATCGGGCGCG TGCCCGAGCC ANTTTCCGGG CGGCAAANA TGCACGNGGC NGTTTAAG 298

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 490 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

GGCAGAGAGA AAGGTTCTGGT TACTGCCGAA GACTGCTGCC TGGAGGCAAA GGGAAGCGCC 60
TTCCTGAAGT TTACTGCATT GTGAAGCCGC CTGGGAATGC TTCACCTCTT TTNAAGGGAT 120
CTTGATGAG GTGGAAAAA GACGAGGCAT CTCTCTGCC CTGGTTCAGC CACTCATGNG 180
AAAGTGTCAT GGGAAGCCCC TTTCCAGCC CTGGGCAAAA CCATCCTTGT NNAAGNAACT 240
TCCTGCCAGG TTTCAGGAAC TGAGGTTGAT CAACTGTGC CGCCCGNTGG GACTTCCCGG 300
CTTCGAGCAA GTGGGACTTT GNAGTCTTCT CTTGNTCNTN CCTTCAGGGT TCCGGCAACT 360

| | |
|---|-----|
| GGTNTNGTGT GTTTGNNCTC CCTGNTTTTT GGNAGAGGAG GGTCACTCTC ATTGCAGACA | 420 |
| AGNTCAAGTA CCCGCCTTGG GTTAATTTTG GTTAAAGGGT TTTGAATGAC ANTGGGTTNT | 480 |
| TGGGACCCNC | 490 |

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

| | |
|--|-----|
| GGCANAGCTG GGGGTGTCTC TGCAGGGTAC TGGCAGCCTT GCTACACTGT CCTCATTTCCC | 60 |
| AGATGGAAAG ACCTGAGTGC CTCTGGCCTT CCTCCGGGAA TGATTTCTTC ATGAAAATGA | 120 |
| NCCAGGCCAC TTCTTCCGAG GGCCAGGCCG CCCCTCCCC GAGAACCTGT CCTGCCGTCC | 180 |
| GCGGGTGTNT GGCTGTAGG GGAAGTGAAG GCTGGGCTTG CTGGGCACCT CTGGAAATCT | 240 |
| GAACCCTGTG GGGCCAAAGA AAGCACCCT GTAGTTTCTG CAGACCCCCA TGCGGTTTCAT | 300 |
| TGTGCATTGT TTGGTTTCTT AGGATGTATG TTTTCTAGT TTTTCTAAT GGAAACCCGG | 360 |
| GANTAATGTA AATAGCTTTT TTGGGNACGG NTTTTAATGT CAAGTATGTN CCGTGTGGA | 420 |
| CTATTTCAAG GTGCTGATGC AACAAATAAT AACCTGGNG GGGGCCGGNA AAAAAAAAAA | 480 |
| AAA | 483 |

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

| | |
|---|-----|
| GGCAGAGGNC CCGCGGTGCG CGGCCCTACG ACCTGGACCG GCGAGATGAT GCCTATTGGC | 60 |
| CGGAAGCCAA GCGGGCCGCC CTGGAATGAG CGCTACCATT CTAACCTTAA CCGCCAGTAC | 120 |
| CGCTTCCACG AACTTTNAAC CACAGGGAAC CGCGGCCGCT NACCCCGNAC CACTTCGGTG | 180 |
| GNACAGGAGA GAAGGTTCAA GGTTCATGA ATGGGNAGAA CGNAGAAGGN ACAGCATTTA | 240 |
| CCCAGAACGC CATGGGAGGN ACCAGAGCGG CCACGGGCCG GGAATTCCCC CGAATGGGTT | 300 |
| GGGGGGGGTT ATGGCTCTGA ACAAGGGNTT TAGNCGAGGG CCNGGGGTTG CCTTCTTCCC | 360 |

| | |
|---|-----|
| CCCAGGGGCA GACGTTTATT GGGGGGACCA TTGGCCNAAG AGAAGATGAC CGTTCATGGC | 420 |
| AGGNAAGGNC NACGGGGGGN NTNNTGGACA GGNTTACAAG AGTTGGCAAN TNGCGAANAN | 480 |
| CATTTCCGTT AATTCCGGC | 499 |

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

| | |
|---|-----|
| GCGTCGCCTT GTTCTACGAT ATGACCATTT TCCATATACA CCACTCGGCT GGCGGTTTTA | 60 |
| CGCGCCACTT CAACTTCGTG GNGTGACGAT CACCTGGGTA ATATTCGTTT CTGCCAGCTC | 120 |
| ACGAATGAAT GCTGACGATT TGTGCCGTAA TTTCCGGGTC CAGTGCGGCG GTCGGTTCAT | 180 |
| CGAACAGCAG TACCTGCGGT TCCATCATCA ACGCACGGGC AATAGCAACA CGCTGCTGCT | 240 |
| GACCACCAGA AAGATGCAGC GGGTAACGAT CGCNATAAGG TTTGAGAACG CAGACGTTNC | 300 |
| CAGCAGTTTT TTCTGCACGG GGCCAGCGCC TGATTCTTTA ATTCAANCCC CATTACAAGG | 360 |
| GCAGGGCGGT TTCAATTCAA GGTTTTGTTN GCACGGTCAA ANTGGGGCCA CAGGTTNTN | 420 |
| TT | 422 |

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

| | |
|--|-----|
| GGCACGAGCA GGGCTAGGTA ACCTGTCTTG GGAGTNTGAG ACCGCCCCGC CCTGCCACGC | 60 |
| CCCTCACCGC CCTGCCCCGA GGCGCCAGCN NANCTCCTTG GCTTCCTTTC CTAGATAGTG | 120 |
| ANGTCCACCA ACCTTGGAGG TGCCTTTTCA AAACACCCGG GAGGCCGTGC CTCAGCATTC | 180 |
| TGTTACTCGG CCTGCAGCCC CAGTGCCAGG AGCCACCCCG AACC GCGAAC CCGGCCAGGC | 240 |
| TGGTTNCAGG GAGGCCGAGG TGGCGCTGAG GTGGCTTTCA GCACGCTGGG GATTGGNTTC | 300 |
| CTGCTNCAGG GATGCTGTTG CATTTCTGCC TGCCACTTTT TGCCNGACAC CAGATNTGTT | 360 |
| TTNAA | 365 |

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

| | |
|---|-----|
| CACAACCTNC TCATGGGTGA CACCAAGGAG CAGCGCATCC TGTAACCACG TNCTNCAGCA | 60 |
| TGAGGTAGCC CTGNGAACGN ACAGAGCGTG CTGGAAGGCC ATTGACACCT ACTNGCGAGT | 120 |
| CA | 122 |

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

| | |
|---|-----|
| GGCAGAGGNN CGGGNGCTGC ATCGACGTGA ATNAGTGCTG GGCCTCGCCA GGCCGNCCTG | 60 |
| TGCCAGCACA CGTGTGAGAA ACACACTCGG CTCCTACCGC TGTTCCTGCG CCTCCGGGTT | 120 |
| CCTGNTAGCA GGGACGGCAA GCGCTGTGAA GACGTGAATN AGTGTAAAGC CCAGCGCTGC | 180 |
| AGCCAGGAGT GTGCCAACAT CTATGGCTCC TACCAGTGCT ACTGCCGCCA GGCTTACCAG | 240 |
| CTGGCTGAGG ATGGGNCACA CCTGCACAGA CATCGACGAG TGTNCTCAAG GCGGCCGGCA | 300 |
| TCCTNTGGCA ACTTTCGNT GTTTTCAAAG TGGCCAGGGG AGGTTTACCA TTGTGCATGC | 360 |
| CCTGAGCAAG GTTACAACAT GTACGGGCCA ACGGTAGGTT CTGCAAGGTT GNGATNAAGT | 420 |
| TTTGCNANCT TNT | 433 |

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

| | |
|---|----|
| GGCAGAGTGG GAACCTCTTT CTGGGCTGGC GANGCCTGAG GCCACTCCCT CAGCTTGCAG | 60 |
|---|----|

| | |
|---|-----|
| GGAGGTGTGG AGGGAGAGGC GCGACGGGNA ACAGGGGCTG CGTGCGGCTC TTGCGGGCCA | 120 |
| GCTGGAGTTC TGGGTGGGCA TGGGCTTGGC GGGCCCCGNA CTCGGANTNA GNCGGCTGGC | 180 |
| CCT | 183 |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

| | |
|--|-----|
| GGCAGAGGGN AAAGTTGTNT TGGCTTTGGC TTGCAACTCT TTGGCAGGAA TTCAGCGAGA | 60 |
| GAATTTACAG AAAGCCATGG GAACTGGTGA CAATCAACTA TTCCTCTGAA CCTGAAGAAT | 120 |
| CTGANTTTTG TATTTGTTGA CTGACCAAAA CAGGATGCGA GTGTAAATGA ACATCATGCC | 180 |
| CATGAATTGG TGCTCGATTT TATACTCAAT TGGATGCTGC TCAAATGAGA AATGATGTCA | 240 |
| TAGAGGAAGA CCTTGCAANG AGGTTCAAAA TGGAAGACTG TTTAGGCTNC TAGCAAAATT | 300 |
| GGGAACATNC AATGAGAGGC CGGGTTTCAG AAGGATCCCA CTTGGTCCAG AGACNNGGAGA | 360 |
| CCNTTATCTG TTGNAACTCT TTAGGGGTCC NNNTTTTCCT CAGGTGACAG AAGCAGTGCN | 420 |
| TCCCTGGATT GACCCAGGC TATNATTCNT TGTCTTNACA GTTGGTGCTG GTNTGCCANA | 480 |
| AAATNAGCCC GNT | 493 |

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

| | |
|---|-----|
| CTCCCACCTC GGCCTCCCAA ATTGTTGTTA TTACAAGTAT GAGCTACTGT GCCCAGTCCC | 60 |
| ATTGGGGTAT TTTTCTGTGG TTCTCAAGGG TTGCCCACAG AGAGACAGAC CACTTTTGGG | 120 |
| ACTCAGGAAA TCTGGGATGT ACCAAGACTA AATCTATATT AACCTTCTGA TCTACTGTGC | 180 |
| AGGATGGCAA AGTGTTTTAT TTCCTGTGNA CAATTCTGGA TCTAAAAATG TAAGGGTTGA | 240 |
| AAAAAAAATG TAAGGGATGA GATCAACTAT TTGTGAANGT TGTCCGAGAG GNTGGGTTTG | 300 |
| CAGGTGTGTG GGTGCAANCA GTNCCCTNCA CACTCA | 336 |

(2) INFORMATION FOR SEQ ID NO:496:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

| | |
|---|-----|
| GGCANAGGNC CCTGGAGGGN TGGAGCCCAG CCTTAAAGAC CCAGGGCAAG CTGAACACCA | 60 |
| GGCCTGGNAA AGGTGATCTT CTTCTCAGAG TCTGGCTGCC ANGGCAGTGG CAGGAAGGTC | 120 |
| TGGGGAGACA TCGTTGATGC CTCAGGCTGG GCCCCCGTAG CCTCCATAAG GGTAGTTCGA | 180 |
| GGCTGCTGGG TGCTGTACGA NGAGCCAGAG TTNCGGGGTC AGAAGCTGGT CCTGCCTGAA | 240 |
| GNGGTCATGG GACTCAGANC CCCAGGGTCA AAGTGGAGTC CCCAAGGTTT CGGNTCCCTA | 300 |
| AGGNGGGTTG TCTGGGGACT TACAAGCANC C | 331 |

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

| | |
|--|-----|
| GCCCAGCCCA ACTCGGGTCT GCTGCAGGCC TCGGTCATCA CCCTCTACAC CATGTTTNTA | 60 |
| ACCTGGTCAG CCCTATCCAG TATCCCTGAA CAGAAATGCA ACCCCCATT T GCCAACCCAG | 120 |
| CTGGGCAACG AGACAGTTGT GGCAGGCCCC GAGGGCTATG AAGACCCAGT GGTGGGATGC | 180 |
| CCCGAGCATT GTGGGCCTCA TCATCTTCCT CCTGTGNCAC CCTCTTGCAT NCAGTNTGCG | 240 |
| ATCCTNCANA CCACCGGTCA GNGAAGCAGC CTGNTGCAGA CCGAGGAGTG CCCACCTATG | 300 |
| GTAAGACGCC ACACAGCCAG CAGCAGCAGC AGGTGGNCAG CNTGTGAAGG GCCGGGGNNT | 360 |
| TGAACAAGAA GNCAGGACGG NGTTCAGTGA CAGTTNATTC TNTNTTTCCTA TTNTTGNCNG | 420 |
| GTGNTGGGCT TNATTGCAAG TTNAGGATGA GGTTCACCAA TTGTTACAAG CCCGTGGAGA | 480 |
| CCGG | 484 |

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

| | |
|---|----|
| ATGACAAGAG GCCCTCTATA TATCTCTTCC CACTCTAAAG CTNACCACAC CAACCTACGG | 60 |
| NATCTTAACC AC | 72 |

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

| | |
|---|-----|
| GGCAGAGCCC CCATCCAGAG CATGATGTGC CAGTACTGGC CAGAGTCCTG GTGGAGGACG | 60 |
| ATGAGATTCA TGCAGGGATT CATCAGGGCT TTCAGGCCCT GCCCAGGCAC CTATGGTACT | 120 |
| TTGCTGGACT TGAACAGAT GGAAGAGCGT GCCGTTTCTA GGTGAGCTCT GCCTGGTCCG | 180 |
| CCTCTGGCTC ACTCCGCCTT CAGAGACCAG ACTCCACCTT CACACTCANG CATGGGATTC | 240 |
| TCTGCCTTNA AGATAACAC | 259 |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

| | |
|---|----|
| GGTTACCCTG GCTACCAGTG CAAACACTAC GCNTGCNTCC GGCGAAGGGC GGCTACTGCG | 60 |
| CTGGTACCNN GGNTGGGCCC CCCCCTATAA AGCATCATT | 99 |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

| | |
|---|-----|
| GGCAGAGGTN AGCTCGCAA AGCGATCGGA GCACAGTGCT ACTTGGAAT GTTCAGCTCT | 60 |
| GA CTCAGAAA GGTCTCAAAG CGGTTTTTGA TGAAGCAATC CTCACCATT TCCACCCCAA | 120 |
| GAAAANGAAG AAACGCTGTT CTGAAGGGTC ACAGCTGCTG TTCAATTATC TGAGGTTGTC | 180 |
| TGGGACCTGC CTCCACCCCA TCCAGGGGAT GAGANTGGNC AGCCAATCTC TGTGGCCAAG | 240 |
| CTTCCAGCCA AAAAGGAGGG CACGACCAGA AAGGAACTCC CTTTGGCAC GGGGGNTTTG | 300 |
| CCCCATTNAC CTTTCTTNAG GCCCTTNCCC NAAA | 334 |

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

| | |
|--|-----|
| GGCAGAGGTG CTGCAGGGGG TCCTGCCGGC CCTGCCTCAG GTGGTGTGCA CTACCGCGAA | 60 |
| TGTGCGCTTC GAGTCCATCC GGCTCCCTGG GCTGCCCCGCG CGGCGTGNA CCCCCGTGGTG | 120 |
| CTCCTACGCC GTGGCTCTCA GCTGTNNAAT GTGGCACTCT GCCGCCGAG CACCACTGAA | 180 |
| CTGCGGGGGT CCAAGGNAC CACCCCTTGA ACCTGTGAAT GACCCNNGGT TCCAGGACTN | 240 |
| CCTNTTCCTC AAAGNCCCT CCCCCGAGC CTTTCCAAGT | 280 |

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

| | |
|---|-----|
| GGCANAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANAAAA CNCCNGGGGG GGGN | 114 |

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

| | |
|---|-----|
| GGCANAGGAC AGGATCAAGC ATGCTTTCCT TATCAAGGAG CAGAAAATCA TTGTGAAAGT | 60 |
| TTTGAAAGCA CAAGCAGGGA GTCAGAAAGC TAAATAAAAG ATGAAGCTTT TTTGNAGTAN | 120 |
| TAAAAATTAA AAGACTTTTT AAAAAATTA GAAGGCAGGG AACCCAGATG GGNAAGTGTC | 180 |
| TTCTGAATG CTCCTTGGCC TTGGGAGGGT CCTTCTGTG TGTTCATG ACAAATCTG | 240 |
| AAAAATGCCG CTAATTGGGC AAAGAGAAAT GTTTATAGGG TCTAGCTCTA GTATNCAGGN | 300 |
| AAGGGAAGC AGNGGAAGG GTGGGTTTGG GACNGNTTAG | 340 |

(2) INFORMATION FOR SEQ ID NO:505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

| | |
|---|-----|
| GGCACAGGTA GAACCCACCA TGGTGCTGTC TCCTGCCGAC AAGACCAACG TTAAGGTNTG | 60 |
| TTTGGGGTAA GGTGCGGNGC GTACCTGGNG NAGTATGGTT TCGGTGGTAN CT | 112 |

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

| | |
|---|-----|
| AAACCAAGCT GTACTTGGCA ATGAACAGTG AGGGATACTT GTACACCTCG GAACTTTTCA | 60 |
| CACCTGAGTG CAAATTCAAA GAATCAGTGT TTGAAAATTA TTATGTGACA TATTCATCAA | 120 |
| TGATATACCG TNAGCAGCAG TCAGGCCGAG GGTGGTATCT GGGTCTGAAC AAAGAAGGAG | 180 |
| AGATTCATGA AAGGGCAACC ATGTGAAGAA GGAACAAGCC TGCAGCTTCA TTTTCTGCCT | 240 |
| AAACCACTGA AGNCCCCATG TTACAAGGNG CCATCACTGC ACGTTCTTCA CGGGGTTTCT | 300 |
| TCCCGTTCTT GGAAGCGGGG ACCCCCAACC AGGGGCAGAA GTGTTTCTG GCGTTGCTT | 360 |
| GAACGGGGGG CAAATNCCNT GGGGCCACAA TGGATCAACG TGG | 403 |

(2) INFORMATION FOR SEQ ID NO:507:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

| | |
|---|-----|
| GGCCCCGAGCA CCAACTTTGG CAACACGACC ATTGTGGTGC CCAAGCCCTT CCGCCCCGATA | 60 |
| CTTGGCCTGC ATCTGGACTT GGAATCCTG TACTATGTCT ACATGGGGNT GCTGGCAGTG | 120 |
| TTCTGTACCA ATGCCATCAA TATCCTAGCA GGAATTAACG GCCTAGAGGC TGGCCAGTCA | 180 |
| CTAGTCATTT CTGCTTCCAT CATTGTCTTC AACCTGGTAG NGTTGGAAGG TGATTGTGGG | 240 |
| GATGATCATG TCTTTTCCCT CTACTTCATG ATACCCTTTT TTTTTCACCA CTTTGGGGAT | 300 |
| TGCTCTTACC ACAACTGGTA NCCCTCANGG GGTGTTTTTT GGGGAGAAAA CNTCTGNTAA | 360 |
| ATTTTGCTGG GNAAGA | 376 |

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

| | |
|---|-----|
| GGCAGGAGGA AAAACAGTCC TGGGAAATGT ACGACACTCA TTCTGCTAAA GAAATAGGCA | 60 |
| AGTAACAATT TTTAACAAGT GAAATATATT ACTACTTAAT TTTATTCAAA ATTCACCAAC | 120 |
| TTAATGTGCT TTATAAATAT TTNCATACCT TTCAAGCTCT ACTGATAAAA CATAATTTAC | 180 |
| AGTTAATTAA AANGTGAAGT TAAAGTAAGT ACAAANCAT TTTCAAGGTG ACAAATTAG | 240 |
| GAAGGTGACA GTNCCGATTG AAACACAGAC ATATCACACC CAAGGGTCAA GTCAAGCCCT | 300 |
| TCTATTTACT TGGGGTATTT TCCCCACTC ACATCTGGTT CAGTGGAAGT GGGGTCCTGG | 360 |
| ACCATCCTAC CAGGNGCCGT TACCCTGTGG TTNCTCTGTG TTCCNTGGG GGTGGCTTTT | 420 |
| AACTTTGCAG GTTTTTGCAC TGCCTCANTA GGTGGGGT CTTTGNCTT TTGGNAATAT | 480 |
| TTTCCTTTNC CCTTAACCAT TTTT | 504 |

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

| | |
|---|-----|
| GGCAGAGCAG CCCTGAGATC GAGGGAGATC TGCAGCCTGC CACACATGGC ATCCGCTTTN | 60 |
| ATTTCTGGAC CAAGTAAAGA TGGGTCCGTG GCCCACACTC GGTCATGTGC TCAGACAACG | 120 |
| ACTGNTGAAA ACGCCCATGN CAGTTTGCAT CGNACTGATA GTGTGTTCTT TCCGGGNNTC | 180 |
| ACAAACATTA ACAAAAAAGT TTAAGTTATG TGAAGTTGGG CAGTTNATTC TATGACCATT | 240 |
| TCCTGTGCCA TNTAAAATTT TTAAGGGATG AAAAATTNTG NAAAAANAA AAAAAGTCTN | 300 |
| GNGGGGGGGG CCCCAGTG | 318 |

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

| | |
|---|-----|
| GGCAGAGGTG AAACCCTACA CTTGTTGTNA ATGTGGGAAG GGTTTCAAAT ATGGCTCAGG | 60 |
| TCTCCTTAGT CATAAGAGAG TGNACACTGG CGAGAAGCCA TACAGATGCC ACGTGTGTGN | 120 |
| GAAAGGGCTA TAGTCAGAGC TCACATCTTC AAGGTCATCA GAGGGTCCAC ACTGGTGAGG | 180 |
| AAACCCTATA AATGTGANTA GTGTGGGAAG GGCTTTGGCC GCAACTCCTG TCTTCATGTT | 240 |
| CATCAGTGAG TCCACACTGG AGAGAAGCCC TATTACGTNT GGTGTGTGTN GGNAAGGCTT | 300 |
| NCAGTTAATT ACCTCAGGTN TTGCGGGAAC CACCAAAGAG TGCCATTTTA GGCGNAGTNA | 360 |
| CCCTTATTAA GTAGTTGTTA CCATAGGGNT TTTCCCATCT TGGGANTTCN AAGGNTTTTT | 420 |
| TATTCCN | 427 |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

| | |
|---|-----|
| GGCAGACCTC GGCCTNNATT CNTNCAAAGG CACATGGACA CAGCCCTTTA ACCTGGCAAG | 60 |
| CACCAGGGAA GGAGAACTTC TATGTGGACG AGACAACTNT GGTGAAGGTG CCCCATGANN | 120 |

| | |
|---|-----|
| GTTGCAGTCG AGCACCATCA GTTAACCTTC ATGAACTCGG AAGCTCCCCT GCCNAGCTGG | 180 |
| TGCAGATGAA ACTACGTGGG NCAATGGGAA CTNTTTTCTT NATCCTTCCG GACAAGGGGA | 240 |
| AGATGAACAC AGTTCATCGC TGCACTGAGC CGGGGACACG ATTNAACAGG TGGTCCGNAG | 300 |
| CNTTGACCCA GNAGCCAGGT GGGACCTGTT ACATTTCCAA AGGTN | 345 |

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

| | |
|---|-----|
| GGCANAGGAC CACTTGAGCT TCCTCAACTC CTTCAAGATG AAGATGTCCG TNATCCTGGG | 60 |
| CGTCGTGCAC ATGGCCTTTG GGGTGGTCCT CGGAGTCTTC AACCACGTGT CACTTTGGCC | 120 |
| AGAGGCACCG GNTGCTGCTG GNAGACGCTG CCGGTAGCTN CACCTTCCTG GCTGGGAACT | 180 |
| CTTCGGTTAC CTCGTGTTTC CTNAGTGCAT CTGACAAGTG GGCTGTGTGT CTGGGNTTGN | 240 |
| CAGGGGNCGA CT | 252 |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

| | |
|--|-----|
| GGCAGAGTAG AAGTCGGGCG GACCCGGAAC CCAGAGGACG CGACACCATG ACTTATGCTT | 60 |
| ATCTCTTCAA GTATATCATC ATCGGAGACA CAGGTGTGGG GAAGTNATGT CTCCTCCTGC | 120 |
| AGTTTACAGA TAAGCGGTTC CAGCCTGTCC ACGACCTCAC AATAGGTGTG GAGTTTGGNG | 180 |
| CTCGTATGGT CAACATTGAT GGAAAACAAA TCAAAC TGCA AATCTGGGAT ACGGCTGGGC | 240 |
| AAGAATCCTT CCGTTCTATC ACCCGTTCCT ACTACAGGGG AGCAGTTGGA GCACTGCTGG | 300 |
| TGTACGACAT TACAAGGCGT GAACCTTTCA ACCACTTGNC CTCNTGGTTA GAGGATGCCC | 360 |
| GGCNACANTN T | 371 |

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

| | |
|---|-----|
| GGNACGAGCA AGCACTGCTC AAACAAGGAG GTGGTGTCTT TNGCCAAAGT CCTTATNAAA | 60 |
| AACTGGAAGC GGCTGCNAGA CTCCCCTGGC CCCCCAAAAG GAGAAAAAGG AGAGGAAAGA | 120 |
| GAAAAGGCAA AGAAGAAGGA AAAAGGGCTT NANTGTTTAN ACTGGAAGCC AGAAGCAGGC | 180 |
| NTTTNTCCAC CAAGGAA | 197 |

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

| | |
|--|-----|
| GGCAGAGNAA CATTCTAGCA GGGGTAAGTG ACCATAGCTG AATTCTTTTC TTATCAATCA | 60 |
| GGAAAATGAA AATCCTTCCT TAATCAATTT CTCCAAAGTC TCTGACACAT AACAACAAC | 120 |
| CCAAAAATGC ACCTCTCTTT CCATCAAACCT CCACTGATAT GAAAAATGGG CAACCTGTTT | 180 |
| TTCCTTGCCC TGTTAGTGAA CTTGTGGGTG TACCCAGTGG CCACTCTAAG GATCTCTATA | 240 |
| ATCAACAAGA CACAGTTAAC AAGTGTGGC AAGCAAGTGG AGAAATCAGA AACTCACAC | 300 |
| ATTGCCAGTG GGGATGTAAA GTGGGAAAAC AGTTTTGGAA GTTNCCTCGA AAAGTTTAAA | 360 |
| CCNGGGATTT AACCTTACAA CTCCGTAATT NCCATTACT TCNAGGGTGA TTNTCCCAA | 420 |
| GGANNTGAAA ACGTNTGTTT AACNCCAAAA NCNGTTACAC AATGTTTCAC AGGGGCNTTT | 480 |
| TTCCTTATTN GCCCAGGGTN | 500 |

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

| | |
|---|----|
| TATATGCGTC TAACAAAAGA GTTACAAAAT ACATGAAATA AAAAGATACA GACATTAAAG | 60 |
|---|----|

| | |
|---|-----|
| GAGAAATAGA CAAATCTACA ACTATAGTTG GAGACTTCAA AGTACCTTTT TCAGTAATCA | 120 |
| ATAGACCAGT TAGAACACCT CAGCCAAAAA TAGCAGAATA TAAATTATTT TTGAGCTCTC | 180 |
| ACAGAACTTT GCTGAGATAC ATTATAACCT GGGCCATAAA ACAAACCTCA ACCAATTAAT | 240 |
| ACAGTTGAAA CCAGAGTGTG CTCTCTGGAC CACAGTAGGA TTCAANCTAT TAATTAGTAN | 300 |
| TNTTANTANT GG | 312 |

(2) INFORMATION FOR SEQ ID NO:517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

| | |
|--|-----|
| GGCAGAGTGC AAGATTGGAG AGGGAATGCT GGCAGACTTT GTGTCCCAGA CTTCTCCAAT | 60 |
| GATCCCCTCC ATTGTTGTGC ATTGTGTAAA TGAGATTGAG CAAAGAGGTC TGACTGAGAC | 120 |
| AGGCCTGTAT AGGATCTCTG GCTGTGAACC GCACAGTAAA AGAGCTGAAG AGAAATTCCT | 180 |
| CAGAGTGAAA ACTGTACCCC TCCTCAGCAA AGTGGATGAT ATCCATGCTA TCTGTAGCCT | 240 |
| TCTAAAAAGA CTTTCTTCGA AACCTCAAAG AACCTCTTCT GACCTTTTCGC CTTAACAGAG | 300 |
| CCTTTTTTGA GGCAGCAGAA ATCACAGATG AAGACAACAG CATAGCGCCC ATGTTACCAA | 360 |
| GCTGTTGGTG GAANTGCCCC AGGCCAACAG GGACACTTGG TTTTTCCTCA TGTTTCATTG | 420 |
| CAGNGAGTGG TTCAGAGTNC NCNTATTAAA TGGGTGT | 457 |

(2) INFORMATION FOR SEQ ID NO:518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

| | |
|---|-----|
| GGCAGAGCTT TTTTGTATTT TTAATTTTGT ATTATTGAAA GCCTTGGAGA TCTCACAGAT | 60 |
| AGATATGCCA AATTCTATAT TTTGTAAATN CTCTATATTA GAAAACAGCT GTGCACACAG | 120 |
| GGCGGGTGTG CTCATTTGTA CTGTGTGTAT GTCGGTGTAT GTACTGGTGT ATATGTGTGT | 180 |
| GTGTTTCATGC TGTGGACTGG TCTCACACAG GATGTTTTCC CTGATTTTCAG ATTTGGCAGT | 240 |
| TTTGGGTTTT CCAAGGTACC ACCAGAGCAG TGGGTGTGTG CTTTTGGGGT ACNTATGCTC | 300 |

CAGATTAAGT AGGAGGATGC ATGGGNCCAC ANTGCCCCAT NTTTCNGGAC ACAGG

355

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

| | |
|--|-----|
| GGCANAGACG GAATTACTCC TTGTNTGTNT ACCTGGTGAG GCAGTTGACT GCAGGGAANN | 60 |
| CTTGTAACANA AACTCAGAGC AAAGGGTATC CGNANCNCAG ACCACTCGGG GGNCCTGAT | 120 |
| CAAGGAGNAA TTGAACTGCT GACCCTGAAC AGTGAAGGTG GCCACTACAA GTCTCCGGGT | 180 |
| GTCACCTCATG TGCCCCGCTAG NAAGNNTGCG CCTGAACTGT CCCTTGTTNGT GCCCTCACCT | 240 |
| GCGNCCACCT GCAGAGCTTN GGATGCTGCC CTTTATCTAC AGATGAATGA GAAGAAGCCT | 300 |
| ACATGGACAT GTCCTGTGTG TGACAAGAAG GTTCCCTATG GAATNTTTAN TCATGANGGG | 360 |
| TTNATTATGG NGAT | 374 |

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

| | |
|---|-----|
| CCANAACGCC AACGCCTCGA CAACTATAAC CATTNACCTA ACACGCGCGA AAAAAACGCC | 60 |
| TGGATGCCTC CCACCCCGCC GGCTGGCCGG CCGGCCTCCT ACGAACCTAC GCTGCGACTC | 120 |
| CNCCCCNGCG GCCTCGCCAC GCGAACTCTC CGACTACTNC ACACGCNCTC NACTCCCGC | 179 |

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

| | |
|---|----|
| GGCAGAGGGN GACCGAGGCG ATGCTATACG ANAAGTTCAG CCCGGCCGGG CCTTATCCTC | 60 |
|---|----|

| | |
|--|-----|
| TCCATCCGGG TCTGCAGGGA ACATGATCAC CCGCCGCTCC TTGGGTACG CGTAGTTAAA | 120 |
| CTTCCAGCAG CCGGCGGTAC GCGGAGNGGC TNNTGGAACA CCATGAATTT TGAATGTTAT | 180 |
| TAAAGGGCAA GCCAGTTACG CATCATGTGN GTCTTCAGCG TGNATCCATT CACTTTCGGC | 240 |
| AAAAGTGGGA GTAGGGCANC ATATTTTCATT TAAAAATCTG GGACAANTCC ATTGNTAATA | 300 |
| AAAGCACTGT ATGATACATN TTCCTGNNTT TTTGGTNACA TCCTTTCCAT GTAAGTTGGT | 360 |
| TTNTAATTGN AATGGGTTCN CAAGGGGNTT TGGGNTTGTA CATTTTTAGA NGTGGTGNNT | 420 |
| NTCCTTACGA TGGTNGTTNN NAAAAANTGA TTGGAATGTT CCNNAATGGA TCNCAAAGTT | 480 |
| TTTTTNGGGN | 490 |

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

| | |
|---|-----|
| GGCAGAGTNA AAGGAGGAAT TGCAGATGCC GATGGAAGAC TGATGCAGGG TGACCAGATA | 60 |
| TTAATGGTGA ATGGGGAAGA CGTTCGTAAT GCCACCCAAG AAGCGGTTGC CGTTTGCTAA | 120 |
| AGTGTTCCCT AGGCACAGTA ACCTTGGGAA GTTGAAGAA TCAAAGCTGG TCCATTCCAT | 180 |
| TCAGAGAGGA GGCCATCTTC AAAGCAGCCA GGTGAGTGAA GGCAGCCTGT CCATCTTTCA | 240 |
| CTTTTNCAC TCTCTGNTC CAGTACATCT GAGTCACTGG NAAATTAGCT TCAAAGAAGA | 300 |
| ATGCATTGGC ATCTGAAATA CAGGGGTAA GNACATCGAN ATGANAAAGG GCCCTATTGA | 360 |
| TTCAN | 365 |

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

| | |
|---|-----|
| NGGGNCAGTG AATCCTCCGN CCTCTTGGA CACCAGGGAC CGCTCGTGGG ACTCCACATC | 60 |
| CTCCAGCCCC CACAATCCTN TTCAGGGCTC CCTGACATNC CTGGGGNTGG NAGAGNCCAT | 120 |
| CCCGGGG | 127 |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

| | |
|---|-----|
| TCCNTCCATA GGCACACTGG NTCATNTNAG AGCCCCTGGG ATCGTTTACA GGGAAGTTCC | 60 |
| CACATGAGGG CCCATGTGTG ACNTGTTATG GTCCGATCCC GNTGNTCTGN GTGGATGGGT | 120 |
| TTTTNACC | 128 |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

| | |
|---|-----|
| GGCAGAGTG GCAGTGGGCA TGGCGACCCC CTCCATTTAA AACTCTAACC ACCTCCCCCT | 60 |
| GGCTCCAGCT CTTNATCAAT GCCCGAACT GGACCCTGGG AAGAGAGNCT GNCTGACTGG | 120 |
| CCANNGGAGC TCACCTGGGA CCCCATGGCN TTTNAACCTA AGTGGGTCCT GCCCCCTCCC | 180 |
| CCATGAACCT TNAGGAGCAC CCCATATTAT TTCCAAAAAT ATCTTGGACA GGCAAGGNCC | 240 |
| AAAATGCCAA AATCTCAGNG GACTTGATGA TCTGCCTGCT GATGTTTCCT TCTGTGGGNT | 300 |
| GTGGTCTATT TTTNAGTTNC TGCTCTT | 327 |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

| | |
|--|-----|
| GGCAGAGTGG AGATGTTTNA TTACCTGGAG TGTGAACTCN NCCTCTNCA AACAGTATTC | 60 |
| AACTCNCCTGG ACATGTCCCG CTCTGTGTCC GTAAGGCAGC AGGGNAGTGC CGCCTCGCCC | 120 |
| CGCTGATCCA GGTCATCTTG GNACTGCAGC CACCTTTATG AACTACACTG TCAAGCTTCT | 180 |

| | |
|---|-----|
| TTTCAAACCTC CACTCCTGCC TCCCAGCTGA CACCCTGCAG GCCCACC GGG GACCGNTTTC | 240 |
| ATGGGNGCAG TTTTACAAAG TAAAGTGGGT TCAAGTAAAC AGGAATGGAG GTGAATTTCA | 300 |
| AGGGCGTTNT AAAATNCATT TAAGGCCTGG GAGTGCAATG GGGGAATTTG GGGTTCANTG | 360 |
| GNAACTGNCT TACCGGTTCA AGGG | 384 |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

| | |
|---|-----|
| GGCAGAGCTC TGGAGAGGCA GGCACAGGGG CACCNGNCNC GTNATGCAGC TTCGCCCTGG | 60 |
| GTTACCTCTA TGGCTCGGAC CAGCTGGTGG TGAGGATCCT GCAGGCCCTG GAACCTCCCT | 120 |
| GCCAAGAACT CCAACGGCTT CTAAACCCC TACGTCAAGT ATCTACCTGC TGCCTGACCG | 180 |
| GAAGAAAAAG TTTCAGAACC AAGGTGCACA GGAAGACCCT GGAACCCCGT TCTTCAATGT | 240 |
| GAACGTTTGC AATTCTGCGG TGCCCCTGGC CGGAGCTTGG CCCAAACGNC AAAATTGCAC | 300 |
| TTTCAGCGTG TTATGAANTT TGAACNNTT TTGGTGGTCA GGACCTCATC GGNNCAGGTG | 360 |
| GTG | 363 |

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

| | |
|--|-----|
| GGCAGAGTNT GACTTCAAAA TCAAACTGT AGAGCTAAGA GGAAAGAAAA TTAGATTACA | 60 |
| GATCTGGGAC ACAGCAGGTC AGGAGAGATT CAACAGCATT ACCTCAGCTT ATTACAGAAG | 120 |
| TGCCAAGGGG ATCATATTAG TATATGATNA TCACTGAGGA AGGAGACATT TGAATGATTT | 180 |
| GCCGAAATGG ATGAAGATGA TTGATAAGTA TGCTTCAGAA AGATGCAGAG CTTCTCTTAG | 240 |
| TTGGGAANTA AGTTGGA CTG TGAACGGGAC AGNGGAATCC ACCAGGCAGC AGGGGAAAGT | 300 |
| TTTGCACAGC AGTTCACTTG GGTGCGGTCT TTTGAGCAAG TTCCCAGGGT AACTTCCATG | 360 |
| TGGGNCGGGN TTTTTTNGAA ACTTGTCGGT GNCCTTCN | 399 |

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| NTGATTGTTT | CAAGAGGTTT | CGTTTTTTGG | GGCCTTGGGT | NAACCTTTGG | GGGGGGTAAA | 60 |
| CATTTTTTNC | CCCTGGTNGG | CTTAAAGGNG | CCCCCTTTAG | | | 100 |

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GGCAGAGCCC | ACGCACAGCA | CTTCCACAAG | CACCAGCTGT | GGCCCAGCCC | CTTCCGGGCG | 60 |
| CTGAAACCCC | GGCCAGGNCG | NCAAAGACCG | CAGAAAGNAA | GGGCCAGGNG | GTGTTTCATGG | 120 |
| CCGCCTCGCA | GTGCTGGTAC | TTTGACGAGA | AGACGATGCA | GAAAGCCCGG | AGTAAGCAGT | 180 |
| GGGATGAGCC | GAGGGTGTGC | TCCCGGAGTT | ACCTGAAGGT | GGACTTCGCA | GACATCGGCT | 240 |
| GGNATGAAAT | GGTATAATNT | CACCGAAATC | TTTTGATGCC | TACTACTGCG | CGGGAGCATG | 300 |
| TNAATTCCCC | ATGTCTNAAA | TCGTTTCGTT | CCATCCAACC | ATGCCACCAT | NCAGAGCATT | 360 |
| GTTCAAGGNT | TTGNNGCATC | ATCCCTGGG | | | | 389 |

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGTGCAGA | GCAACCNAGT | GCTCTATACG | CCCGGCAAAG | AGCCTGAACC | ACTGNTAGNA | 60 |
| TNCGAAGTAT | GTGCCCCTAC | GTGGGTNAAC | AGCAAGCCCG | CGCTGGAATG | NGTATACCTC | 120 |
| GGAGNCTGAA | TGCTGGGAGG | NAACCAACAC | ACTGGTGCTG | CACAACACGT | GTAAGGGTCT | 180 |

CGCTGCTGGC CGCACCCATC ATGCTGGAAC CTAGCGCTGC TGAACCGAGC TGTGCAAGNG 240
AGTGAGTTTT CTGNCNCTGA NCATGGGACC CCGAAGNCG 279

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GGCANAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAANGNCCN GGGGGGGGNC CCCN 114

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GGCANAGGNC TGCTCAAGGC CACGGAGCCC GGGTTATTCG GCGTGTGGGC GCACAATGGC 60
GAGGTGCGTA CCGCCAGTCT GCTGAGCGAG CGCAACGCAG CCAAGCAGAG GCTGGTGGTG 120
CTGGTCAAGG ACAATGGCGA GCCTCCGCNC TTNGCCACCG CCACGNTGCA CGTGCTCCTG 180
GTGGACGGTT TCTCCCAGCC CTACCTGGGG CTCCCGGAAG GCGGCCCCGG GACCAGGCCA 240
ACTNCGCTCA CCGTTTTACC TGGTGGTGGC GTTNGCCTTC GGTGTCTTCG GTTCTTCCTN 300
CTTTNTNGTG CTTCTGTTTT CGTGGGCGGT GNGGNTTNC ANGNAGNAGC ANGGGGGNCC 360
CCGTTGGGGT TCGTTGNTTC GGTGCCTNAA GGGCCCTTTT CCAAGAAAAT TGTGATTT 420
TAGGGGNAAC GGAACCTATT CCANAGTTAC CATT 454

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

| | |
|---|-----|
| AATGCCGTTT TCTGTTTCGT GGGGCATCCT CCTGCTGGNA GCCTGTNCTG CCTGGTCCCT | 60 |
| NNTTCCNTGG NTGAGGATCC CCAGGGAAGA TGCTGCCCAG AAGACAGATA CATCCCACCA | 120 |
| TGNATCAGGA TCACCCAACC TTTCAACAAG ATCACCCCCA ACCTGGCTGA ANTTCGCNTT | 180 |
| CAGCCTATAC CGNCANTGGN ACACCAGTTC CAACAGGACC AATAT | 225 |

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

| | |
|--|-----|
| CATCTNGAAA ATNCATGNGA AAATTAGTGN AATGAAGTTA ACTGANATTT GTCAAAAACA | 60 |
| TGTGTTGCTG ATGAGTCAGC TGAAAATTGT GAACAAATCA CTTTCATACC CTTTTTGGGA | 120 |
| GACAAATTAT GTCACAGTTG CAACTCTTGG TGAACCTATG GTGAAATGGC TGA CTGCTGT | 180 |
| GCAAAACANG GAACCTGNGN GAAATGNANT GGT TTTTGGC AACCACAAAG | 230 |

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

| | |
|---|-----|
| AAGAAAAGAC CCAGCCTCCC TTCCAGCCCG TCTCCTGGCC TCCCAAAGGC TTCTGCCACC | 60 |
| TCAGCCACTC TGGAGCTGGA TAGACTGATG GCCTCACTCT CTGACTTCCG CGTTCAAAAC | 120 |
| CATCTTCCAG CCTCTGGGCC AACTCAGCCA CCGGTGGTGA GCTCNACAAA TNAGGGCTCC | 180 |
| CCATCCCCAC CAGAGCCGAC TGGCAAGGGC AGCCTAGACA CCATGCTGGG GCTGCTGCAG | 240 |
| TCCGACCTCA GCCGCCGGG TGTTCCCACC CAGGCCAAAG GCTTCTNTTG GCTCCTGCAA | 300 |
| TAAACCTATT GCTGGGCAAG TTGGTGACGG CTCTGGGCCG CGNCTGGCAC CCCGAGCACT | 360 |
| TCGTTTGCGG AGGCTGTTTC CACCGCCCTG GGAGGCAGCA GTTCTTCGAG AAGGATGGAG | 420 |
| CCCCCTTTTG CCCCAGTGC TACTTTGAGC GGT TTTTGCC AAGATGTGGG TTCTGNAACC | 480 |
| AGCCCA | 486 |

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

| | |
|---|-----|
| TNAAATTTTA ACCATGTGGG AAATCNTGCA CATCCAGGTC TGGNCAGTTT GGCAACCANA | 60 |
| TCGGTGCCAA GTTCTGGGAA GGTGGATCAG TGATGNAACA TGGCATCGAC CCCACCGGNN | 120 |
| ACCTGACCAC GGGGACAGCG GACCTNGCAG CTNGGACCGG TATCTTTGNG GTACTGACAA | 180 |
| TTGAAAGCCA CAGGNGGCAA AATATGTTNC TGC GTGCCAT CCTGGGTGGA TT | 232 |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

| | |
|---|-----|
| GGCAGAGCTC GNCNTNCGNC CTCCAGCCTG CAGCTCACGG TGACCCAGGT AAAGACTTGG | 60 |
| TTCCAGAACC GCCGCAACAA GTGGAAGCGG NCANTCTCGG CTGAGCTGNT AGGCGNCCAA | 120 |
| NATGGCGCAC GNNTCGGCGN AGACTNCTGG TGGAGCATGC CGCTGGTGTT CCGGGAACAG | 180 |
| TTCGCTGCTG NCCGTGCCGG TNCCGCNTTC GCTCGCCTTT CCCGCGCCGN TCTACTACCC | 240 |
| GGGGAAGCAA CCTCTNGGGC TNACCNTTCT ACAACCTATT ACAACAAGCT TCGACTAATG | 300 |
| GACCGGGCC | 309 |

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

| | |
|---|-----|
| GGCAGAGAAG ACATTTCCCA GCAACCACTG GTGCAGGTGG CAGCCTGGGT GCATTGGGGA | 60 |
| GTATGGGGAC CTCCTGCTGG CAGGAAGTGG AAGTTGATTG AGCCCCTTCA GGTGGACGAG | 120 |
| TAGGAAGTGC TGGCATTGCT GGGAAAAGGT GCTGCAGTCC CACATGTCCC TGNCAGTTA | 180 |

| | |
|---|-----|
| CTCGAGGGAT ATGCCCTCAN AGCCCTTCAT GTAAGCTTCA GCACTTCGCC TCTTTGGGGG | 240 |
| ACAACAACCG GCATCCGCCA GTGGNTGTTT CATCTACGGG AAGCTGNTTT GGGACGTGGA | 300 |
| GCTGTCANCA NCGGTGCTTT GGGAGTTNGG ACACAATTTT TCCGGAA | 347 |

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

| | |
|---|-----|
| GCTTAATAAA ACACATCCGG TAATTTATAA CGTCTGCAAT TATCAGAAAC CCGTGCCCGG | 60 |
| TGAGCCTGCG TTGTTACTCT GGGATGATGT CATAACCTTA TTCCATGAAT TTGGTGATAC | 120 |
| GCTGCACGGC CTTTTTGGCC GTNCAGNNTT ATGCCACGCT TTCCGGCACC AACACGCCGC | 180 |
| NGTTTTTTTT CGAATTTCCG TCGCAAATGC AACGAACACT GGGGCAACGC ATCCGCAGTA | 240 |
| TTTCGCTCGC TACGCCCCGC ATTATCAGAG CGGGGCAGCA NTGNCTGACG AACTGCAACA | 300 |
| GAAAATGCGT NATGNCAGCC TGTTCACAA GGGTATN | 337 |

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

| | |
|---|-----|
| GGCANAGGGN ACCATGGAGG GTGTAGAAGA GAAGAAGAAG GAGGNTCCTG CCTGTNCCAG | 60 |
| AAACCCTTAA GNAAAAGCGA NGATTTTCGC AGAGCTGNAA GATCAAGCGC CTGAGAAAAG | 120 |
| AAGTTT | 126 |

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

| | |
|--|-----|
| TTAAATCCAN NTCCATACAA CGCTCCGCCG CCGNTCCTGC CGNGAACCCG GAACTGCCCCG | 60 |
| CCACNCGCCC CCTGCCCCGAC AGCTCCGTNA CTATGGAGGA TATGNANCGA ANTACAGCAA | 120 |
| TATAGAAGGG AATTCGCCAG AGGGGATCCA AGATCAACGC GAGCAAAGAT TCAGCAGGAT | 180 |
| GGACGGTGAA AATNTTTATT GGAGGCTTGA GCTGGGNTAC AAGCAAANAA GATCTGGACA | 240 |
| GAGTACTTTG TNTCGTTTTG GGGGAGTTNT AGACTTGCAC ATTTA | 285 |

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

| | |
|---|-----|
| CTGGGGCCGA CGCTCTGNCC GGNTGCTGCC CTGAAGGAAA GCCGGGACGC GGNGCCCCGC | 60 |
| CGAGAAGCTT CTTTGCTCCG GAACGCCCCT GGACGTGGCG GGCAGCCGGA AGGNNTAACC | 120 |
| ACCATGAATC CCCTGGGTGC TCCTGGCCTG TGNCCCTCCC CTGTGNCTGC TGACCCACTG | 180 |
| CTTGGCGCCT TTGATTGCA GGGACTTCCG GAAAGGGTCC CCTCAACTGG TCTGCAGCCT | 240 |
| GCNTGGCCCC CAGGGCCCAC CCGGNCCCCN AGGAGCCCCA GGGNCCTTAA GAATGATGGG | 300 |
| ACGAATGGGG TTTTCTCTGG GAAAAAGGG TCCAAATTGG ACNAAGAANG GGGAACCGGG | 360 |
| GGGGACAAAC GNGNAGGAAG AAATTTTTTT TTTCNAA | 397 |

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

| | |
|---|-----|
| AGCACGAGCT GGCATGTNAC AACCCAGGGC TGCCTGAAAA TGGATACCAA ATCCTGTACA | 60 |
| AGCNACTCTA CCTGCCAGGA GAGTCCCTCA CCTTCATGTG CTACGAAGGC TTTGAGCTCA | 120 |
| TGGGTGAAGT GACCATTNNT TGCATCCTGG GAACAGCCAT CCNACTGGAA CGGGNCCNNT | 180 |
| GCCGTNTTGT ANAAGTAGGC AGAAGCGGCA CAGAGACGTC GCTGGAAGGG GGGGGAACAT | 240 |
| GGCCCTGGNT ATCTTTCATC CCGGTCCTNA TCATNTNCTT TANTGTTGGG AGGAGG | 296 |

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

| | |
|---|-----|
| ATGNTTTGTG CCGCTGAGCA GTACACACCC AAGGCCAAGT ACCATGGCAA CGTGATGCTA | 60 |
| NTGCNCGCCA AGACGGGTGG NGCCTACGGC AGGTNCCTGG GCGCGGACTA CAACCTNTCC | 120 |
| CAGGTATGCA ACGGGAAAGT ATCCGTCCAC GTGCATCGNG AGGTGACCAC CGCACGCTGC | 180 |
| TGGTAGGGCA GGGNCCTNGT AGTTCCATCA TCAGCATCAT CCACAGNTCC CTNG | 234 |

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

| | |
|--|-----|
| GGCAGAGGTT TTAANATCTT CTTCAAGAGA CGTCTGATGA ACCTCATGCG GGATGTGGAG | 60 |
| CGGGAGGGCC TGGACTGGGA ACCTCATCTA TGTGGGCCCG AAGCGGATGC AGGTGGAGCA | 120 |
| CNCCGAGAAG GCTGTGCCTC GCGTGAAGGT AACCTGGTGG AGGCCGACTA TTCCTACTGG | 180 |
| ACCCTGGCCT ACGTGAATCT CCCTGCAAGC GGCCCGCAA CTGCTGGCTG CTGAGCCGCT | 240 |
| CTCCAAGATG CTGCCTGTGG ACGAGTTCCT GCCCGTTAAT GTTCGACAAA CACCCAGTGT | 300 |
| CCGAGTTACA AGGCCCCACTT CTCCCTCCGC AACCTGCATG TTTCTCTGTG GAGCCGTTGT | 360 |
| TCATTTTACC CCACACATTA CACAGGAGAC GATGGGTATN TGAAGTTAAC ANCGAGACTT | 420 |
| CATCGTATGG AACAAATGAGC AAGTTAAGAC CGATTGGAAC NGGCCANTTC CAAAGTTTNG | 480 |
| GGGNAGCAGG ATT | 493 |

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

CCTCAAAAAG TCCGGGAAGC TGAAATCCCC GAATGGNTGG TATACCGTCA NGCTGGNCAA 60
GCACAAAGAG CTTGACTNCC TNACGATGAA GGAAGTGGTT TCTACACGCG AATCT 115

(2) INFORMATION FOR SEQ ID NO:548:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GGCANAGGNC ATTTTNCCTG GCTATAAAGC GGGGTCTCCG GAACCAAAGG NNGCACACAG 60
CTCTT 65

(2) INFORMATION FOR SEQ ID NO:549:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GGCACAGCTC GGCGAGANAN AGCTTACTCA AATTGGCCAA CATACCCTCA GCTGTATGTG 60
AAAGGGGAGC TNGTGGGAGG ATTGGATATT GTGAAGGAAC TAGAAGNAAA TGGTGAATTN 120
CTGCCCTATAC TGGAGAGGNG AAAATTNAAT AAATCTTAAA CTTGGTGCCC AACTATTGTA 180
AGAAATATTT GAATTNACAT TGGGAAGCAG TTTCATGATT TTAGTCCTCA GAAATGGGTT 240
CTAGGGNNTT AGGAAAATTT CCTGNCTTTN CT 272

(2) INFORMATION FOR SEQ ID NO:550:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

TACAACTGAA ACCTCCAGTA CCTTAGAGGT AAGANCTCAG GGCCCTATCC TCACAGCAAG 60
TGGCAAAAAC CCTGTAATGG AGCTCATTTGA AAAAGAAGA GGTCTCAAGT TATGANCTCA 120
TCTCAGAGAC TGGTGGNAAG CCATGNACAA GCGCCTTTGT GAATGGAGGT AGCAAGTAGA 180

| | |
|---|-----|
| TGGACAGAAA TTCAGAGGCG CAGGTCCAAA TNAAGAAAGT GGCAAAGGCG AGTGCCAGCT | 240 |
| TTTGGCTCCT TGNGNAGTAA ACTTTTTTTT GGGACCCAAT GCGGGCAAAT TAATTAAGGA | 300 |
| AAAAGNAAGA TTTATTCCCT TCAGGGCAAA GGGGNCGTTT GTGGAATTAC AGCTNGTTTT | 360 |
| CTNNCAGCAG TCCCAAG | 377 |

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

| | |
|--|-----|
| GGCAGAGCCC TGATCGACCC CAACATCTTG TNTCTNAACA TCCTCTCTTC CGGATACATC | 60 |
| CACCCAGCCC AAGATGACCG GACCTTTTAC CAATTTAAGG CTGCGTGGGA CAGCTCCATG | 120 |
| CACAACTTTN TCCTGCTGAA CCGGGTCACC CCTTATCGAG AGAAAATCTA CATGACACTC | 180 |
| TCCGCTTATA TCGAGATGGA GAACTGCACC CAGCCGGCTG TTGTNACCAA GGAAC TTCTG | 240 |
| CATGGTCTTC TATTCCCGTG AATGCCAAGC TTGCCAGCCT CGGGGTNCCA TCCGCAACCT | 300 |
| CTTTGGGCAG TGGGAGCCTT CGGGCCTNCA NAGGAGTNAA CCGTGTGAAC TGGTGTNTTA | 360 |
| | 360 |

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

| | |
|---|-----|
| GGCANAGNAT TTTTNACTTT AGCAACGTGA TCTTCCTTTA AGGGGAAGTA TGTCCCCTCC | 60 |
| TAGAAACACT CCCGCCTTGG AGAAGGGGTT GAGTTCGCAA CTCCACTTAC AGACTACGGA | 120 |
| GGGAACCCCA GGGTCAAACC AAACCAAACC AATTCTGGCC AGTTGCTTAG CGCATTCAAG | 180 |
| TTACTTAGTG CGCTGGAAGG GCATTTTCAG GCAATCCAAC TTCTGGCTCG AACCTTCTCG | 240 |
| GAGTATTCCA AGGGATGGGA ATACTCTNCA CTTGAGGCGC TTGCCGAGGG TGGCCGCTTT | 300 |
| GAGGNAAAAC GTGANTTTNT TGAAAGAAAT GTTTTGTGTTNG CCAGATTACA GTTTCCACCA | 360 |
| TTCTNACATN AAGTATGTGG GAAAACAGGA NGTTATCCCT TTTGGGTTCC NGGGGTCTTC | 420 |

CAGAACCATT AGGGGGCAAA CATCCCAATT TGNTTNTGGG CACTTCCAAG AGNC

474

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

| | |
|---|-----|
| ATGAAGATGG GTGGNCTGCC GCGTACAACA CCTCCAATC AAAAGCCCCC TAGTCCCCCT | 60 |
| ATGTNAGGGA AAAGGGACAC TTGGGCGGCA CTCCCCCTAT CGCACACTGG AGCCAGTNCG | 120 |
| TGCCTCCAGT GGTACCAAAT GAATTACNTA CCTAGCCCAA CCNGTAAATA TGGCTCCCTC | 180 |
| GCAGCAAAGC CCTGTGAAGG ACAGTTTCTT TGAAATCAAA GAAATCGAAC TTACAGCAGC | 240 |
| ANTGGGNGTA NTGGAGGGAA GCCACCCAAN TAGTCGGAGC ANCAATCGAG AGAACATTGG | 300 |
| AATGGGTTAT TTGGGGG | 317 |

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

| | |
|--|-----|
| ACTNGGCCCC TTCCGCGCCA GCAGTTCCCC TATGAACCGC AAGCTNNNTT CCACTGCNTT | 60 |
| TTTGGCAAAC AGCGAANGGG ACTTCTATTA TGAGTGGGGC AGTTTTTCGGG GGGCAAAGTG | 120 |
| GCCAGGGTAT ATGATTTTAC TAGGGGCTGC CACATGGCCA TCCTGGNGGA CAAGGCCATG | 180 |
| GGCATCATGG NTGCNTGGNG GGGNGG | 206 |

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

| | |
|---|----|
| ANATGGCCCC CGGGAAACAC AGCAAGANTG CCAGCTTCCT GTTTGGNATG CGGAACAGTG | 60 |
|---|----|

| | |
|---|-----|
| NCAGCCAGTN AATGAGGACT CAAGCTGGGC TACCTTTATC CNAGGGNCAG CCCCTGCCTA | 120 |
| ATGGNTCCCC AAAGGACACA GAATTCCTTC TGGAAACCCC AACGCCTTCA AGAACGGATT | 180 |
| CCAACCTGCC GGTGGATGG TTGAGGGTCC AGGACACCTC AGGGACCTAT TNACTGGCAC | 240 |
| ATTCCCAACA GGGGACCACC CAGTGGGGAA CCCCCGGGC CGGGNTNTCC NNTTTAAAGG | 300 |
| GG | 302 |

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

| | |
|---|-----|
| NAAGCCCATA GCTCAGCAGG CGGCACGGCG GCCTGACCTT NAGGGCAGCN AGCTCCCTCC | 60 |
| CGGTTTCGCN TTCCCTCGCG GTCAGCATGA AAGCTTTCAN TCCCGTGANG TNCCGTTAAG | 120 |
| AAAAANAGCC TGTGGGAACC ACAGCCTGGG NATCTTCCCG GTGGCAAANN NCCTNTGGGA | 180 |
| CGACCCGNTG AGCCTGCTAT TACAACATGA ACGANTGTTA NTCCAAGTTC AGGAGTTGGT | 240 |
| GCCCAGCATC CCCCAGAACA GGAGGTGAGC AAGNTGGGAA TTNCTGCAGC ACGTCATCGA | 300 |
| TTACATTTNG GACNTGCAGT TCGCCTGGGA TTGGNTTCCA TTTTGTT | 347 |

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

| | |
|---|-----|
| GGCAGAGGGN CGGGCCTAG TAATGGAAGG GGTGANATGT GGGCGGGCG AGCTGTGGGT | 60 |
| GGGGCCTAGC CATGGGAAGA GGTGAGCTGT GAATGGGGCT AGCTATGGGT GGGGTAAGCT | 120 |
| GTGGACAGGG CCTAGCCATG GGAAAAGGTG AGCTNTGGGC GGGGCCTAGT CACGGGAAGA | 180 |
| GGTGAGCTGT GGGCGNGGCC TAGTCATGGG AAGGGGTGAG CTGTGGATGG GGCCTAGCCA | 240 |
| TGGGAAGGGG TGAGCTGTGA GTNGGGCTGA GCCATGGGAA GCAGCAAGCT NGTGGAGTNG | 300 |
| GCTNGGCCGG ACTGTGGN | 318 |

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

| | |
|---|-----|
| TGAACCAGCA GTATATGTAA TATNNTNATG CCCAGGACAC AGAGACTTTA TCAAAAACAT | 60 |
| GATTACAGGA CATCTCAGGT GACTGTTCTG TCCTGATTGT NGTGTGGTGT TGGTGANTTA | 120 |
| AGTGGTATCT CCAGANGGGC AGACCCGAGG CAGCCNTCTG GTTACACACN GGGNAACAAC | 180 |
| TATTGTCGTG TTACAAANGG TTCCATGNCC ACNACANCAA NGATNNGGAA TTGTTAGGAG | 240 |
| TCACATTACA TAGNATTGGT ACACCCGACA CATAGCATTT NCCANTNCTG GTGGATGTGC | 300 |
| ACNGTGGNCC AGTGNTACAG CTTGNTCAGG GTGGAAGTCA CNTAGGTGGC ATGCCATGGA | 360 |
| CCNGTTGTTG GGCNTGGATG CNTCTACCAC CACTGTCCAC TGACAGCCTT GGGCTGCNTT | 420 |
| CCAGGTGTTT CAAATTGGTG GTTTGGTANG TTCC | 454 |

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

| | |
|--|-----|
| GGCANAAAAG ACGCAANCCC ATGAAGCTNA GGTCTTGAAG CAGCTGGCTG AGAAAACGAG | 60 |
| AGCACGAGAA AGAAGTGCTT CAAAAGGCAA TAGAAAGAGA AACAACAAC TCACTGAAAA | 120 |
| TGGCAGANGA GAAAAC TGAA CCCACAAANT GGGAGGCTAA TTAAGNNGAA CCGAGAGGCA | 180 |
| CAANTGGCTG CC | 192 |

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

| | |
|--|----|
| TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCCCCCT NNAGGGNCCC CC | 52 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

| | |
|--|-----|
| TGAAGGGCCA TGGCTATGCT TCCCTGGCTC CAAGGGCCCA TTTCCCTCCTA GATGCCCTTT | 60 |
| TGGCCTTTNT GAGGGAGCGA GGAACAGGCT CGAAGGCTCC GGGGTATCTG CCTTCTGCTG | 120 |
| GGCTCCTGTG AACAGGCCTT CTGTGCCAG CGTTTGTACT TGCCTCCCC AACAGTGGGC | 180 |
| CTGTTCTTNN CCGTGCCAGG CCCCAGGAGA GCCGCAGGGG CCTGNACAC ACTCCCAGCT | 240 |
| CACCCTCACC CCAGCCTTTT TCCCCACATT NAGGGGTTTT TTGGGAAGCT GGGTTCTCAA | 300 |
| TCCCTTCCAA CTCAGNTAG AGGTTAGGT TNTCCCTGAT TTCCTGGGG TTNCCAGCCT | 360 |
| TAAAAANTNA ATTGGCTTTC CCAAGGGGC CCCTTTAAGG GAGGGTTTTG GGGG | 414 |

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

| | |
|---|-----|
| TTTCCAAACA TTCTATAGAA ACTCACAGTG TATATAAATA TAATACATTC TGCTTTTACC | 60 |
| TTTTTNACCA GATTCTTCAT TTTCCTGATG GAGAAAGGTA TAAAAATGTC AATATCATGA | 120 |
| TTCTTGATGA TGACATTCCA GAAGGAGATG AAAAATTTCA NCTGATTTTA ACAAATCCTT | 180 |
| CTCCTGGACT AGAGCTAGGG AAAAATACAA TAGGTAATTA ATAATTNCTT ATAAACAGCT | 240 |
| TCCTCTCCTT CATGCTGGGT TCCTTAATAT GGGGGAAGAT GTAAAAGGGN TGAGGAAAGT | 300 |
| CTTGGTGGTT TTNCTGTGGN TTAAATGGG GAATGATTTT TAAGTTCNNG GCATTTCCAG | 360 |
| AATTTCCCGT GNTCNGGTGT AACATGGNCC CTTTCCACGG GTGTAATGTT GGGNGGTATA | 420 |
| TATGCCAGTT ATGTNAAAAG GCCAAGGTAG GGTGGTTACC CCCGG | 465 |

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

| | |
|---|-----|
| GGCACGAGGT CCTGCAAAAG NGTTGTGGGA AAAGCTTCTA TGTCCTGCAG AGGCTNAAGG | 60 |
| TGCACATAAG GNNCCACAAT GGAGAGAAGC CCTTNATGTG CCATGAGTCT GGCTGTGGTA | 120 |
| AGCAGTTTAC TACAGNTGGA AACCTGGAAG AACCACCGGC GCATNCACAC AGGAGNGGAA | 180 |
| ACCTTTCCTT TNT | 193 |

(2) INFORMATION FOR SEQ ID NO:564:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

| | |
|---|-----|
| GGCANAGGGA AAGGTGCGTN TGGGGCTGGG TCTCGGAGTG GGAGACGTGG AGTNCAGGGT | 60 |
| GGAATGTAGC AAAGCCCATC CACCAGCCAT GTACTACCCC CCAACCCGGN CAGGCTGGAG | 120 |
| CAACCGTTTN TGGGGAGCCG AGCCCCGTTT CTNGCTGCGG TGAGCCCGGA CTGGGGCACG | 180 |
| NACTGGCCAN ACT | 193 |

(2) INFORMATION FOR SEQ ID NO:565:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

| | |
|---|-----|
| AGCCAGANTT CGTCTCTTGT CCTGCACTAT AGATTTTACA CTGGAGAGAA ACCCTACAAA | 60 |
| TGTAATGAAT GTGGACGAGC CTTTGGTCAC ACTTCATCCC TTATTAAGCA TCAGAGGACT | 120 |
| CATACTGGAG AAAAGCCCTA TGAAATGCCG GGTAATGTGG GAGAACCTTG AGCCAGAGCT | 180 |
| NCATTCACTG CATTGTGCAT TACAGATTTT ATACTGGNAG AGNAAACCTT CACAAATGTA | 240 |
| ATAAATGTGG GAGAGCCTTC AGCCAGAGTT CCATCTCTTC ATTCAACATT TACAGNTTTT | 300 |
| CACACTGGGA GAGAAACCCT ACAAATGTAA TGAGTGTGGG AAGGGCCTTT GCNTCCTAAT | 360 |
| GTATNCCTTN GTTAAACATC CGGTGAAGTC NTGTTGGGGA AAAAAACCC TATAAATTCC | 420 |

469

AGTGGATTTT AGNAGGGGNT TTCAAGTGGG NGTGCCAGAC CTTTCATTGG

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

| | |
|--|-----|
| GGCACGAGTG CCACCTGACT GGANGAGAGC ATCCTTCCAA CAGGGCAGTC AGGCCAGCCC | 60 |
| TGATTTAAAG CCAAGTCCAC AAAATGGAGC CACGTTCCCG TCCTCTGGAG GATATGGCCA | 120 |
| GGGAATCACT GATAGCCGAT GAGGAGTCCC AGGAGTTTGA ATGATTTAAT ATTTGCATTA | 180 |
| AAAACTGGTG CTGGTCTCAG TGTCAGTGAA TANTGAAATC TGGTCAAGGC AGCCAGGAGG | 240 |
| GGGGCACCTT GGA CTGACTC CCAGATCGTG GAGCTCCAGG AGGATACCCA TCGCCGACAC | 300 |
| TCACCTGTAG CACCTTCACT TAACCATTTC GACTGAGGCA CATTTTCCAT ATTTGTATTC | 360 |
| AGCTTTTTGT GGT TAAAAAT CTCTAAGTNA CATCCACCTG TGTAATTAGG AACCNGTGGA | 420 |
| ATTGTTACTG GGTGGTTTAA TACCAAACGT GGTTTGTTGN TATTTGGNGT ATAAATTACT | 480 |
| GGNTTGT | 487 |

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

| | |
|--|-----|
| GGCAGAGTGC CACTGNCCAC CCGGTTTCCA AGGCTCCAAC TGTNAGAAGA GGGTGGACCG | 60 |
| GTGCAGCCTG CAGCCATGCC GCAATGGTGA GGCCTGGAGG CTGNANCGGC GAGGGNTGGG | 120 |
| GTGGGGGTCC TGGATGGCTC ANACAGTNCA GGGTTGGGAA TCCTGGCTTT GAACTCTTCT | 180 |
| GAACCCTAGG GCCTGGGGAC CTGACCTTCT ACCTGCAAGC CTGTAAAATG GGCAAGGAGA | 240 |
| CATTCCCTAT CTNATACTA TTAATATTTA CTGAGGAATT ACTGTGTGNC CAGGCCCTAT | 300 |
| TTT TAGGCAC TGNGGTTACA GCAGGGAATG AAACCGACAA AGTCCCTGGG CCTGCCTGTT | 360 |
| AGAGNTNAGG TGCCCGGTNT | 380 |

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTNTNGGGG 60
GCCCN 65

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

CTAGATGAAA TGGCCAAACA AGCTCGAAAT CTCATCACTG ATATTTNCAC AGANCAGTGT 60
ACCCTTAGTG ACCAGTTGCT ACCCAAGCNT TGTCCCAAAN CTATCAGTCA AGCAGTGNA 120
TAAGAAATCA AAAAAGCAGA CTGGTAAGAA AGGGGAACCT GNAAAGGNAG NAAACCAGGT 180
GTTGAGAGCA TGAGGAAAAA CAGGCTGGTT GTGNACCAAC CTTGNATAAA TTGCACACTG 240
CACTTTNTGN AGTTATGCTT CTNTATGATT T 271

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GGCAGGAGCN ACAATCCGGC CAGTGCCCAG GCTGCCATCC AGGCCATGAA TGGNTTCCAG 60
ATCGGCATGA AGCGCCTCAA AGTCCAGCTA AAGCGGCCCTA AGGATGCCAA CCGGCCCTAC 120
TGAGGGCCCC CAGGTCTGGA GATCCCANAG GAAGGGGCGC CTCANACCCT CTTCCCACGA 180
CTGGCCNCGG CCATCTCCGC ACACCTGCCC TGGGCCTTGA CTGGGTTCTG GGGCAAACGA 240
TGCTTACGTG GCCCCGGGGG CGCAAGANNA CCGGCCNTTC CCACNCCCCT GNCTGTTTGA 300
AAGGGCCATG GGTGATGATT TCCCTGGGT 329

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

| | |
|---|-----|
| GGCAGGAGGN ACACCAAAGG CTTGGTGAGA NCGCTCGGGG AGGAAGCCCT GCTGAGAATA | 60 |
| CGTTCTCTCC ATAAATNAAG AAGGGCTAAG GCGATGCGAN GAGAATACAA AAGTNTTTGG | 120 |
| TCGGCCTATC AGCTCATGGA CCTGCCTGGT GGAATTGGA GGGCTGAACA TCGCCCACTT | 180 |
| NTGGAGNCCT TGTGTNAAAA GCGCTNCTGC GGTATNCATC G | 221 |

(2) INFORMATION FOR SEQ ID NO:572:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

| | |
|---|-----|
| CTCCTACCTG CNGGCTNCCC TAGNGGTNAA CTCCTCCCTT AGTGGCCAAN GACATCAAGA | 60 |
| AGATCTTGGA CAGCGTGGGT ATCGAGGCGG ACGGACGACC GGTNCAACAA GGTATNCAG | 120 |
| TGAGCTNGAA TGTGGGNAAA ACA | 143 |

(2) INFORMATION FOR SEQ ID NO:573:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

| | |
|---|-----|
| GGCAGAGGTG CTCACTGGAG CTGTGCAAAA TGGGCTTGCC CTGGTGAGGC CTCCCGGGCA | 60 |
| CCATGGTCAG AGGGCGGCTG CCAACGGGTT CTGTGTGTTC ANCAGCGTGT CCATAGCAGC | 120 |
| TGCACATGCC AAGCAGTAAC ACGGGCTACA CAGGATCCTC GTCGTGGANT GGGATGTGGA | 180 |
| CCATGNNCAG GGGATCCAGT ATCTCTTTGA GGATGACCNN AGCGTCCTTT ACTTCTCCTG | 240 |
| GGCACCGTTA TGAGCATGGG CGCTTNTGGC NTTCTGCGA GAGTCAGNTG CAGCGCATNG | 300 |

323

GGCGGGGACA GGGCTCGGCT TNA

(2) INFORMATION FOR SEQ ID NO:574:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

| | |
|--|-----|
| AGTAGAGCCA CTTTCATCTCT GGNATGGTNT TACAAAGTCA GNCAGNAAAG CAGAGCAGGA | 60 |
| CANGGAGGGC CTTTTGTCCC TGGTAATGTG TTTGGGATCT ANTTCCCGAT GCTGCGATGC | 120 |
| TGCGGGAAGC CTTGGGAGGG CTTTAAAGCA GGGGCGTGGC TTGCCTGTAT TTATTNCAGC | 180 |
| TGTGTNGGAG AATGATTTGT AATACAGCAA ANGNTTNAAA GGAAGGGCAG | 230 |

(2) INFORMATION FOR SEQ ID NO:575:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

| | |
|--|-----|
| GGCCATAAAA CAAGGCTTCC AGTTTCGCCG AGTTTGGNAG GGTGTTTTTCC GGCAACGNCA | 60 |
| GTANCCAGAT TGGTCACATC ATCGTAAATA CCAACCGTAA AGCGCGCTTT CGGTTTAGCC | 120 |
| GCGTTGAGCT CGGCAAATAC CGCCAGTACA CAGTCTGGGC CAAATTCTTT GGATGAANGA | 180 |
| CCATAGCGCC CACCAATGAA CACGGGGCAG AGTTTCGCCG TCGCNATTAT TGAAAGGCTT | 240 |
| CTGCCCAGTG AGGGTACATT TACATCCAGA TAGAGCGGTT TTGCNTGGGG GCACCGGGGT | 300 |
| TNCTTTGGGT TCTGTCCAGT TACCGTCANG GTTGGGTACG GGNTNCCGGG CAGAA | 355 |

(2) INFORMATION FOR SEQ ID NO:576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

| | |
|--|----|
| TCGCCAGACG GCAGCAAACCT GGCATTTCGN TTGTGCAAAA CCGGTAGTNT GAACCTNTAC | 60 |
|--|----|

| | |
|--|-----|
| GTAATGGATT TGGCTTCTGG TCAGATCCGC CAGTGAAGTG ATGGTCGCAG TAACAATACC | 120 |
| GAACCGACCT GGTTCCTCGGA TAGCCAGAAC CTGGCATTTA CTTCTAACCA GGCCGACCGC | 180 |
| GTGNGCANTN TAAAGCCGGG CGTGGCTTGC GCCANTGCGG GCTGACGGTG GAGCAACTGG | 240 |
| CCAGACAGGT GGAGCCGGAA TACACACCGG CGCGAAAAGT TCATTTTAC CATTGCGAAC | 300 |
| CACCGGGGCC TGNCGTGGG GGTTCATCAG CNAAGACGGG CATTACGGCG TGGCGCGGGG | 360 |
| GTATTTTAT TGANTGGGGC AACCAGTTA ATGAGGNGAA CCCGTTTCAC TTGCAACAGC | 420 |
| GTACCTTTNN CCAAGG | 437 |

(2) INFORMATION FOR SEQ ID NO:577:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

| | |
|---|-----|
| ATCAGCAGGC GGTACGGTT AACTGCTGA ACCTGGAACN NCGGGNANAC CGGTTGNNGT | 60 |
| CGCGGCTTGT GTGCAGCGTT ANNGCACGGA GATGATGAAC GTNATTTNGG CCGGTNTGGA | 120 |
| TNGATCTGCC ACTGACGNCG CGANCAGTCG ACCGATCATT CGAGTTCAC CTTCTTATTC | 180 |
| AGCAANCGAG AAGCGCGCCA TAAAGGGGCA ACATCAGGCC CATNACGNTA NCAGCGTAAT | 240 |
| GCTTGTTAGC TGCANCCAAA CGGGCAGTCA CGNTTTTAA GGGACTGGG CCTTGGTG | 298 |

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 194 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

| | |
|---|-----|
| NNTANAAGGN GGCCAAGTG GCACAAATGC AGNAACTCC CTCTGGTGAT GATTTCAGCC | 60 |
| TCTCCTTGGC AGATACTAAA TCTACCATCC GGAAGTGGAG CCAGAGCTNC GCATTTGCAT | 120 |
| TGCTAAAGCG TCTTTCAAGA GGTGCAGTCT TTGAAGGGCT GGGTANNGTN GCATCTGTGG | 180 |
| GANCTGAAAA TTCC | 194 |

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GCTGGCTGAT GAAACGCCGG AAGCCGNCAG TATTGTAATC CTCGCCAAGC AGCGTTTTAN 60
CCTNCGCGAC CCAATGTGCA GTCGCTCCAT GCCACCTTT 99

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAGGAAGCCA ACACCTTTAA ATTACCCGT TCGGGGCCAG CTGCGGTGCC CAGCATATAG 60
TGC GCGGTTT CGTAACTACC GGACCAGTCG CGCNGCCTCG TTACAGGCAT CTTTNAGCGT 120
CGCGAAACCG TATGCACCGG GATCACTTCC GCACCCATTA AGCGCATACG AAAAACGTTA 180
GGCGACTGGC GTTCAACGTC TTTGGCACCC ATATGAAATA CGGCATTTNA GGCCGAGCAG 240
GGCGCTGGCA AGGGCCGACG CCACGCCATG CTGACCGGCA CCGGTTTCGG CGATGATTTT 300
GGTTTTACCC ATCCGTTTCG CCAGNAAAGG CTGNCCCCAG CACTTGTTAA TTTTATGNNG 360
GNCGNCGTGC AGCAAATTTT CAGGTTT 387

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

AACATCAACG AAACACGCC GCGTTTTNAA GATGCNTTTA TTGATTTCCCT GGGCGGTGCC 60
GGAACCTCGG AATCGCCGNT GGGNGCAATA TTACATACGG TAGAAGGCAC ACCCGGCGAG 120
ACGGTGATCG AAGCGAAAGA NCTGACCAAG AAATTTGGGG ATTTTNCCGC CACCGATCAC 180
GTCAACTTTN CCGTTAAACG TGGGGAGATT TNTGGTTTGC TGGGGCCAAA CGGCGCGGGT 240
AAATCGACCA CCTTTAAAGA TGATGTNCGG TTTGCTGGTG CCGACTTCCG GCCAGGCGCT 300

GGTGCTGGGG ATGGATCTGA AAGAGAAGTT NCCGGTTAAA GCGCGCCAGC ATCTTCGGGC 360
TATTATGGCG GCAAAAATTT TTCGCTTTTA CGGTNAACCT GGACGGTCGA ACAGAATTTA 420
CGGTTTTTCC TCTGGTGTGT ATTGGCTTAC N 451

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GGCACGAGTA AGGCTGGGGT ATCCTGGTGA NAACTGGAGA GGATCTACTC GGNTCCCTGC 60
CTGGCCAGTG GGGAAACACC GGTCCCCCAG GCACCTTCAC CTAACCAAAG CGATAGATTT 120
CCACCGCCCC TNATGCCGCC CTTTGGAGGN AAAGTGAAAA GTGAAAAGGA AGGAAGAGGA 180
GGCTTCATGG CTGAGGAGGT CGCAGCGCCA TGAAAGTCCC TGTTTCTGCC TCCTCGCTGT 240
GGCTTTGGGT GAGCNAACCC CGCGAACTCA TCGCCCAAGA AACTAGAGGG AAGCGGAGGG 300
GAGGTGGCCC CACTGGGAGC CGATGCCANG NTTGGGGAGT GGGGCAGGTT CACCAGACAT 360
ACAAACCGTT TCTTNATTNG TTTCCCTATN AGGCAAG 397

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GGCACGAGAA CGGAGACTGC ATTGACATAG ACGAGTGCNC CAACGACACC ATGTTTGGTA 60
GCCNCGGCTT CTNTAACAAC ACTNATGGCT CCTTCCGCTG CCTCTTTAAC CAGGGCTTCG 120
AGATCTCTCC CTCAGGCTGG GACTGTTTGG ATGTAAACNA NTGTAAGCTT ATNCTGGCGG 180
TATGTGGGGC CGCGCTCTGT NAGAACGTGG AGGNCTNCTT CCTGTGCCTC TTTGCCAGTA 240
ACCTGGAGGN GTACGATGCC CAGGAGGGGC ACTGCCGCCC ACGGGGGGCT TGAGGTCAGA 300
GTATGTTTGA GGGCCNCAAC GGGGGGACCA TGCCCCGGCC CCCACCCGGT TGGACTGCNA 360
TTCCGGGNAG AAGGGNCATG CGCCCTGCTC CAGTNTCCTG GGCCGGAACA NCACANAGGC 420
TGAATNNNTG TTGCACCCAG GGC GTTAGTT GGGGAGTGCT NTAAACCTGT GCCCGTTTTA 480

GGAATTAGTT GAATTCAGGG AG

(2) INFORMATION FOR SEQ ID NO:584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

| | |
|--|-----|
| CCAGCCATTT CCTGCTCTAC GTACGTAATT CCNCCGCCGG ATGGCAGGGT GACATGGATT | 60 |
| TACCGCCGCA GCCGCTGATA CCTTACGCCG ACTGGTAAGT TTTCAGANAG CGCCTCTCTT | 120 |
| AATGCCGCTG CGATCGGGTA TACTCGGGCG GCAATCTGGG ATTTCCGGGG GGAGACAATT | 180 |
| TGCGCGTAAG TCGCTCGTTA ACAATCAAGC AGATGCCAGC NCTTGCCAGA ATNAGCGCGT | 240 |
| CGGTGAAAAA AACAGCCGCA TNAATTGAGC ATCGAACAGG GTGCCGCCAG CATTGCGCCA | 300 |
| AACAGAGGTT TCAGGACTTC TCTACGNTGT GAAAAGAAAG CTGGCGACTG CTTCCAGGAA | 360 |
| GAATGAAAAA TAGCAAGCCG ATTTTCAGGAT GCCCGGCAGC CCGNAAAGCG NCTTTNATGT | 420 |
| GCGTCGCCAG AAAAAGGCAC ACCACATTGA AGGGGGACAA AAANCAGCAG GTTTGCCCCC | 480 |
| GGCCCAACGT T | 491 |

(2) INFORMATION FOR SEQ ID NO:585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

| | |
|---|-----|
| GGCAGGAGCN AGNCCCGACG CCGCCGACGC CCCTACGACC CCAACAGCGT CCGCATCANC | 60 |
| TTNGCCAAGG GCTGGGGGCC CTGCTACTCC CGGCAGTTCA TCACCTCCTG CCCCTGCTNN | 120 |
| ACTGGAGATC CTCCTGCAAC AACCCAGAT AGTGGCGGCC CCGCGGGAA GGGGCGGGTG | 180 |
| GGAAGGCCGN GGCCACCGNC ACCTGCCGGC CTCGAGAAGG GGCCGATGCC CAGAGNACAC | 240 |
| AGCCCCCAG GACAAAACCC CCCNGATTAT CATNTTACCT AGATTNAAT NTAAAATTTT | 300 |
| ATATATTATA TGGGAAATTA TNTGATTATA ATTTGTT | 337 |

(2) INFORMATION FOR SEQ ID NO:586:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

| | |
|---|-----|
| GTTTTTTTAC TGGCAACCCC NACGCTGTGG CNGTTTTNCG CNTGGGGCGG TAATGCAGTC | 60 |
| AGCGTAACGG TACTGGTGGC GCTGCTGGTC TGTNTNATCC CAACCACTAT TGGCGGCCTG | 120 |
| TNGTCAGCGA TCGGNGTCGC CGGGATGAGC CGGATGCTAG GCGCGAATGT AATTGNCACC | 180 |
| AGCGGACGTG CAGTTNAAGC GGCAGGTGAC GTTNACGTTC TGCTACTGGA TAAAACCGGC | 240 |
| ACCATCACAC TCGGTAACCG TCAGGCGTCG GAGTTTATCC CCGCGCAGGG CGTGGNTGAA | 300 |
| AAAACGCTGG CTTGACGCCG CACAACCTGGG CTTGCTGGC TGATGAAACG CCGGAAGGCC | 360 |
| GCAGTTATTG TGAATCCTCG CCAAGCAGCG TTTTAACTT GCGGCGGACG CGATTNTGCA | 420 |
| GTCGTTCCAT GCCACTTTTT ACCGTTTANT GCGNAAGCCG GTTNAGCGGG GTCAACATCG | 480 |
| GCAACCGNAT GNTCCGTA | 498 |

(2) INFORMATION FOR SEQ ID NO:587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

| | |
|---|-----|
| GGCAGAGCNA ACGGCGNGGC AGCGCACNGC AGGCGGNATT CATTCCACTT AAAACCTGAA | 60 |
| AACATTGGAC CACACAAAGT CTTACTGATT TCAGGTAAAA ACAATAATTG AAGATGTCCA | 120 |
| GCAAAACAGC AAGCACCAAC AATATAGCCC AGGCAAGGAG AACTGTGCAG CTTTTAAGAA | 180 |
| TTAGAAGCCT CCATTGAAAG AATAAAGGTT TCGAAGGCAT CAGCGGACCT CATGTCCTAC | 240 |
| TGTGAAGGAA CATGCCAGGA GTGACCCTTT GCTGATAGGA ATACCAACTT CAGAAAACCC | 300 |
| TTTTCAAGGA TAAAAAATT GCATCATCTT ATAGTGGATA GAGAAACAGT TCTTGGCTCT | 360 |
| TCCAACAAG GCAATTTTGA GCNGTCCTTG NAGNGTTTAC CTCAGTTATT TGATAACCNN | 420 |
| GTTATAATTA A | 431 |

(2) INFORMATION FOR SEQ ID NO:588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

| | |
|---|-----|
| GGCTGCGGTC AGGGCTTCAA ACATGAGTCC TTTGCCCTGC CATTTTGGCC CAATCGAATA | 60 |
| ACCGAGATAG CAGGCATGAA AAGAGCCACG AACAACATTG GAAAAATTGG CAACGCATGA | 120 |
| AATCTCTTTT TCGTCCGGGT CGAATAAGCC AAAGTAGAAA GCTGNAACCT TGTTTATGAA | 180 |
| AATTGGTTAA ATCATCCCCA GCCTGGCCTG CCAACCTGAT GGATAAACAG TGGGCTTTGC | 240 |
| GTCGCGGCAC TGGCTTCCCA GGGCTTTGAG GGAAATGGGC GNTTCTNCT GCGTGAATAA | 300 |
| NTCCGCAAGN ACGGCCAGGC ATTCACGNTT CATGCACCA | 339 |

(2) INFORMATION FOR SEQ ID NO:589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

| | |
|---|-----|
| AATTTGTCTC ANCCGATGCC GGCTACCAAG GGGCGCCACA GCCGNAGGNG CTGGTCCGAG | 60 |
| GTGGATGTGG ACTGGCTGAT CGCCGAGCGC GCCGGCAAGG TAAGAACCTT GAAACAGCAT | 120 |
| CCACGCAAGA NCAAAACGGC CATCAACATC GANTACATGA AAGCCAGCAT CCGGGCCAGG | 180 |
| GTGGAGCACC CATTTCGCAT CATCAAGCGA CAGTTCCGGG CTTCGTGAAA GCCAGATTAC | 240 |
| AAGGGGTTGC TGAAAAACGG TAAACCAACT GGTGATGTT ATTTACGNT GGTCAACCTN | 300 |
| TTTTCGGGNG GNACCAAATG ATTACGTCAT GGGGGAGAGN | 340 |

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

| | |
|---|-----|
| CGCCTTAATG GTCCGACGNG CCTAAAGTTA ATTNAGGATT TAAGTAAGCG GAAAACGCGT | 60 |
| NATCGAATGG GTACGCCATT TATGCGTGAN CTGGAAGAGA AACGCAATCN NTTAATGGTA | 120 |
| AATCGGGGGC GTTCTGCGC CCCCATGCTG CCAACATTTA CAAATNCTTT NCACTTCCCT | 180 |

GCACTATCCG ACACTGTCAC CATCCATAAT TNAGGCTTAT NTGTTTGTTA NCAGTAACCT 240
TATGTTT 247

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

AACAACACCG GTATTACGCA AAACCTATCG TACATTGGCG GCTAAAACGN CAAAAGGAGA 60
GATCAGATGA GTCAGGTAAG CACTGAATTT ATCCCGACCC GTATTGGCTA TTCTNACGGT 120
TTCNAATCGN CGCGGTGAAG AAGACGATAC CTCCGGTCAC TATCTGCGCC GATTCGGCGN 180
AAGGAAGCGG GCCATCACGT TGTCGATAAA GCCATTGTGA AAGAAAACCG NTGACGCTAT 240
TNGGGCTCNA NGTATCT 257

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 277 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

AACCTGGTCA CAGTNAGCGA TCCACAAGAC CTGGCAGGCG ACGGAGTGTN CCTTGATCAT 60
AGCGAGCCCT ACGAAGCCTC GCGGGAATTT ACCCAGGTNT GGCGGCGTTT ATTGCAGAGA 120
AGAAACCGTC GNATTTCAAC GGTAACATA TTCATGTGCC GCGGAGCAAT AACTNCTCTT 180
CCCGGCGAAT TTCAACAGCC GTATCCGCTC ACTTTANCTT TGGCGGATCG TNNAGATGTN 240
GCCCAGNAGC TGGCGGCAGG AACAGGTTGA TCTCTAA 277

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

| | |
|---|-----|
| TGCCCAGAGN CGGGGGTTAA AGAGGAGGAA GATGGCAGAT AAGGTTCTAC CTCACCNAAT | 60 |
| CCGGGAGCTT GTTCCANAGT NTCAGGCGTA CATGGNTCTT TTGGCTTTTG AAGCGGAACT | 120 |
| GGTACCAGAC CATTGCTNCG CAAGCGGGAT GGAGATCCAN GTAGGCCATC AAAAAGCCTC | 180 |
| TGNNCACAAA AGCGAAGTTT CGGGATCTGA CATTTTCCAA TAAGTTCATT CCCAGCAAGG | 240 |
| AGGNAAGGNG | 250 |

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

| | |
|---|-----|
| ACGTTTTNAG CGGAGGCCCA GCTAATGTTT NAGTATTTAC CCGAACTNAT GAAAGGGCTA | 60 |
| CACACNAGCC TGACGCTAAC CGTNGCCTCG CTGATTGTGG CACTNATTCT GGCATTNATT | 120 |
| TTAACCATCA TCCTGACGCT GAAAACGCCG GTNCTGGTGT GGCTGGTGCG GGGTTATATC | 180 |
| ACGCTGTTTA CCGGTACGCC GCTGCTGGTG CAGATCNTNC TNNTTTATTA CGGGGCCGGG | 240 |
| CCAGTTTCCG ACTTTCNAGG AGTATCCGG | 269 |

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

| | |
|--|-----|
| AAAGAAGCGA TTAGCATNAA ACAGGTTCTA TCGGTTTCTC NGGTTTNCAC AGCTTCACGC | 60 |
| CACGGAANGA TTACGCGGTG CATCAGGCAC AGNTTTTNCG GCGGTGTAGA AGTATCANCC | 120 |
| TGCGGTTNAT TCAGCAAGCT GCTGGCTTTC ACCAGCNTAA TGTCTGGCGG CAGGTTATAA | 180 |
| ACCATCTTTT GCAACACGCG TACCGTTGCC AGGGTGAGGA TGCCCAATGG NAATGGTTCCG | 240 |
| ANCCGTTGCG AACGCGGCCA GGTTCAATTG NGCCGATTGA AATTGTCACA CGGNTGTCCC | 300 |
| GTTTCATTTT GCGGAANCGT TCGAGGGATG ACCTTCCCGT TTNGGTCCNA CC | 352 |

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

| | |
|---|-----|
| AATAACGCGG GTAAACGGAA TCATCCATAC AAGCANGATA ATGANCGGGA ATGGAACGGA | 60 |
| AAATNTTCAC AATCGCAGAA ACGGTANNAT ACAGCTTCGC NTTNACAATG AATTTGCCCC | 120 |
| GGAACGCGTG AACATAAAGC AGAACGCCAA CCGGCAGNAC CAATGCACAA AGCCAAAAAA | 180 |
| ACCGGATACG AAAGGTGCAT TGCCAGCTTT TCCCATTACG GCCACGGAAC CAGCAGCCAC | 240 |
| ATGCTNCGGC TTCAGAACAT TAACCCAGTT ACCTCTGATT TTAAACATGG TGTTTCCTGG | 300 |
| CAGCCCAGGC AATGGGGGGN TTGCGNTNAT NCT | 333 |

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

| | |
|---|-----|
| CAGCAATGGC GTCAAGTTGG GCAAAAANTAA CATNTCCTG ATCGGNCCGA CCGGTTCCGG | 60 |
| TAAAACCTG CTGGCTGAAA CCCTGGCCGC CCTCCNGGAT GTCCCGTTNA CCATGGACCG | 120 |
| ACGNGAACTN AACTGAACC GAAGCCGTT ATGTGGGTGA AAGACGTTGA AAAACATGCA | 180 |
| TTNNAGAAAG CTGTTGCAGN TAATGCGAAC TGNGAATGTC CCAGAAAGCN CAGGTGGTTA | 240 |
| TTGTCTTACA TGGGTGAATG GACCAAGATT TCTC | 274 |

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

| | |
|---|----|
| ACAGACCTC CTTNNTCCGT TTNTGGGGAA TACTTCCCTC GGGTGAAC TG AAAGTAAATT | 60 |
| TTTTTTTTTTT CCCAAACA | 78 |

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

| | |
|---|-----|
| GTNAAAAAAG GGCTCGGTGT ATTCNAAAAT AGCGGCGCGA ATTACCTGAA NCGCAATTGG | 60 |
| TGGTGGTTCT CCACAGGNTA CTTGTAAAAG CNAATTGGGA ATTATCAGCA ACAACCCGGA | 120 |
| AGTTTGCCGA TGTGCCGTAC CTGGGAAGGG CTTTCCCCGA CCAATAAACC CAGTGTACCG | 180 |
| ATTCTGGCAA TTCCTAACCA CAGCAGGTTA CTGGNCCAAA GGTGAACCAT TAACTTACG | 240 |
| TGAATNCACT GNACGGAGAA GGAAACGGGC GCCAATTTTT GTTTTGCTTN ATGGATNCCG | 300 |
| CATGATATTC CCCGNCGGTG | 320 |

(2) INFORMATION FOR SEQ ID NO:600:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

| | |
|---|-----|
| GGCAGAGGTA AAATGGACAT TTTAGGGGAA ANTCCTGTGG AAAGATAGCC CCTCCTCTG | 60 |
| TTGTGTCTTC AGGGCCATTT CTTTTTATCA AATTTGTCTC TGAACACGA AAACACATGG | 120 |
| TGCAGGGTTT NCCATACGTT AATGAAATTT TCAAGANAGG TCCTGAATGT NCCCAGTAAC | 180 |
| TACACAACAC CTNAGTGGGA GTGAATGAAA GTCCCCGGG ATTNCCCTGA ANAAAATAAT | 240 |
| GCCCAACAGC CTTGGAATGT CACTTNATNA TTGGTNCTTT TNCGCNCAAA GAATGTCCAG | 300 |
| AGAATTTATT CCTGGGAATT TGAAAAGGTT TTG | 333 |

(2) INFORMATION FOR SEQ ID NO:601:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

| | |
|--|----|
| TGTAACCTC CCAAAGGNGC AGCTGGCCAN AAAACCATCG NTGCCCTTCT CNGTTGCCTT | 60 |
|--|----|

CTGGTGAAAG GANTGATGAG CCACCGTGAA CGGAAGTTCC GTGCCCTCAG CATTANCACC 120
CTT 123

(2) INFORMATION FOR SEQ ID NO:602:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGCTACGTAA AGAATAAAAT CAATCTCCCT NCNCAACGGT GGTAATTACN TTAAATGAT 60
GGCCTCAAGT CGGTAAGCCG CTATGGNTGA TCCNGTTTTG AAACATTATG GCATGAAGGC 120
GAACGGCNTT TATTGTTACC TCANGCATCA AACGTCACCC GCAGAAGTGG AACCCAAAAT 180
CGCNGCAATT TATGAANCGT TTNTAAGCTT AACGGAAATT CGCGAATGTA TTTGATTTCC 240
CAGTCACCAT ACCCCTTTTT TNGCCATCGG GGTTAGGTGG GTTATGCGGN NGACCCNTAN 300
TTACTG 306

(2) INFORMATION FOR SEQ ID NO:603:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

CTGCACTGGG NNCATGAACT AGGCCTGGCC TTCACCAAGA ACCGANTGAN CTATACCAAC 60
AAATTCCTGC TGATCCCAGA NTCGGGAGAC TACTTCATTT ACTCCCAGGT CACATTCCGT 120
GGGAATGAAC CTCTGAANTG CCAGTGAAAA TCAGNCAAGC AGGCCGACCA AACAAGCCAG 180
ANTCCATNCA CTGTGGTCAT CACCAAGGTA ACAGACAGCT ACCCTGAGCC AACCCAGCTC 240
CTTCATGGGG ACCAAGTTTG TTTGCGAANT AGGTTAGCAA CTGGTTCCAG CCCATTTTAC 300
CTTGGGGGCC AGTTCTNCTT GNCAAGAAGG GGACAAGCTT ATGGTGGAAC GTTCATANCA 360
TCNTTTTTTG GTGGNTTTAC ACAAAGG 388

(2) INFORMATION FOR SEQ ID NO:604:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

| | |
|--|-----|
| AAGCTTTACT GGTGCGCGAA AAAGTTGAAG CCGCGCGCAG AGCANTGCTG CTGTATCCGC | 60 |
| AAGGTTTAAG CTGGGAATTG GTGGGATGAC GTCACCGTAG AGATCCGTTT CTGGCTTCCG | 120 |
| GCGGGTAGTT TTGCAACCAG CGTTGTCAGG GNAACTTATC AACACAACAG GTGATTATGC | 180 |
| CGCATATTGC TGAGTAATGA TGACGGGGTA CATGCACCCG GTATTNGAAA CGCTGGCGAA | 240 |
| GCTTGCGTGA GTTTTNTCTGA CGTTCCAAGT GGTCGCCCCC GTTCGNTAAC CGCAGGGCGN | 300 |
| TTCAAATTCT TCTGNCATGG GATTCTCTCC TGCGNACGTT TTACCTTTGG AAATGGGGGN | 360 |
| TTATT | 365 |

(2) INFORMATION FOR SEQ ID NO:605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

| | |
|---|-----|
| TTACAGANNT AAGCCGCCGT GCCCAGNCAC AAAGTTCTTT AATNACAACC ACGNAAGGGG | 60 |
| CACACATGGG TCCTGTCTCT GGTATGGATT CACACACACG TGCACAAATT GAAGTCCAAT | 120 |
| AAAAAGCATN TGCCACAGA CCCACCATGT GCCATTAAAG ANCTTCTCTN CCAGCACAGA | 180 |
| CTNGTTGGTG TTGTTCTTNG TGCTTGNAGC TCTTCAACAA AGAGCTTTTG CCGT | 234 |

(2) INFORMATION FOR SEQ ID NO:606:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

| | |
|---|-----|
| TCTCTNCGAC TCATTGAGCC AGATGCTGAG GAAAAATGTA GAAAAGCGAG CACANCCAAG | 60 |
| NACAGCGGCA CTACCGGNCA CGNGACTCGC TTGTATAAAA GGTTTTTN | 108 |

(2) INFORMATION FOR SEQ ID NO:607:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```
TGGTGGAGCT CNGCATCCAC GAACAACCGC ATCCGCAAGT GCCCAAGGAA GTTTTCAGCG      60
GGCTCCGGAA CATGAAGTGC ATCGAAATGG GCGGGAAACC CACTGGAGAA CAGTGGCTTT      120
NAAACCNNGA GCCTTCNAAT GGCCTGAAGC TCNGCTACCT GCGCCATCTC AAAGGNCAAG      180
CTGGACTGGC ATCCCCAAAN ACCTCNCTNA GAACCCTGAT TGAAACTCCA CCTAGACCAC      240
AACAAAATNC AGG                                                                253
```

(2) INFORMATION FOR SEQ ID NO:608:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```
GGCAGGAGGN CCCTCAAAG NAGNAATCAG CTNCANTGAC AATAAAGATG GGACATGCAC      60
AGTGACCTAC CTGCCGAGTC TGCCAGGCGA CTACAGCATG CTNGTCAAGT ACAATGACAN      120
NNACATCCCT NGCAGCCCCT TTA                                                                143
```

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```
CCCNTNCTCA TGGGGNTGTT TCCTACTAAC CCCAAAGNGA AGACCCAGGA GGAACCCCTT      60
GGNCCAGAGC AGGGCCCCCTG TTTTGACCGT GGTGTCCAAG TTCAAGGCCT CACTNGAGCA      120
GNTTGTGCAG GTCCTNNACA GNACCACGCC CCACTNCATT CGCNGCATCA ACCCAACAGC      180
CAAGGNCAGG CGCAGACCTT TTTCCAANAG GAGGTCTTAA GCCAGCTCGA GGGCTGTGGN      240
TT                                                                242
```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

CCCCTCCATG TACAGCCGCT CCATCCAGGG NCACCATGTC TGNCTCCTGG TGAAAAAGGG 60
TGAGANCTCT N 71

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

AGTACACTGG TNCCCGTACC GGGCAATGTA CCANTACAGG CCCCAANCGA AGACGAGCTG 60
GAGCTGCGCN AGGGGGACAG GGTGGATGTA ATGCNGCAGT GTNACGATGG CTGGTTTGTG 120
120

(2) INFORMATION FOR SEQ ID NO:612:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

CGTGNGCCCC NCAGAAATG GNCCCGGGTG CAGAATCGGC AGAGCGGGTC TGCTACTGGT 60
CCCNTAAGCC AGAGTAGCCA AGACTGAAGT CACTGCTCAT CCGGAATGGA AATCCCGCCG 120
ACCAACTACC CAGCCTCCAG GCGGCCTTG GTGGCACAGA ACTACATCAA CTACCAGCAG 180
GGGACCCGCA CAGGTGTTTN AGGTGCAGAA GGTCAACAAG CCAGCATGGA GGATATTCCA 240
GGAAGAGGAC ATAAGTATCA CCTTTAAATT TGCTGTTGAA GAATTATACA AAAACAANTA 300
AGGTGAACTG CACAGNTGAA GTACTTTACC CTCAACGGG ACAGAACTGA CCAGAGTCAC 360
TTCACATTTG AAGGGGAACT GGAAGATNCA GATGAGAGAC AACTTTNTC AAGCTTAGTC 420
CTGAGGACGT AGAGACAATT TCNGCATTTG GATNN 455

(2) INFORMATION FOR SEQ ID NO:613:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

| | |
|---|-----|
| GGCACGAGCT ATGCCAGCA GTGCCAGTNA CTTTGGGGAC CTGGAGCCCA GCCCGCTGCG | 60 |
| CCACTTTGCC TCCAGACAGC TAATACTCGG GGAAATGCTT TTGGGAGCTG TGGGCGCAAC | 120 |
| CCCAGTGGCA GTTATGTGTC CTGCACCCCT AGAGATGGCA TTTGTGGGCA GCTCCAGTGC | 180 |
| CAGACAGGTA GGACCCAGCC TCTGCTGGNC TNCCATCCGG GGATCTACTC TGGGAGACAA | 240 |
| TAGATGTGAA TGGGACTGNG CTGAACTGCA GCTGGGTGCA CCTGGGACCT GGGCAGTGAT | 300 |
| GTGGCCCAGN CCCTCCTGAC TTTGGCCTGG CACAANCTGT GGCCCTGGNC TGGNNGTGTA | 360 |
| TAGACC | 366 |

(2) INFORMATION FOR SEQ ID NO:614:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

| | |
|---|-----|
| TTAAGGTTTC GCTGACCGGG ACATAATGGC TTACACCTTC TCCAGTTTGA CCGCGCACTT | 60 |
| CTTGAAGTCC GTCTCTTTCG AGAGCGGATC GGTGCGATCC AGCGTCAGTT TGTTAACCAA | 120 |
| CTGTGCCGGC GTCGAAGAAC GGCATGTACA CCAGGCCCTG TGGCGGACGG TTANNACCGG | 180 |
| CCGTTTCAAC AATCGAGATC ACTTCGCCAC GGCGAGAAAC CACTTTNACT TTGTGCCAC | 240 |
| GGCGCAGATC GCGCGCTTTC GNATCCAGCG GGTGGAATAA AACAGGACCG CTTCCGGGGA | 300 |
| AGGCGCGGTG CANTTCTGGT NACACGGCGA GTTCATAATT GCCGGTTNTG NCCAGTGGTT | 360 |
| CCAGAACGTG TTCCGGTTAG AGAGCCACAA GTTCGTAATT CTTCATCCGG TGGTTCCGC | 420 |
| CGNCGGTTTC NATGGGNATT CGGAAGATCA NCGTTTTGCC ATTCCGTTTT ACCTTAGAAT | 480 |
| TTTTAGCTTT GGGC | 495 |

(2) INFORMATION FOR SEQ ID NO:615:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

| | |
|---|-----|
| GGACTGCACC GGCACAGAGG CCCACATCTC CAGCTGCAAN NGTTNCCCCA GGTGTCACTG | 60 |
| GACCCCATGA AGAATGTCAC CTGCNAGAAT GGGCTACCGG CCGTGGTGAG TTGTGTGCCT | 120 |
| GGGCAGGTCT TCAGCCCTNA CGGACCCTCG ANATTCCGGA AAGCGTACAA GCCAGAGCAA | 180 |
| CCCCTGGTGC GACTNAAAGG CCGTGCCTAC ATCGGGGAGG GCCGCGTGGA GGTGCTCAAA | 240 |
| AATGGAGAGT GGGGGACCGT CTGCNACGAC AAAGTGGGTA CCTGGTNTCG GNCAGTNATG | 300 |
| GTCTTGACAGA GAGCTTGGGG CTTTGGGAA GTNCCAAAAA GGCAGTTNAC TNGNTTTCGG | 360 |
| ACTTAGGGTA AAGGGTTTCG GACCNATTCC AACTGGAACG GAGTTTCCA | 409 |

(2) INFORMATION FOR SEQ ID NO:616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

| | |
|---|-----|
| GGCAGAGCNC GANTTNAAAA AAGGAAGGCA ATCATTGGAT TATACAACTA TGCCCATGAA | 60 |
| ATAACTCATG GAGCAAGTGN ACAGAGAAAT ACCCAGCCT TGGCCAGATG ATTGTGGATT | 120 |
| ATGAAAAACC CTTTAAAGAA GATGATGGNA AGATTTNNTN NCCCCATNAG CAAGTNTCTT | 180 |
| TNAGATGCAC TAATTTCCCT TCCAAATGGT ATATCCTCGA AAGGAATCT TTTCACCTGG | 240 |
| ACCAGTGGAG AAATGNCCAG TTATTGAGNC TCATCAGTGN NACCTTNGT | 289 |

(2) INFORMATION FOR SEQ ID NO:617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

| | |
|---|-----|
| GCCCCAGGAA AACCGTGTNC NATNAGCCAT GAGTCAACNC CACCGTGTTC TNCNANATTC | 60 |
| CCGTCAACGG GAAGNCCCTT GGGCCGCGAT NTNCCTTTAA CCTGTTTGCA GACAAGGTCC | 120 |

| | |
|--|-----|
| CAAAGACAGC AGAAAATTTTC CGTGCCTCTG AAGCACTGGN NGAGAANGGA ATTTGGTTAT | 180 |
| AAGGGTTCCT GCCTTTNCAC AGGATTCATT CCAGGGTTTA TGTGTCAGTG TGGTGGANTT | 240 |
| CACACGCCAT AATGGCACTG GTGGGCAAGT CCTTTNTGGG GGGGAATTTG AAGGTGNGNN | 300 |
| TTT | 303 |

(2) INFORMATION FOR SEQ ID NO:618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

| | |
|---|-----|
| CCCATTTANN TCGGATANTT GCCGNGAAAT CGGCCGGATT AATGGCGAGT ATTTGGCACA | 60 |
| TCCNTTGGCA ATGCTGAAGG TGGTCAGGAA GCCACGGGTC ATCAGGTTTN N | 111 |

(2) INFORMATION FOR SEQ ID NO:619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

| | |
|---|-----|
| GGCAGAGNCA GAAAACTGCC CCAGGGGATG CAGCTGGATT NTTGGAAGAA ACGAGAGTTT | 60 |
| TGGGAAACCG TCCTGGCATC CTGGAAGGGG CCTGAAAGCA GCCCCTTATT CAGAAGCAGA | 120 |
| GCCGGCNCCA CAAAAGGAA GCCCCCAAGA AACTAGGNGA GCTTGAAATT AAAACATGA | 180 |
| GTAAAAATNT CATAAANCA GGGAAGCTTC AAAGACACAG GGNACATTGC CAGAAGCCAG | 240 |
| AGAAGGTGTA AGNAGAAAGC CGTGAACCTC CCGGGGCTGT NTGTGGAGTC TNGCAGGGGC | 300 |
| TGCCTGGTTT GCCGAGTCCC ACGTTTTCGN CAGTGTGGTG GTNCCGNTGG GGAGG | 355 |

(2) INFORMATION FOR SEQ ID NO:620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

| | |
|---|-----|
| GGCAGAGGGA AGACACAAGA TAAAATTAAC ACCAAAAATA AAGAAATACT TAGGTATAAN | 60 |
| TCCAAGAAAG CATGCATAAG ANCTGTATGA AGAAAGCTAC AAAACTCTTA TAAAAGACAT | 120 |
| AACATTTTCA CGATAATAAG TACAAAGTTG GAGGGATGAC TTCGAGACTT ATTAGAAAGG | 180 |
| TACTGTGAAT GAAGACAGTN TTGTATTGGT CCAAAAANTC GGCCAATAGA ACACATTGGA | 240 |
| AAGCCCAGAA AATAGACTCA GTGCCAGGCC GGGCGTGATG GTTCAAGCGT GTAAATCCTA | 300 |
| GCACTTTGGG GAGGTCCGAG GCGGGCGGGT TCACAAGGTT CAGGAGNTCG AGACCNTCCT | 360 |
| GGGCCCAACN GGTAAACC CCCTGTTNTA NTAAAATTAC CAAANNATTT AGCTGGGCGT | 420 |
| GGTGGCAGTG CCCGTAGTNC CCGCAANTTG GNGGTTTGG GCAGGCGATT GGGGTGACCC | 480 |
| GGGGTTGGA GTTTTCATTN NGGGGTTTG | 510 |

(2) INFORMATION FOR SEQ ID NO:621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

| | |
|---|-----|
| CAGCGGATCG GTCTGCCCCT GTANNCAGTT AGCTCTTCAT GCACCCGCAG CATAAACGG | 60 |
| TGNAAGTGCA GGCNCTGTTT CCGGTCTCCC GGCAGGCTTT GATAGAAAAG GTCCATCAGC | 120 |
| CAGGTTTTCC CGCGTCTAC ACCGCCCCAN ATATATAAGC CACGCACTGG CGTNATGCTT | 180 |
| TGTGTCTTCG CGTTTACCCC ACAGCTTACC GACCCGGGCC ATTAGCCAC TCGTCCTGGG | 240 |
| GGCTGGTGGC GTGCTATTGA TGAGTTCCTG ATAAATAAAT TTCCAGGCGG CTGACGGCCT | 300 |
| CTTTTTTGAA CGTNGTCGGG TTGATGGCTG NCNTTCATTA AAGCGNCTTC AGGTATTGCG | 360 |
| ATGTTGGGGT AACGGTTTGC ANGATCNTAA TGTANTCCN TGGATAAATC GGTGNGCCTT | 420 |
| TGTTCAAGGT NNAGGAAAAA AAGGCCGTTT ACATTACGGG TATNCATCGG GGTTCATTT | 480 |
| TTGGNTTAAC GGTAAAGGGG GA | 502 |

(2) INFORMATION FOR SEQ ID NO:622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

| | |
|--|-----|
| ATTGAACGTN GCCCAGGAAT CAAAAGTCGC CGTTTTTCCA GACAAGCCGG GNACGGTTTTT | 60 |
| TTTGGTGGTG GATTTGTACA CCAGAACTC ACGCCACATT CGCCAATTCT CACGGAGAAC | 120 |
| AGGCCTTCCT GCTGCNTNGA GTCTATCGGA CAGTCAGAAA TGAATCATAT CCAGTTTATG | 180 |
| CTGACTTAAT TGCTCCAGCA GNATTTCGTG GGTGGNTTCG AAGCAGNGGA AGATGAATGG | 240 |
| GCTCGTCTTC TACCACTGCG GCGTTAAGTA CGCTACTGAC CAGGCGTTTG GTAAAGTGCA | 300 |
| TCAGCCACGN CAACGTCAAN CAATGAATTG GATTCTTTGC GATAGTTCAC AATATCCCAG | 360 |
| CCATTTCGG GNTNAGGTGA ACATTTTTTT CGGCTTAGNG TTAGNCCATT TTT | 413 |

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

| | |
|---|-----|
| GNCACGAGTG GGTNATNATA CCCCTGNCAT TGACAGACAT CTAGNGAAC CACATAAATT | 60 |
| TAAANAGAG TGGTCCAGTG TAATGCGGTG TGTAGCAGTG CTTTGTGGT ATAAATCATG | 120 |
| NCAGTNCTAA AGTGGATTTT NATAACAACA TACAGTTGTC TCTNACACTG GCTGCACTAT | 180 |
| CCATTGGACT GTGGTGGNCT TTTGNTAAGA TCTAGANGTG GTTTTGGCCT TGGAGTAGGA | 240 |
| ATTGGCCNTC TTGGCAACTG TGGTCACTGC AACTGCTAAG TNTATAATGG TGTTTTACCA | 300 |
| ATATGACCTN CTCCAAGATN TCCNGTGAT GGT | 334 |

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

| | |
|---|-----|
| GGCAGAGNCC GANCCACCAT CTNCTNGAAC GTCAACGGCA NACAAAGTAA ACAGGACCAA | 60 |
| GATCCACAGC GNAGTCCTGA GCACCCTGGA NTNTCCTCGT AAACCCCGGC NGCTGTTNGA | 120 |
| GANANGTNGT TGAATNCACG GCCCTCCNAN CGACCTGGGT CAAAACACC AGCATCCTCT | 180 |
| TCCTGGAGCT GGTCAATTTT AACCACCNTC ACACNAGACT CTCACATAAC CACTGGACTC | 240 |
| AGCACTTCCA NTGNCAGTCC CGNATA | 266 |

(2) INFORMATION FOR SEQ ID NO:625:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

```
GGCAGAGCTC ATAGCTTGTT GGTACCTCC ATGGGGCACA TAAAGCTGAC AGATTTTGGA      60
TTATCTAAGG TGGGACTAAT GAGCATGACT ACCAACCTTT ACGAGGGTCA TATTGAGAAG      120
GATGCTAGAN AGTTCCTGGA TAAACAGGTC TGTGGCACNC TGGAATACAT TGCACCAGAA      180
GTGAATTCTG AAGGCAGGGT TATGGAAAGC CGGTGGGACT GGTGGGGCCA TGGGGATTTA      240
TCCTTNTATG ANATTTCTG GTTGGGATGC GTGCCATTCT TTTGGGGATA ANTCCANGGG      300
NCTATTTTGG GACAAGTTCA TCATGATGAG ATCAATGGGC CTA                        343
```

(2) INFORMATION FOR SEQ ID NO:626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

```
CTGCGGNGCA AAAGCGGTTT GCCAGATCTT GCCCAGTCTG CGANGATAGT TGGTCAGCAA      60
CACCAGCGGC AGGCCTTTAT CCATAATCCC GTGCAAAAAT TCCGCTGCAC CCGGTAGNCG      120
NACGTTATCG TGCATCAGCG NCGCGTNCGC ATATCGCAAA TTACATTTTT GAATGGTCAT      180
GGACTACCCA GAATATTGAC AACAATTAAG CGCCACTTAT TAAAAGCACA TTAAATTTTC      240
CAGCAAATGC TGGAGCAAAA TACCGTTGAG CATGGCGCGT TTTTACCAGC GGCAAAAGCN      300
CCGTTTGCCG AGCGGTTGAT TCCAGCTTCA GAACGTNACC ACCGGNCAGN TTAGTGCGN      360
AAA                                                                363
```

(2) INFORMATION FOR SEQ ID NO:627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

| | |
|---|-----|
| GGCAGAGGGC ACCCTNTCGC CGCGAANCGG TGC GCGCGCA CTCGTCCCGG CCCTGGCCCCG | 60 |
| CCGCAAACAA GGATCCGCTG CGCTCGGGGA ACGCAACNNN CGNCTCGTGG CCCC GGACCT | 120 |
| GAAAGACCCT TCCAGCATGC NAAAGGAAAG TTCCCCCAGG CGGACCCCGC AGAGCATTCC | 180 |
| CTACCAGGAC CTCCCTGCAC CTGGTNAATG CAGACGGACA GTAACCTNTT CTGGCAGGTA | 240 |
| CTGGGAAACC CACAGGCACA CCCAAGGCC TCATCTTTTT TTTCCCATGG AGCCGGAGAG | 300 |
| CACATGGGCC GTTATGAAGA GNTGGNTTCG GATGNTGAT GGGGCTTGGA NCTG | 354 |

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

| | |
|---|-----|
| TANNCGTAGT GGTGGTTAAC CACTATAACT GGGAAAGATG ATGCCCCGCC GNGCAGCCG | 60 |
| TGGGGCAGCA CCATCATRNA TAAAGCCCAT GTNAAAGGAT TAATGTACTT GCCNCCCGGA | 120 |
| GATCCCGGTC AAAATCCGTG GCACTTATNA AAGCCCTCGG GCATCCGGTG AATGNTCGCT | 180 |
| ATTTGAAACA TTTGGGCCAT TACCGNGCTG GGAAGTCTG CCATGGCGCA TTTTGCCAGT | 240 |
| NAAACCAGTT TGNAAAGCNT GGGGGGTNAG TAACTTATTG GGGTTTACAA CCCG | 294 |

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

| | |
|---|-----|
| AAAATCGTTA CCACGTTAGG CCCAGCAACA GATCGCGATA ATAATCTTGN AAAAAGTTAT | 60 |
| CGCGGCGGGT GCCAACGTTG TACGTATGAN CTTTTCTCAC GGCTCGCCTG TAAGATCACA | 120 |
| AAATGCGCGC GGTATGAAAG TTCGTGNAGA TTGNCCGCAA AACTGGGGCG TCATGTGGCT | 180 |
| ATTCTGGGTG ACCTCCAGGG GCCCAAATC CGTGTATCCA CCTTTGAAAG AAGGCAAAGT | 240 |
| TTTCCTCAAT ATTGGGGATA AATTCCTGGC TTCGACGGCA NCCTGGGGTG AAAGGTTGTA | 300 |
| AGGCGNCAAA GTAAAAGTTG GTGTCGTTN ACAAAGGNC TGNCGGCTGA ACGT | 354 |

(2) INFORMATION FOR SEQ ID NO:630:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

| | |
|---|-----|
| CTGGCTTTGT GTTTTGGTCA TTAATGGGGT GAGTGTGCGG NTCACCGCTG CCATGTATTC | 60 |
| CTGAGCTTTC GCTTTCGCGG CTTTTTGCTN TGGCCCCTGG ATGGGTAGCC AGGTCATTTG | 120 |
| AATGCTTTTG AATTTTNAAG GTACCGCGCT CCAGCTGTTA GNAAGCATAC AAGTNCTCAT | 180 |
| TAATTTTACT TGCAGCACGA GTGAAGATTG GCTTTGTCGG GACTGCTGTC GATGGCACGA | 240 |
| AATTCGTTCC AGTGGCAGGC TGGGATTCTG GCTGTAAAG TCTTCTCGAA ACTGGCTGAT | 300 |
| GGAGAGATCG AANTNNGGGC TTAGCCAGC AGATAAGGCG CGGTNNTTTG CC | 352 |

(2) INFORMATION FOR SEQ ID NO:631:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

| | |
|---|-----|
| GGCAGAGCGC ATGTGTGNAG GCGCTCAACA TGAAATTCAA GGCCGAAGTG CAGAGCAACC | 60 |
| GGGGCCTGAC CAAGGAGAAC CTCGTGTTCC TGGCGCAGAA ACTGTTCAAC AACAGCAGCA | 120 |
| GCCACCTGGA GGNACTACAC TGGCCTGTCC GTGTCCTGGT CCCANTTCAA CAGGGAGNAC | 180 |
| TTTNCCGGGG CTGGNAACTA CACCTTCTGG CANTTGGTTT TTACGGGGTG ATGGGAGGTT | 240 |
| GTTGAAGAAG CACCACAAGC CCCACTTGGA ATNNATGGGG GCCATCCTAG GGTTTTTGTG | 300 |
| AATTAAGCAA CCAGTCCCCA NGNNCTGGTT | 330 |

(2) INFORMATION FOR SEQ ID NO:632:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 428 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

| | |
|---|-----|
| GGCAGAGAGC ATACCATCTT TGGACGGGTT GTTGGGGGCT TTGACGTACT GACAGCCATG | 60 |
| GAGAATGTGG AGAGTGACCC CAAAACTGAC CGCCCTAAGG AGGAGATCCG CATTGATGCC | 120 |
| ACTACAGTNT TCGTGGACCC CTATGAAGGA GGCCGATGCC CAGATTGCGC AGTAGCGGNA | 180 |
| AGNACACAGC TCAAGGTAGC CCCGGAGACC AAAGTGTAAG AGCAGCCAGC CCCAGGCAGG | 240 |
| GAGCCAGGGC CCCAGACCT TTCCGCCAGG GTGTGGGCAA GTTACATCAA CCCAGCAGCC | 300 |
| ACGANNCGAG CAGCAGAGGT AAGGAGNCCT TTAACCATTG GCCATTTTTC CCCNNTTNCA | 360 |
| AGAAGAAGNC CATTTCGGGT TTTTGGGGAT TTCAGTTCTG GTTAGCAGCA NAATTTTtag | 420 |
| GTTTTACT | 428 |

(2) INFORMATION FOR SEQ ID NO:633:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

| | |
|--|-----|
| TTTGCAGCTC ACGGGNAAAT TTNTGCGCCA CTACCGCATC ACCAAGCATG ACCGGAATAA | 60 |
| TGGCGTGATC GGNTCCCGCC AGGNTAAAGC CCGNCGNCGA CATTTGCTCA CGGAACTGAC | 120 |
| GCGCGTTCGC CCACAGACGG TNACGNAGTT CGCTGCCCCG TTCGACCATC TCCAGTACTT | 180 |
| TNATGGACGC GGCAACAATG GCCGGTGCCA GCNAAGTTGG AGAACAGGTA CGGACGAGAA | 240 |
| CGCTGGCGCA CACTNCAACC ACTTCTTTGC GCGCCGCGGT ATTAACCACC AGAAGCCCCG | 300 |
| CCCAGCGCTT TTACCAAGCG TACCGGTGGN TAATATTGCA CCCGGCCCAT CACATTCGCA | 360 |
| GTATTTTCATG GGGGAACCAC GGACCATTTT TNAACGGACA AAACCGACCG GNTGGGGAGT | 420 |
| TCGTNTTACC TTCANCAGGG NA | 442 |

(2) INFORMATION FOR SEQ ID NO:634:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

| | |
|---|-----|
| TGCCGCTCTT TATGTGGGCC GCGCGTCACT GTCAGCCCCC AGGTAATCAG CGGCGCGGCC | 60 |
| ATCTTCCGGC CAGCAGGTCA TAATGGGAAT GCNATTGANA TCGNCGTCAT CGCCAGANAC | 120 |

| | |
|---|-----|
| GATTTTTTGT TGGCAGGGCG CACCACGCAG CCGCTTTGTC GGCATGTTCA ATACTTGCTT | 180 |
| AAACTGCGGC AGTTTATCAA ACAGGTCGCG GAAACCTTTT GCGGCTCCG GCTCTTTCAG | 240 |
| AAACGCCAAT AATTACCAA CTTACGCAG CGCCGNAAAC ATCTTCCTGC CCCATGCCCCA | 300 |
| TCGCCACGCG CTTTGGCGTT ACCGAACAGG TTGCACAGCA CCGGCATTGN GTAGCNTTNA | 360 |
| GGGTTTTTCG GAACANCAGC GGCAGGCCCA CCGGGAAGGC AAATGCGGTT CAGCAATTTT | 420 |
| CATGGTTTTN CAGATGGGGG ATNCCACCGG GAGNGTNGTA AGTTTTTAGG | 470 |

(2) INFORMATION FOR SEQ ID NO:635:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

| | |
|---|-----|
| GGCAGGAGCG CTCCTGGGG GACCGAATCC GGGATCTTGC TCAGCTCAA AATCTCTATC | 60 |
| CCAAGAAGCC CAAGGATGAG GCTTTCGGA GCCACTACAA GCCTGAACAG ATGGGTAAGG | 120 |
| ATGGCAGGGG TTATGTCCCA GCTACCATCA AGATGACCGT GGAAAGGGAC CAACCACTTC | 180 |
| CTACCCCA GCTCCAGATG CCTACCATGG TGCCTTCTTA TGACCTTGA ATGGCCCCTG | 240 |
| NATTCCTCCA TGAAGCCCCC TTTNNNTNT | 270 |

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

| | |
|---|-----|
| GGCANGAGCT GGACCCCCCA ATGCGGGCAA GAGCAGCCTA GTGAACCTGC TCAGTCGGAA | 60 |
| GCCTGTGTCC ATCGTGTC CCGAGCCAGG GACCACCCGT GAACGTGCTG GAGACCCAG | 120 |
| TCGACCTGGN CCGGATTTCC TGTGNCTGCT GAGCGACACG GCTGGGTTGC GGGNAGGGCG | 180 |
| TGGGGCCCN GGAGCAGGAG GCGGTGCGN GCGCCCGTGA AGTAGGCTTA GAGCAGGCTG | 240 |
| ACCTCATTCT GGCCATGNTG GGATGCTTTC TGAACCTGGC CTCTCCCTCC ANTTGGCAAN | 300 |
| TTCTTGGGTC CACCGTNGTT AGNCTCT | 327 |

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

```
GGCAGAGCTG AGCCTTGGAG ATTATCATCA AGCCAGACCC CTCAGCAGCA AGTGGAGCTG      60
TTTGA CTTGG AGAATAACNN AGAGTACGTN TCCAGCGGAG GGGGCTTTGG ACCGGTTGCT      120
GATGACGGCT ATGGTGTGTC GTACATCCTT GTGGGAGGAG AACCTCATCA ATTTCCACAT      180
TTCTTCCAAG TTCTTCTTGC CCTGAGACGG ATTCTCATCG CTTTGGGAAG GCACCTGAAA      240
NNAAGCAATG ACTGACATCA TCACTTTGTT TGGNTCTTCA GTTCTNAATT TCCAAAAGTA      300
ATTCCACTGG AGCTGCTGGG GAAGGTAAAA CGAGCTCTTT NTGATGCAAA CCAATGNAAA      360
ATTAGGCATT AATCCNGGNC CTNAGTTCGG GA                                     392
```

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

```
ACTTTGCCGG AACATCCTGC TGGGGCTTGA TCCACGTCGC AGTTGCTTCT CGCATGACTG      60
CNTCGGTGGG CAGTTTGCAA AACTTTGCCA GCTTCATCTG CGCCTCTTTT GCGCCGATCA      120
TTACTGGTTT TATTGTTGAT ACCACCCACT CATTCCGTCT GGGACTA                                     167
```

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

```
AGAGCNGAGC AGTCAAGATG TGTGAACTCC ACCGAAGACC AGACCGNAGA GTTCAAGGAG      60
GCCTTCCAGC TNTNNTAACC GAACAGGTGT ATGGCAAGAC CCTGTTACAG NCA                                     113
```

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

| | |
|--|-----|
| AGATAGCAGC CTTGTAAC TT ATGANCTACA TTNTCGGCCT GAGCAGGACA AGTTCTCTCA | 60 |
| AGCTGCCAAA GTCCGAGAAC TTGAAAAGCG CCTGANAGAG CTGGAGACAC TGTNACGTTG | 120 |
| TGAATCAGGA ATGCTCAGAA ATCCCCTTTT TGNCAGGTNT ACAGGGAAGC CTGTNCTCAT | 180 |
| GGAGACTGTA GGAGCTGTTG CAAAGCAAAA GGTGGAGCGC CCTAGAACCT TGCAGTTTTG | 240 |
| GGATCAAGTG GGAGGCTCGG CTTACAGAGT GTNCCTGGGG AAAGGTTGAA CGAGATTGTC | 300 |
| CCAAGCTTAA AAGCCTCTNT TAGGAAGTTG CAGTTTCCNC AAAGCAAAGT TGCNCCNGTT | 360 |
| TTTTGGNAAC TTTT | 374 |

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

| | |
|---|-----|
| GGCAGAGGAT GACATTNGNN TNANCTACAA GATTGGAGAG ANGTGGGACC ATCAGGTGCN | 60 |
| AANTGGNCAT ATGATANGNT GNACATGTTT TGGGAACGGA AAAGGCGAAT TCAAGTNTGA | 120 |
| ACCCTTCATG GAGGTCAACG TGTTATGNAT GTTGGGTAAG ACATACCACN TAGGCNGTAA | 180 |
| CAGTGGNCAG AAGGGA | 196 |

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

| | |
|---|-----|
| GGCAGAGCTG AGATCAAGGG CCACAGGGGA CCTACGTGGG CGCNATGCCG GGAAAGATCA | 60 |
| TCCAGTGTTT AAAGAAGACC AAGACGGAGA ACCCCCTGAA TCCTNATCGA CGAGGTGGAA | 120 |

| | |
|--|-----|
| CAANATCGGC CGAGGCTACC AGGGGGACCG TCGCTCGGNC ACTGCTGGAG CTGCTGGTAC | 180 |
| CCAGAGCAGA ATGCCAACTT TCCTGGNACC ACTACCTGGN ACGTGNCCCCG TGGGANTTGT | 240 |
| TCCAAGGTAG CTGTTTNATC TGGCACGGGC CAANGTTCAC GGGACACTTA TTCGCCNAGC | 300 |
| CGTTGGAAGG ACCGTTATGG NGGTTGATTC AACGTGTCGG GGTANTTGG NCCCAGG | 357 |

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

| | |
|---|-----|
| GGCACGAGGT GGCAGGNNNT GTGTGTGCTG AGGCGGCTGA GCGGCGGACA TGCACACTAC | 60 |
| AGTGCGTGGC GATGGAACAG TAACCGGGTT TGTNAGAGGG CTCTGCAGTA TAAACTAGGA | 120 |
| GACAAGATCC ATGGATTAC CGTAAACCAG GTGACATCTG TTCCCGAGCT GTTCCTGACT | 180 |
| GCAGTGGAGC TCACCCATGA TGACACAGGA GCNAGGTTTT TACACCTGGC CAGNGAAGAC | 240 |
| ACGAATAATC TGTTACGCGT GCAGTTTCGT ACCACTTCCA TNGACAGTNG TGGTTGTTC | 300 |
| TCAAAATTCT TGAGGCATAC CGTNCTTTNT GGGTTTTTCTG AAATATTCGT GNAGAGACC | 359 |

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

| | |
|---|-----|
| GGGGCAAAAA TGCCGAAGAT GCGGTGCATA ACGCATCGT GCTGGAAGAG GTCGCTTATA | 60 |
| TGGGGATATT CTGCCGTCAG TTAGCGCCGC AGTTACCGGC ATATGCAGCA AACGCTGCTG | 120 |
| GATAAACACT ATCTGCGTAA NATGGNCGCG TNGGCATATT ACGGGCAGTA ATGNCTGTAT | 180 |
| AAAACCACAG CCAATNCAAA CGNAACCAGG CTATACTTCA AGCCTGGTTT TTTGNTGGNT | 240 |
| TTTCCAGCGN GGCGCAGGTC AGGTTTTATC TTAACCCGNA CACTGGCGGG GACACCCCG | 299 |

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

| | |
|---|-----|
| CGGCCGCGCT GCTGGACAAG CTGTATGCTC TCGGCTTGGT GCCCACGCGC GGTTGCTGG | 60 |
| AGCTCTGCAC TTTCGTCACG GCCTCGTCCT TCTGCCGCCG CCGCCTCCCC ACCGTGCTCC | 120 |
| TCAAGCTGCG CATGGCGCAA GCCTTNCAGG CTGCCGTGGC CTTTGTGGAG CAAGGGCAGC | 180 |
| TACGCNTGGG CCCTGACGTG GTTACCGACC CCGNCTTCCT TGTNACGCGC ACATGGNAGG | 240 |
| ACTTTGTNAC TTGGGTGGAC TCGTCCAAGA TCAAGCGGCA GTGCTTAGAG TNACAATGAA | 300 |
| GGAGCGCGAT GATTGNTCT GGAAGCCTAG CGGATTTCCT ATTTGCAATG TTGTNTTTTN | 360 |
| ACAGTGGGAA AATTGAGGCC TGATGTTGGA GATTTTANGA GGGTGTTTTT CTCAAGGGTT | 420 |
| NTNAAACGGT TGTAGTTTTT TAAGAATTG ATTCATCATT GGCANGCCAG NATAGAGCCA | 480 |
| GGG | 483 |

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

| | |
|---|-----|
| TCAGCTGCCC TGGGGGCTGC TTCCNTGGG CACGGGCTCC AGGGATCATN TNTGGGCACT | 60 |
| CCCTTCCTGC CCCAGGNCCT GGNTCTGCCC TTCCTTGGGG GGTGGAGCAG GGTCCAGGTT | 120 |
| TNAACTTGC NACCTCCTGG AGGTCAAGAA GAGCAGAGTC CCCGTCCCTG NT | 172 |

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

| | |
|---|-----|
| GGCACGAGGG GATTACAGGC GTNAGCACCA CACCCGGCTT CATTTAAACC ATTTTAAAGT | 60 |
| GGCATGAAGT ACATTCAAAT TGTNGTGCCA CCATCCATCA CCCAAACCGA AATCCATAAC | 120 |
| CATTAAACCA TAACTCCTCA TTCCTACAGT NTGTTTCTTT TCATTACGGG ATAATATTCC | 180 |

| | |
|--|-----|
| ATTGTNTGGA TGGGCCACAG TTTGTTTATC CACTCACCTA TTGANGGACA NCTTGTTTCT | 240 |
| TCCCACATCT TGCCAATNAT AAATNANGCT GCTATAAATA TTTGTNTGCA GGTTTTTGTG | 300 |
| TGCACATAAG TTTTCANGTC ATTTGGGTAA ACACAAGGGG TGTGATTGCC GGGCCTCTGT | 360 |
| CTGACTTTAT TTCCATCAAC CGCNTCAAGC ACCTGGNGTG NGGGCAGGAG CCANGCCCCAA | 420 |
| CANTTATGTT TGTAAACCTA TTTAATTAAC AGNCCACAAT ACAGNCCAGG CACATGGGTT | 480 |
| CNGCNGNAAA AACTTGGGAC TTTTGGGAGG CCCAGGCG | 518 |

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

| | |
|---|-----|
| GGCAGAGCAA ACTGTGACTC AGTGGATATT TGTATGCCCC CCAAAAACAT TTAAAGCTG | 60 |
| AGCAATTTTT AATAAGATG TATAATAAT TTTGNATTAT TCTCATTGTA GTTAAGTTAC | 120 |
| TGTTAGTTTG GTGCAATACA TTCTTTCCTT CCTCATCCTT TTAAAATTAA ATATATAAGA | 180 |
| NGTATGTTTT GTTTTATTAC ATTAAGTGCT ATTTTTAAAA AATTCATTGT GTGTATATGN | 240 |
| AGNCTAATAC TTGATTTGTT TCTGTATAGC ATGATTAAAG GTAATTGGAA ATTTTGCCAC | 300 |
| CNATTTAGGN CCNTGGGAAA TT | 322 |

(2) INFORMATION FOR SEQ ID NO:649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

| | |
|---|-----|
| AACCGCTTCA CCGCGCGANT GGTACCAGTC AATCAGGCGG TTAGCGACAT CCACCGTACT | 60 |
| GTCACCTTCC GGCACGGCGN AGCGCGCCAC CAGCACAGAA ATCATTTTGT AAATCGACCA | 120 |
| GTAACAGGGC GCGAGGGGGC ATTACAGTNT CCTTAATCAT CCGGCGTAAG TTCGCCGCGC | 180 |
| AGGTTTTGGC TCATGGCCTT GCGAATGGTT TCAGTATCCA GTTCCTGGGC TAAAGCAGGT | 240 |
| AAATGCAGTT TGGTTAGCTT GGGCTTTCTT ACAGTCATAT CTGCACCGGN GAATNACGCT | 300 |
| GGTATGGGGC GAGGGGGTTN ACCGGTTGGG GATAACCANC CATGTTTCAN TTTAACGGGA | 360 |

CATACATTGT GTTCAGGTTN ACCACCACAA TAACCGGGGN TCGCTGGGTT TTTTGTTAAT 420
TTNCTGNCAG GAAAGGTTTT TTTTTTTTGG GNG 453

(2) INFORMATION FOR SEQ ID NO:650:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GGCAGAGGGA GAGGCGCTGA GGTGTGCTGG GTGCACTGGA GCCACCGGGA CCCCTTGAGG 60
ACATCGCCAG GNTCNGTGGC TTNTTCCCGA GCGGGAGAGG TGGAGATGCT TATAGCAGTT 120
ACGCNTTAGG AAGGGGACAA CCAGGNCCCG CCACACGCTT CACACACAAA CCTGCTCACG 180
CAACTGTGAA TGCTTGGCAC GGGGTGGCCA GTNCAGATGG AGCCCAAGGC CCCNTCGGNC 240
TCCTGGGGCA ACTTGGGGTA CACAGGATAC TNGGGGTGCC CGTTCCTTAC TTAAACCCCA 300
GCTAAGGGTT ACAACTGACC CAGTTGGNCT TGGGCCCGGG GCACTTTGGG TTGGTTCNTT 360
TGGGGCCCTT GNACGTTGGG CCCATTGTTG GNAAGGTTN TTCTT 405

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

GTTGGGCATG TNCAGGTGGC ACAGGTNCCA GGNCGAGGGG AGCCCAGCAG CCCCAGAGAG 60
CTGAATTTCC CCTATCTGTT TCAACTGCTG GNAAGNTGAA GGCTACAAAG GTTTCGTGGG 120
NTGTGAAGTA TCAGNCTCGA GGAGACACAG TAGAGGGCTT GATTGGGCTA CGTTCATACT 180
GGGNATAGGC GGGGCCACCC AGAGGCTGGC CAGTGAAGGG CCCGCACACC ACCCACGTGC 240
CTNCAGNCAG NGAAGTGAAC ATNGCCAT 268

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

| | |
|---|-----|
| TCTTTCCTTT NACCTACAAG GGATCTGTTT ACTTCACTTG CACCCATATT CATAGCTTAT | 60 |
| CCCCTTGGTG TGCCACCAGA GCCGTGTACA ACGGCCAGTG GGAAGTACTG CCAGAGTGAA | 120 |
| AGATTACCCA CGCTGTATCT TCCCTTTGNA TCTATCGAGG AAAGGCTTAT NAACAGCTGC | 180 |
| ATCTCCCAGG GNAGCTTCTT AGGCAGTCTG TGGTGCTCAG TCACCTCTGT TTTCGATGGG | 240 |
| GAAACAGCAG TGGGAAATTC TTGTGAAACG GAATGAAGTA TGGGGGGAAA TTCTTCTTCA | 300 |
| GGNAAGGCCC TGGCATCTTN CCCCTCCATN TTACAGGAAA TAATGTGGGT CTNN | 354 |

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

| | |
|---|-----|
| AATGGAAATC GGTCCAGTAA GGCTGTNATC TGGANGGTGC TGCGCAAGTN GGGGCTGCCC | 60 |
| CTGGGAATAC ATCATTNACT NTTTGGGGAC GTGAAGAAGC TCATCACTGA ATGGTTTGTG | 120 |
| AAAGCAGAAA GTNCCTGGGN CTATGNCCNG NNTCCCCANT AGCAATCCCC CTGATTATGA | 180 |
| NGTTCTTCTG GGGCCTGCGC TTCTTACTAT GAGANCCNGC CAAGNTGAAA GTCCTACAAG | 240 |
| TTTTGCCTGC AAG | 253 |

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

| | |
|---|-----|
| CCATAGTCCT GGACAAGCTG GAACGNAGGG NCTTCCTTTT CCTGAGCATG ANGGGGGTGG | 60 |
| GCCAAACGCT GGTNTGGTGT NTGCACAAGG AGTGAACCTT TT | 102 |

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

| | |
|--|-----|
| CCACTGGTGC TGTGCTGTAC GGTGCAAGGA ATGCAGAANT ACTNTGGACG TCCATACTTG | 60 |
| CAAGCCCCCA AGANGGCAGA NTGGCTGGNC CAAACCTGAA NCACNCAGAT ACCTCATTTTC | 120 |
| TTCCTTCCAA TTCANGNNTC TNAACTCNAA AGCACNAGGT CCTTTGTTTG NACANTTTTT | 180 |
| TNCACCCTTC ACCCTGGGGT TGTACNTTT TTTTTTTAAG GGTNTTGGG GGGTTATTCC | 240 |
| TTGGGGGCCC TGGGGTTC | 258 |

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

| | |
|---|-----|
| TTCAAAGTTG CNTCCNATCC TGCCTGCAGA AAACCCAGAC TGCATTCACT GTCCCTCAGT | 60 |
| TAGCCACCAC TTTGNNTCCC AAGGTGGCTG AGCAACANAT TCCCAAGTNT AAGANCCATC | 120 |
| A | 121 |

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

| | |
|---|-----|
| GGNTTTTTTCG CTCGGTTTAG CTAAATCNTC CAGCCCTTTC CGGCNTCGC GGTAATCTTC | 60 |
| CAGCGCTTTA TCCAGAACT TGCATCGGT TTTTCNTTCC ACCAATGGNA AGCAATGCAC | 120 |
| GCAGAGTCGG ACTTGATATC GCCGACAGT GCCATATCCA CCTTGCCTGT GAAGCGCCCCG | 180 |
| ATGCTGGCTG GNTTGAATAT CCAATCTGNA ATGAATTTTG GGCATCGGTC GGGTAGNAAG | 240 |
| GCGCGGTAGG GGAAATTGCC GTTGCCGNAG TTAGCCACTA AACGTNTTCG GCGGGTTTCA | 300 |
| TCATGGGTAT GGGAAACCTG NACGGNG | 327 |

(2) INFORMATION FOR SEQ ID NO:658:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

CTCCTCCTCC TCCCTCCTAC AAGTCCAGTG GCCTTGGNCT TGGAAACTAA AGGANGAAGG 60
TCTGGCCCCC AGGGTGGGGC TCTCCTTTCC CTCCCANCAN CCCC GCGGTN AGCACTGCCC 120
CCTCTGTGAG GTTCGCTAAC TTN 143

(2) INFORMATION FOR SEQ ID NO:659:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

ANCGGCCCTT TGAAGGTGC NTCCCGCAAG ANGAACGGAC GCCACTTAAT CCTCCGTGAA 60
AATTCCAAGA CCAGNAANAA CATCCAGAAA TCCCTGGTTG GNAGCTCCAG GCCCCGGGGC 120
TTCNAGCGGC ACCANCGGTG AACCACGGTN AAGCTCGTGG AACCGGTTTG CAAGTTTGGA 180
AGTGGNG 187

(2) INFORMATION FOR SEQ ID NO:660:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GGCACGAGAA AAAGTAGAGC ACAAATAGTA CAATGGCGAA TATAGACCCA AGCACATCAG 60
TAGTTACATG GAGGANGACT GTNTACTNAA AGANTTAAAT GTAGGCTAGA TTAAAAAAA 120
AAAAAAAAA CCNCG 135

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

| | |
|--|-----|
| AGGCGAAAAG TTTCCACGGC AACTAAAACA CTTAGACGCT GTAGTACAGC TCAAACCTCTA | 60 |
| CCGGATGCGG AGTCATACGC ACGCGGTCAT CTTCTTCGCG ACGCAGAGNA TGTACGCATC | 120 |
| ANTTGCTTCG TCAGTGAAAC ACGCCACCGG CTTTNNAGGA ACTCGCGGTC CAGATCCAGT | 180 |
| TCGTTCACTG CTTCTTCCAG AGAGCCTGCA ACCTGTGGGA TCTCTTTNGC TTCTTCTGGC | 240 |
| GGCAGGTCAT ACAGGTTTTT NTCCATGGTT TCGCCCGGTA TGGGATCTTG TTCTTGAATA | 300 |
| ACCNNCAGGA CCGGGCCNTC AGCCAGGGCA GNCAAAGCAC AGGTTACGGG TTAAGATTGC | 360 |
| CGGGTTCCGG GAAAACGTNA CTTTGNTTAN GACGTGNTTT TCGGNGGAAG NAAACCACCG | 420 |
| GNATTACGGN TTAGANGCGG AACGGTTTAA GNGNCNNNT NAGGCCAGCT TTACCGTGTT | 480 |
| TCTAGCCGGG AC | 492 |

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

| | |
|---|-----|
| ACCACCCCCC GCCCCATACA CACACACACA CATGCATACA CAAAGAAAAG CTAATAAAAA | 60 |
| TTGCATATAG AAATTTTTTT TTTTTTTNGG GGGGGGGTNT CGTTNTNTNA CCCAGGT | 117 |

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

| | |
|---|-----|
| GGCAGAGAAT TAGGTTTAGC ATAGCCTATC TTTCTCCATC CNTTTACTTT NAATCTGTCT | 60 |
| TCATCTTTAT ATTTAGAGTG GGATTTTGT AGACATCATA TAGTAGGGTC TTGTCGTTTG | 120 |
| ATTTGCTCTC GGACAGCATG TGTCTTTTAA ACTGGTGTAT TTAGACCACA GATGTTTAAA | 180 |
| GTAATTATTG ATATAGTTGG ATTAATGTCT ACTGTATTTA TAACTGTTTT CTACTCCATT | 240 |

GTCCCTTGTT CCTTNCCTTT TTCGGNCTTT GNACTTTGTG CTCTGCCTTC TCCATTNGNA 300
ATTG 304

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

NTTCCATTCC ATTNGATTCC ATTCCATTCA AATNAATTCC ATTCCATTCA TCTCCATTCC 60
ATTCCATTCC ATTCCATTCC ATTCCATTCC ATCCAATTAC ACTNGCTTTG AATCCATTCA 120
ATTCCATTCC ATTCCATTCC TTTTCNGTTCC TTTGCATTCC ATTCCATTCA ATTCCATTCC 180
ACTGGGGTNG TTTCAATTCC ATTCTATTCC ATNCCATTCA ATTGNA 226

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GGCAGAGTTT TCCAGACGCA GGTAAGAGCC CATGAAAGGC TGCCCTCTTC TCCCCTGCCA 60
GGAGGGCACC TGGGCAGGCT AGGAGCAGCC TGGGCCAAGG GCACCCCAGG GACCAGCCCC 120
AAGAGGCACT GCTGCTGACT CCCTGTTCTT GTTTTTTTTT TGTGTTGTTT TTTGAGANAG 180
GGTNTCGNAN TGTNCCCCCA GGTTAGAGTG 210

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GGCANAGCAA ACTTTTTCCT GTTGAGTGCC CTAAGACAGT GGAAACTTC TGTTTTTACA 60
NCAGAAATGG TTATTATAAT GGGCATACAT NTCACCGTAT AATTAAGGC TTTATGATTC 120

| | |
|---|-----|
| AAACTGGAGA TCCAACAGGT ACTGTNATGG GAAGGAGAAA GCATATGGGG AGGAGAATTT | 180 |
| GAAAGATGAA TTTCCATTNC AACATTACGN ACATGACAGG CCGTACACAC TTCAGNCATG | 240 |
| GGCTNAACGC GGGGTTCAAA TACTAATGGG ATCCCAGTTT TTCCATNAAC GGTNGTTACC | 300 |
| CAACGGCCTT TGGGCTTTGG ATTAATTNAG GCCTTTACCA GTTATTTTTG GGGACCGGAG | 360 |
| TTGGACTTAA AAGGGGAATT TGGGGGGNNN N | 391 |

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

| | |
|---|-----|
| GGCANAGTGG CCATTTTCGT TGGTGGTGTT CANTTGCNGC GGTNCTGGT CAGTAACAGC | 60 |
| CAAGANGCTG CGGGAANCTG CTGGNTCTTC GTCAGATTGG GCAGAGGACG ATAAGGACTT | 120 |
| GCTTCCCGCA GCATTTTAAA AATAAAGTTC CGGTAGGAAG CAAAACTGT TCCAGGAGGA | 180 |
| TGATGAAATC CACTGTTATC TAAAGGGTGG GGTAGCTAA TGNCCCTCTG TTATAGNGCC | 240 |
| ACCANGNTTT TTACAAGTTG GGTGTAACA TCNTTA | 276 |

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

| | |
|---|-----|
| GGCANAGTCA TATTTCTACA GTATGCCAGT ACTGAGGTTG ATGGAGAGCG TTACATGACC | 60 |
| CCAGAAGACT TTNTTCAGCG CTATCTTGGA CTGTATAATG ATCCAAATAG TAACCCAAAG | 120 |
| ATCGTGNCAG CTCTTGGCAG GGAGTAGCTG ATCAAACCAA GGATGGGTGA AGTATCTTCA | 180 |
| TGTCATTTNC TGNAAACTN AATGTTCTCTG GGAATATATT GTTGAAAAAT TTNAAAAACC | 240 |
| AGCTGGGNCA CAGTGGGCTG CATGCCTGTN AATCCCAGCG CTTTGGGAAG GCTTGAGGCG | 300 |
| GGCGGTNTCA CCTGGTGGGT CGGGGNGTTT TTNAGA | 336 |

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```
GGCACGAGAG AAACCTCTATC TAGTTAAAAA GGCGANGAAG AAAGATAATC ATGCTCCTGT      60
TCCCATAAAG AAAGGGCAAG GAGTTGGGAA GGAGNAAGGG ACCCTCCTGG NTCCTGCAGC      120
CTGAATCTCC ACTTGTGCCC TCTGTCTTCC CCACTAGACT CT                          162
```

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```
GGCAGAGNCT CTGAAAAAAC TCGCCAAGAA AAAAGTAAGA AATTGACTTT ACAGAAGTAA      60
AACCACACCG GGCTAAGTAC AAATACCTTC TAGTACTAGT AGACACCTTC TCCAGATGGA      120
CTAAGGCATT TGCTACTGAA AACGAAACTA CCAACACAGT AGTTAAGTTT TTACGCAATG      180
AAATCAACCC CCAATATACG CTGCCTGCTG CTATTAAAGT CTGATNAATA GAGGCAGCCT      240
TTACCTCGNC TATGAGCTCC AGTTCAGTCC AGTTAAGGCG TTNAAACATT TCAATAGGAG      300
GCTCCATTGT GGCCTATNCA ACCCCAGAGG TTCCAGGTCA AGTTGGAACG CATGGAACCA      360
CACCTNAAA AAAAATTTCGN GGGGGGGNCC GNTACCCATT T                          401
```

(2) INFORMATION FOR SEQ ID NO:671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
GGACAGTGCC ATTATCCACA CCAGCATGGG AGACATTCAC ACCAAACTTT TTCCTGTTGA      60
GTGCCCTAAG ACAGTGGAAG ACTTCTGTNT TCACAGCAGA AATGGTTATT ATAATGGGCA      120
TACATTTTAC CGTATAATTA AGGGCTTTAT GATTGAGACT GGAGATCCAA CAGGTACTGG      180
TNATGGGAGG AGAAAGCATA TGGGGAGGAG AATTGNAGA TGAATTCAT TCAACATTAC      240
```

| | |
|--|-----|
| GACATGACAG GCCGTACACA CTCAGCATGG CTAACGCGGG NTCAANTACT AATGGATCCC | 300 |
| ATTTTTCATA ACGGTAGTAC CAACGCCTTG GCTTGNTAAT NAGGCTNACA GTNTTTGGAC | 360 |
| GAGTGANTAA AGGATGGTAG TTGTTACANG GTTNTCCAAG TCAAGTTCAT TCCCCAAAACN | 420 |
| GTTAGCCNTT TGAGGGTGTT CAGCTNCTTA AATTTTACTG TTCAGTTAAA TTAGGTTTNT | 480 |
| TTTNATGT | 488 |

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

| | |
|---|-----|
| GGCACGAGAA AATATCAACT CCCAAGTTG ATCTGTAGAT TTAACAGAGT TTCAGACAAA | 60 |
| ATCACAGCAT AATTGTTTAT AGATATAAAC AGGCTGATTC TAAGATGGAT AAGGAAATGC | 120 |
| AAAGGAACTA GAATAGGCAA AACAATTTTA AAAAATAAAG TTGAAGGAAT CACTATCAAA | 180 |
| TTTTATGACA GTATAAACT ACAGTAATAA AGNTAGTATG TTAATAGGAA CTGTGTAAAC | 240 |
| ACCAAAAGCA GTGGTACAGA ATAGGCAAGT CTAGTAATAG ACCCATATAC ATNTGGCCTT | 300 |
| TTGACAAGGT GCACNGGGAA TTTTATGGGG AAGAACCCTT AATAATNAGT NTCGGACCAT | 360 |
| TGACCTNCCT TTAAANACCA AAAACTCGGG GGGGGCCC | 398 |

(2) INFORMATION FOR SEQ ID NO:673:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

| | |
|---|-----|
| GGCAGAGNCA GAGGCCAGGC ACGGTGGCTT ATGCCTGTGA ATCCCAGCAC TTTGGGAGGC | 60 |
| TGAGGCAGGC GGATCATGAG GTCAGGAGAT CGAGACCATC CTGGCTAACA CAGTGAAACC | 120 |
| CCATCTCTAC TAAAAATACA AAAAATTAGC CGGGTGTGGT GGCGGGTGCC TGTAGTCCCA | 180 |
| GCTACTCGGG AGCCTGAGGC AGGAGAATGG TGTGAACCTG GGAGGCGGAG TTGCAGTNAG | 240 |
| CCGAGATCAG GCCCCTGCAC TCCAGCCTNG GAGACAGAGG GAGATTCCAT CTCAAAAAAA | 300 |
| AAAAAAAAAA AAAAAAAAAAN AAAAAAATT TNTNGGGGGG GCCCCCNTA | 349 |

(2) INFORMATION FOR SEQ ID NO:674:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

| | |
|---|-----|
| GGCAGAGCTT TCCATTCCAT TCCATTTCAT TCCAGTTGAT TCCATTGGAT TCCATTCCGA | 60 |
| TCCATTCCAT TTCGTTCCAT TCCATTCCAT TCTATTCCAT TCCATTCCAT TCCACTGGGG | 120 |
| TTGATTCCAC TTCATCCCAT TGCATTACAT TCCATTTCAT TCCACTNNNG GTTAATTANN | 180 |
| ATTCCGTTCC ATTCCATTG | 199 |

(2) INFORMATION FOR SEQ ID NO:675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

| | |
|---|-----|
| GGGAGATCGT TGCCGGAATA TCCTCCAACG ACGCTCGACG GCGGGGTTTG TTAAACAGGC | 60 |
| CTTGTGCGGC AAGGTGAAGA TTACGCGCAT CAGCAAGGGN GAGGTGCGGC ACGACATTCA | 120 |
| TGACTCCATC AATCGAACGC TGCCGCGGCG TAACTAGTTG CCAGAAGCCA GCAAGGTTAG | 180 |
| TTGCGTAAGA GTTTCGCTGG TTCATCACCT GAAAGCTGTG CGTCTACAGG CAAATACCAC | 240 |
| CAATTTTNTT CTGCAAAGNC CCGGCATTTN ACCGCATCTT TTTCAGTCCA TTACCAGCGT | 300 |
| TTGCCCCGGCG CTTTACCAAC GGCACTTGAC ATCCGNATGG TTNCAAAGAT TGATGGTTTCG | 360 |
| GCCCAGGGGT TACACNTTTT TNNCGGTTGT ACGGCCACAC ATNTTTCAGC GTGGGCAAAA | 420 |
| AAGCGCGGCG GATGCCCCAT TNCCCCGCCN TGGCATTACA TGTTCAGTT GAGCAACGTC | 480 |
| ACAANGGTAC CGTACGTAAT | 500 |

(2) INFORMATION FOR SEQ ID NO:676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

| | |
|---|-----|
| AANTAATGCG CCGTCAAACA TACTGCTCAT AATGCGGGAG GTGTTGTNAT CAAGCACGAN | 60 |
| ACGCTGGCGA ACAGGAAGGT AAACATGATT AATCAATTGA TCTACTGGGT ACTCTCGACC | 120 |
| CAGTGAAATA ATTCTCGCGC GTAGTTTGGC AGGATTAGCC ATGCGAAGAA TTGACATCAT | 180 |
| CTCTTCTTGC AGGCGGCTCC AGTCATCTTC CGTATCCTGG CTGGTGGTTT CCAGTAATGC | 240 |
| TTTAACTTTG CCTACAGGN CGCCATTACT TATCCAACGC TTGATCTCTT CGATGCGTTG | 300 |
| TATGTCTTCT TCATCAAAGA GTNGGTGTTT CGCCTTAATN GNGTNGGGGT TTAAACAAA | 360 |
| CCGTGGGNGG T | 371 |

(2) INFORMATION FOR SEQ ID NO:677:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

| | |
|---|-----|
| GGCAGAGCCA GTTTTAAAG TATCTTAAA ATTTTNAATA AGACTTTTTC CAAATATAT | 60 |
| TTAAGGATCA AAGTACTTCT TGATGAATCA CTTTTTATCG TATTGATGCC TTTGAATCA | 120 |
| TCTTAGTTTG TCTGCATGTN GTTATTACCA ATTCGTGAGG AATGGCCATT TCAAAGTTTA | 180 |
| CCATAAATGA NGTAAACGT CTTCAAGTCA CACTGCTTGG CTTTGAATTC CTTACTCTAC | 240 |
| TCTTTCTTAC TGTNGTGAAC ATATGGCAAG TTAACCTTAG CTTCTGCACT TCCTGTTTGT | 300 |
| GGTTTTCCCC TTTATTGGGT GGTNATAAAC AGTCTCTGTC NTCCTAGGGA TCTNCCNGG | 360 |
| TTGTTGTGGG NGTT | 374 |

(2) INFORMATION FOR SEQ ID NO:678:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

| | |
|--|-----|
| GGCANAGGNA CAGTGCCATT ATCCACACCA GCATGGGNGA CATTACACCC AAACCTTTTTC | 60 |
| CTGTTGAGTG CCCTANGACA GTGGAAACT TCTGTTTTCA CAGCAGAAAT GGTTATTATA | 120 |
| ATGGGNCATA CATTTACCG TATAATTGAA GGGCTTTATG GTTCAGACTG GGAGATCCAA | 180 |

| | |
|---|-----|
| CAGGTACTGT TATGGGGAGG AGAAAGCATA TGGGGGAGGA GGATTTGNNG GATGAATTC | 240 |
| CATTCAACAT TACGGACATG ACAGGCCGTA CACACTCAGC ATGGGTTAAC GCGGGGATCA | 300 |
| AATACTNATT GGGTCCCCAN TTTTTCATA ACGGGTNGTA CCCACGNCT TTGGGTTTGN | 360 |
| T | 361 |

(2) INFORMATION FOR SEQ ID NO:679:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

| | |
|---|-----|
| CTCAGTTTGG TATATTCTCC TGTNAATGCT TGCAATTNCA TTATCAAATT TTTGTAGTGT | 60 |
| GTTTTTAAGN TCTATCAGGT CAGTNACATT CTTTCCTATA CTGGCTATTT NGTGTGTAA | 120 |
| GTNCCTATAT CATTTTATTG TNAATTCTAA GCTTNCTTGG ATTGAGCCTT CAATGTTCTC | 180 |
| CTGCATCTNA ATGGTCTNNA TTCCCTACCC ATATTCTTAA TTCTGACTCC TGTGNATTC | 240 |
| CAGCTATCTG CAGCCTAGTT AAGGAACCTT TGGCCTGGTT NAGGAACCCT TGNTAGNGGA | 300 |
| ATTACTGTGA CAGTTTAGAG GAAGGAATNC ANTCGGGCTT TTGGAGTTGT CCAGGGTTCT | 360 |
| TGCGG | 365 |

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

| | |
|---|-----|
| GGCACAGGGA ATAGCTCTGG CTAAGCGGTG GCCAAGGATG TGGGCAGAAG ACAACCCTCC | 60 |
| AGGGTNGCNA ATCAACCAGG CCCCCATACT CATAGAATTT AAGCCTGGGG CCCAGCCAGT | 120 |
| NCAGGCAAAA TCAGTACCCG GTCCCCAGNG AAAGTTNTTG AAGGTATCCA GGTCCATCTC | 180 |
| AAGTGCCCTG AGGGCCTTTG GAATTAATAG TTCCTTGTCN AGTTTCCATG GAACACTCCC | 240 |
| CTCCTGCCTG TTCCCCAAGC CTGGGNNCCA AGGACTACAG GCCGGTAACA GGTTTTGCGC | 300 |
| TTGTTTCCAT CCAGGCTACA GTGAACCTTA ACATCCAGGA GTGACCTAAC CGGTNANACA | 360 |
| TTGTNGGGGT TNGNTG | 376 |

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

| | |
|--|-----|
| GGCANAGGGA TCTTTGGAAG TTTGATTAGA AAATGCCTTG AGGTAGTCTT CTTTGGGGTTA | 60 |
| AACCTGCTTG ATGTTCTATA AGCTTCTTGT ACTTGAAATA TTGATAACTT TCCCTAGGTT | 120 |
| TGGGANCACTT CTGTNATTAT CCCTTTGGGA TAAACTTTCT ACGGCTATCT TCTTCTCTAT | 180 |
| CTCCTCTGTA AGGCCAANAA CTCTNAGTTT TGCCCTTTTA AGGCTATTTC CTGTATCTTG | 240 |
| TAGGTATGTT TCATTCCCTT TTAAATCTTN TTNCCTTTNG TATCCCCTGG ACTATACATT | 300 |
| NNCAAGTAGC CGTCTTCAGA CTCACTAATT CTTTCCTCCG GTTTGGAACC AGTTC | 355 |

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

| | |
|--|-----|
| GGCANAGTGT AAGCTCAGAG AGGAGTGAAG CTCGCCGGA ACTTCGGGAA TGTAATGGTT | 60 |
| TAGTTAATGC CCTCATTTTN ATTGTTTCAGG CTGAGAATTG GGCAGAAGGA TTCAAACAGC | 120 |
| AAGCTTGTA AGAACTGTNT TTGCCTTCTN CGGAACTTAT CATATCAAGT TCACCGGGAG | 180 |
| ATCCCACAGG CAGAGCGTTA CCAAGAGGCA GCTCCCCAAT GTTGCCAACA ATACTGGGCC | 240 |
| ACATGCTGCC AGTTGCTTTG GGGCCAAGAA GGGCAAGGGA AAAAACCTAT AGAGGNTCCA | 300 |
| GCAAACGATT ACATGGGTTT TCCCTTAAAA GNACGGGTTC CCATTNGGGG GGGGGCCCCG | 360 |
| TTANCCCAT TGGNCCTTTA GT | 382 |

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

| | |
|--|-----|
| GGCANANAAG TAGCTGTAAC TACACTCCCC ANATGTNAGT AATTACTGCA GTGGTTTTTAA | 60 |
| CACAGGGCCA CACATCCTTG GCTCTCCTCT CCCAGGAGG TGAAGCTTCC TTTTCTCTTT | 120 |
| GCCATGTGNG TCTNCAGCTA GTAAAGCAAA AGCTATACCT TGAACAGTGG GAGTCCAGGC | 180 |
| AGACACTTCC TGCCCCAGTG AACCAGGGTT GTCCCCGGGC AAGCCATGGG CCATCAGGNN | 240 |
| ACCCATGTNT TTCAGCATGG ACTCCGGGAT GACAGGATGA GNAACCTCAT TCTGTGGGGT | 300 |
| TTTTTTCCNA AAACCCATCA NCCCCAGTTT TTAANCTGNG GAAATTTTCG GGGCAAACCC | 360 |
| AACCTG | 366 |

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

| | |
|--|-----|
| GGCAGAGCGG CANGAGTTCT CAGGAGCCAC TCATCTGCTG GCAGAGGTAG CAGAAGAATG | 60 |
| CCCTTAGTGT AAGTCCTCTA CAACCATAACA CCAAATGTGC TCCCTGCATT TCAAATTCCA | 120 |
| TTGTAGAAAG TCTCTGNATA ATCTCACTTA TACTATGAGC CATTCCTCAG TATCTGTGCC | 180 |
| TCTTCCTGTT AGTGTTCTAC AATTCCTTTC TCCTTAATTT TTCTCCGCTT TACAAAATGT | 240 |
| CACACAGAGA AGTGCATAAT ACTTAANGCA AGCTTTTGAA AAATAATGCT CCATNAAATA | 300 |
| GCTTTGGTTC TGGTNCATGA TNATTGCGTN TTTATGAAAC ATTTTAAGGT GCATT | 355 |

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

| | |
|---|-----|
| GGCAGAAAGC AGAGGCAGGG NACGGNTCTN AAACCTCCAG TNTGGAGGGC CCTGGGAAAN | 60 |
| TGGCCTCAAA TGTTTCCTTG TNCTCANTGG ATAGGCCTGG TCCGCCATCT GCAGTCCTCC | 120 |
| TCCCAGCCCA AGCCTGGTCA TCTCCAAGCC TAAGGACACA CAGCACAAGG NGCACTTNTN | 180 |
| CCGGTTGGTC AGCTCAGGTT GCCTCATGCT NCAGAGACCT CGCAGGGGAA TGGCTTAAAG | 240 |

GAGAGAGTNA ACAGGTTTGT TAGAATTGGT ACCAGGNCCA NGTTTTNTN TTCTTCCCCC 300
AGCTATAAAA CA 312

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GGCAGAGGTG CAGAAANTA ANTNTCCAAG NAAGTNTGCC AACGGAGTCT TTCTTACGGN 60
CAAAGCTTTT TAGCCCATT CNTCACTGTG GTCTTGTCTT GGTACAAAG TAAAGGCACA 120
ATGGGCCCCC TGGCCTTCCT GTTGNAAAT CCCCTTCCCA GGCTGTCTAA TCATNGTAGA 180
TCTTTTCCNN GAGGAAGCAT ATCCTNTTGG TCTTGT 216

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

CTGCAGTTAT CCCAGGGCTT AAAATTAAAT TAAATTAAAA ACAAAGACCC AAATCAAAAC 60
AAAATTAAAA AAAAGCCAAC CAACCAAATA AACAAAGAAA AAGNACTGCA GTTAANCCAA 120
TCAGGTTTCA CTAGTAGGGA AAAGGAAAN TTATTAAAGA TATTGGGTCT TTTTATTTCC 180
TTGCGGGATT AAATTAACCT CCCCTAGGGC TGTGCCAAGT CCTGGANCTG AACATATTAG 240
GNGGTTTTTN TTNAACTCC AGNGNGGTGT AATTATNTTT CCCCTTAGTG TGATTGGTGG 300
ATTTTAAGGG TTTCCNTCTG NCCGGGTTTT AACCCACCAC CTGGGGGGAC NTGGNGGGGC 360
CTTTTTTTGN GGGGGGT 377

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

| | |
|---|-----|
| GGCACGAGGA AAATNATGAT TCCTGTCCCA ATGCACAATC TCAGGAGTGG TTATTGCCTT | 60 |
| AAAGACTTAA TCAGTATCGT TCATGATATC CTTTTTTTTT TTTTTTTTTT TTNNNNNGN | 118 |

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

| | |
|---|-----|
| GGCAGAGCNG AGAACCACAA GGCGAGATGT CTGCTCATGC CTTCCCTGTG CAGACGTGCG | 60 |
| GGGAGGAAGA TCAGAAGAAA ACCCCACAAG TTCCTATCAA TTTCACAGAA CTTTCCAAGT | 120 |
| GCTCTTAGAG TTGAAAGATA ATGTCTGGGG AAAGAGNAAG TCTAAATCTG NATGAAAGGA | 180 |
| CAAAGGTGGA TAAAGTAGGC TGTGGGGGGA AAATGAAAGG ATGATGGACC AGCTTAAGGG | 240 |
| AGGCAAGGAG AAGGCCCTA AATGCCCCC CAAAGACCAC TGCCTGTTCT GTTCANGATT | 300 |
| CCCCAGCATC NAATTCCCTT AGNCCNTNGG GG | 332 |

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

| | |
|--|-----|
| GGCACGAGNA TTACAGCGGC ATAGAGACAT ATTGCAGGAT TATACACATG ANTTCCATAA | 60 |
| AACCAAAGCA AACTTTATGG CAATACGGGA AAGGGAGAAT CTTATGGGAT CAGTACGAAA | 120 |
| AGATATTGAG TCATATAAAA GTGGGTCTGG AGTAAACAAC AGAAGANCTG AGCTATTTTTT | 180 |
| GAAAGANCAT GACCACCTNC GAAACTCAGA TCGTCTGATT AGAAGAGACA ATAAGCATTG | 240 |
| CTATGGCAAC AAAAGAAAAT ATGGACTTCA CAGAGAGGAA TGTTGAAGTC AATTTACAG | 300 |
| CAAANTGGAA CACTTTGGGC CATTCGTTTT NCCTGCTGTA AAACCGTNCG GNTCCAGAGG | 360 |
| GTCAACCTGA GGAAGNGGCG GGACTCGTTC CTTCTAGGGG GTGTTATTNG GGTCTGTTAC | 420 |
| CTTCNGTTGC TGTTGTATG CGTTCCNTTG NTGGGGCTC TTCCGGGACT NTGACAGNCA | 480 |
| CCGTTTTTCA CACCTGGTTT G | 501 |

(2) INFORMATION FOR SEQ ID NO:691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```
GGCAGAGGTC ATATCCAATN AATGTCCCCT GGTAATTTT GAAAGTNATT TAATGTTTTTC      60
AGTTGATCCC TACATATGGT TACTTTCTGT GGCACAATGA TAGTGTTCATT TACTGAAGTC      120
TCCAAGTAGG AGTAAAGGAG TAGCAGTCTG AATTTTGTCA GGAGCTATNA ATTAAACCAG      180
CATGAGAAAT CAANTTTTGC AAGT                                             204
```

(2) INFORMATION FOR SEQ ID NO:692:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```
GGCAGAAAGT CATTCTATAG TAACATCATC CCAGACTGCC TTCTGTATTC CCCTGTGTAC      60
AGTCTCCTTC TGTTTCTAGG TTTAGAAGTT CAGAGGTGAC TGTTTTTTTC CATTTCACACA      120
GCCAAATGGG GGAAGAGGTG AGGCTAGGGG AGTGCTGTGC TGATTCTCCA GCCATGGTNA      180
GACAGGTCAC CCAGGNAGCC TCGAGGAAAG CCCTGGAGGG GAATCACATG TGTACTTTTT      240
NNATGGAAGC TTTTGTGAAA GCACATCTGT GATTACACTT AGTTTATTGG AACTAATGTC      300
CCAGGAGTAG ACATGGATTG GTGGGCCAAG TTATTTNGGG GACACCTAAA CNGNTCATGG      360
ACCCGANNGA CTTTTTCAAA CCTTTAT                                             387
```

(2) INFORMATION FOR SEQ ID NO:693:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```
GGCANAGGGA AACTGTGCC AGTTTCCAGG AGGAAGTCAA TTTTCATGGCC CTCAATGGTT      60
```

| | |
|---|-----|
| AAATATACTT GGGGCTCAGT GAAGGGTGAT GACATGAGTT GGTGCTTGCC CTGGGCACCC | 120 |
| TCAGTCCTGT TGTGAGTCA TCTGGTTGGG GGCTTCTGGC CCAGAGGAAC CTTTGTCTC | 180 |
| TGGGGCAGTG CACCTTCCAG TGATTGTCTC TGCATAGCGG TTAATGGGGT GAGGGGGCAA | 240 |
| TTTTTCTTT GTTTGGACAA NNCNTTTTTA AGGTGTTTNT TGNAACCAC ACTTGTTAAC | 300 |
| AAAGCTTACC CGGG | 314 |

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

| | |
|---|-----|
| AGTCGGTAAA GTAGAGCGGC GACACGAACT TCTNCANCCG CTCCANNGTG GTACGCCAGT | 60 |
| CCTTCAAGGC CGGCGCACNC ATACGTGCGG GNNTCTCGCT CCTCTTTCCG NNAAGGCCCC | 120 |
| TTGCGACTAC CGTTCCGCTC CACGGNCAGG AAACCAAAGG TTCCGGCGTC CAGAGGGCGT | 180 |
| CTNCCAGTCC CGGGNCANCT TTTCTTGGGA ACACCGNCGG CTGTTGGTAA GCC | 233 |

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

| | |
|--|-----|
| TGAGNTGTTT ATGGAGTTTT TAATCAGTAT GTCTNAAACC ATTAAATNTA NTNNGCATGA | 60 |
| TCATANAACCT GTGTTTCTAA AANCACTAAA TNAACAACGC CTGGGAGGGG NNATTTTGTG | 120 |
| ATGATNGCTA TTGTGGTTGA GGATGTGANA ATTCAGAGCA CNCAGNTGTG TTCTTGCCTG | 180 |
| CCTGCAGACC TACTTTGAAA AAGCTTTTGC ANGAAGCTTG TGGTTGNTAG TTCTTCGGGT | 240 |
| TCATAGTNAT TTAGGTTTCC TTCGTTCTGG GTGTGTTTGA TAGAGGGTCC TGGAACNNC | 300 |
| | 300 |

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

| | |
|---|-----|
| CTNCTCTGGG NATGCAGCGT CTGTTGNCTC CAGTGAAAGN CNATTCTGCA ACTGACAAGA | 60 |
| GCGGTGCAGG AAACCTCCCT CACACCTGCT CGCCTGCTCC CAGTAGCCCA CCAAAGGTTT | 120 |
| TCTACAGCCT CTGCTGTGCC CCCTGGCCAA AACAGATACT TGGCCAAAGG ACGTGGGGCA | 180 |
| TCCTGGGCCC TGGGAGGTTT TACTTNCCAG CCAATNTGT GGGNCCAAAN TTGNCCTGGA | 240 |
| G | 241 |

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

| | |
|---|-----|
| GGCAGAGTTG CAACATCTCG GAGGGGAATT GTCCGGAGAG AATCATCACC TGACCGGCCC | 60 |
| CACCAATGCC ATCTTTAAGG CTTTCGCTAT GAATCATCGA CAAGCTGGAG GAAGATATCA | 120 |
| ACAGCTCCAT GTACCAACAG TTACCGNGGG CCAGCAGGNC CCCGGTTCAC CCTGAAGGCT | 180 |
| GGTGGTGCCG GCCACCCAGT GCGGCTNCCC TGNATTGGGA AAAGGCGGGT GTTAAGATCC | 240 |
| AAAGAGATCC GCGNAGAGTN AGGGGGCGCA GGTTCAGGT GGCGGGGGGA TATGCTGCCC | 300 |
| AAATTCCACC GAGCGGGGCC ATTCACCATC GNTNGNGT | 339 |

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

| | |
|--|-----|
| GGGCANNGAG GTGAATTGAG GGNGGAGCAC GTAAGNGGTT TTCCCAGAAG AACAATGACC | 60 |
| TAACAAGTTG CTGCTTCTCA NATGCCAAGA CTATGTATGA GGTTTTCCTAA AGAGGACTCG | 120 |
| CTGTGTCTGA ACAATTGGCC CTGCTTGGGA ATNATAGTAA AACCAAACCA GCCCTACAAA | 180 |
| TGGCTATCTT TACAAACAGG TGTTCGTGNTA GAGNCAGAGT ACCTGGGGTT CCCGTCTCTT | 240 |

| | |
|--|-----|
| GNCATAAAGG TGTGTNAAAN CATTACCCA GGACCCAGTT TTNTTCGGGG GATCTTTTTG | 300 |
| GTTCCAGAAT AGGNGCCCAT AGGT | 324 |

(2) INFORMATION FOR SEQ ID NO:699:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

| | |
|---|-----|
| GGCAGAGNCA GAGATGGCCC TCCCCTCCGT GGATCCAACA TGGNATTTAA AAGANCCAC | 60 |
| AGAAGNGGGT NGAGCACAGA GACCACGAAC TCCAGNTTAA ACCTCGAAAC ANTCGTGAAC | 120 |
| CCCCCTNCAT TGNAAGTAGC CAATCCNAAC TCTGCCTAAT GCTTCCGGGG GTGCCCCA | 177 |

(2) INFORMATION FOR SEQ ID NO:700:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

| | |
|---|-----|
| GGCAGANAAT GGGCCCTNCT TGGAATATAG TGAACCAAAT AANCTCTNCA NATGGCTATC | 60 |
| TTACAAACAG GTGTCTAATA GGCAGAGNN CCTGGNTTCC TGTCTCTTGG CATAANGGTT | 120 |
| ATGAAATCAT GCACCAGNCC AGTTTGTGCG GACATCTTNG CTTAGCAAT AGGCCAGAGT | 180 |
| GGGATCCANC TCCNAAATTG GCCTTGTTAA NACGTG | 216 |

(2) INFORMATION FOR SEQ ID NO:701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

| | |
|--|-----|
| GNAGGCAGGG TCTTNTGTGTT CCTAATGTNC ATAACCCTCC TTAAC TTAA CGCCAACTTC | 60 |
| TTTCCTATNG TCCAGAACAT TGTGAGCACA GCTCTAATGA TTNAGAGTGG NCATTGGTTT | 120 |
| TAAAAACCAA GCTGGGCTTC NTTGAACTCT NGT | 153 |

(2) INFORMATION FOR SEQ ID NO:702:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GGCACGAGGA GACTGCAGTG NGTGTCCGTG TCTATCAAAT ACCTAAGGAG TCCCCAGGAG 60
CTNGCTGGCC ATCGTAATAG GATNTNTCTG TCCTGTAAAC TGTGCCAATT NA 112

(2) INFORMATION FOR SEQ ID NO:703:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

GGCACAGGNT TTTNGGGATC ATGTCTGGTG GCTCCCCGGA TTATAACACC AGAAAACATG 60
GCGGTCCAAA GG 72

(2) INFORMATION FOR SEQ ID NO:704:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

AGCTCCACCA GCATCAAATG AAACAATAGT NCAGTTNTNC TGCTCANAGA TATTCTCCCT 60
TATCCACTTC AGGNACACCT GGCTCTGCAT GACAGATAGT CCACTGGGTT ATCAAAAAAG 120
CCCTGNNATT TNAGAAGNAT GTAGGTCCAT GGTGATAAT 159

(2) INFORMATION FOR SEQ ID NO:705:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

GGCANAGCAG GAATACCAGA GCAAGAACT GATGTCTGAC AACGGANNNG NAGTTCAAAG 60
ATTCTTTGTA GCAGACACTG CAAATGAA 88

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

CAAATCTCTN AACGAATCAT GTAATTAATA AATATTTTAA GCACTCATCA GTATTCTCCA 60
ATGTAACCTT CTNATTGGAG TACACAGANG GAAAGCAAAG AAGAGCATCT AACTTCTAGC 120
TCTGGCTTNN AGCCTCTCTA CCAGGCCGAN GCAAG 155

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

NCTNAGGCTA TCCCCTTGTA AGNGTTTTGT ATCGGCTCGG AACCCCAAGT AACATACCAA 60
CAGACANCAC GNGGGCAGTG TGGGAGCAAC ATGCTGGTTT TAATNAGTGG CCTGGGANGC 120
AGNTA 125

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

GGCANAGGNA CGGTGGGCAC TCTGTCCCAG CGGATCACAA ACCAGGTCCA TGGTTTGAAG 60
GGACTGAGAC TCCAAGCTTC TGGATATNAG GNGCTACCTG GNAAAAAGTC GCCACAGGCA 120
AGCTGCCCAT CAACCACCAG ATCATCTACC AGCTGCAGGA ACGTCTTCAA CCTGCTGCCA 180

GATGTGCAGC CTGCAGGAGT TCGTCAAGGC CTTTTAACCT GGAAGACCAA TGAACCAGAT 240
GGTGGTAGTG TACTTGGCCT CGCTGAATCC GTTCCGTGGT CGCCCTGCAC AACCTTCATC 300
ANCAACAAGN TTGCCAACCG GATGCAGAGA GGAAGNANGG CAGGGAAAGN AGTGAGCAAA 360
AAG 363

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GGNAGAGGTA AAAAATGGCG CCACCCAGTA CCCGGGAAGC CCAGGGTCCT GTCGGCAACC 60
AGCNCAACCA AATCCATCGG AGAAGAATGG TGNTGANAGC TTCCCGGACG CCNACN 116

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TTTTCCGCGA AATTTCTGN NGGAAAGGTC CCAGCATTTA AGGGTGAATG ATGGATTCTT 60
TGTGNTTAAN AGNAACGCCA TTGCTCTACT ATGTGAGAAA TGAGG 105

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

ATTCCGGCAA GTCCACCACT ACTGGCCATC TAACCTATAA NTCGGGTGGC NTCGACAAA 60
GACCCNTTGA AAATTTTAGA AGGNGGTNC TGAGATGGGA AAGGCTTCT 109

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

| | |
|---|-----|
| CGCNAAAATC CCAAATTTTT GGGTAACANC ATTTGNAAAA CCATCCACAA GTGTCTGNCC | 60 |
| TGCTTGGGGA GGAAGATGAA GAGGCATGCN TTATTTGAAC CGAGTTGAAG TGAACGATTT | 120 |
| TGANGTNTTG AATCCGGTTT CCGN | 144 |

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

| | |
|---|-----|
| TAACTGGGGG AAAACCCAGA GGGCATTGGA NAACAGGNTT NCGTAGAAGA ATTCAAGGGC | 60 |
| CAGATTTTNA ATGCCCAANA TTGGTTTATG GGAAGCAACA AAAAAANAAA GCACATGTTG | 120 |
| CCCANTGGGT TTCCGGNAAG TTCCCT | 146 |

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

| | |
|---|----|
| GGNAGAGGCC CAGGTTCAAG AAATTCTCCT GCCTCACCCCT ACCANGNAGC TGAATTNCA | 60 |
| GGTGTGTGGN A | 71 |

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGAANACCGG TNCCAAGTGC CTGCCCTCTT TCCCCGGGGC TGGNTCTCGT NTGCCCCGGT 60
TCCTGGG 67

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

TGCTGCTGGG AAAGATCTGG AGGTCCAAGT CCTGCAAGGN CATCTCTGGA AAGAGCCAGA 60
TCCTGTTTNC CCTCGTCTTC ACCACCAGGT ACCTGGACCT GTNCACCAAC TTAATCTCCA 120
TCTACAACAC AGTAATGANG GTGGTTTTCN TCCTCTGTNC CTATGTNACA GTGTACAT 178

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

GAGCAATATG GGATCAAACA CAAATCACT AGATAACAAC TATTCCACAC CAAATGAAGA 60
GNGGAGACCA CAATAGAACA CTGGATCGAT CGGGGGATCT AGGCGACATN GAAGCCATTN 120
ANAGGGAAAC AACACCCTTG AATGCAGAAAG AATTTAGCCA CCACTATCTC CGTNCCATCT 180
GGGCTTATAT GNGACT 196

(2) INFORMATION FOR SEQ ID NO:718:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

ATTGTNATGG GNTGCCCAT T GAAATAAAAG TATTATCAGA ACTTGGTAGA GAAGCTCAGA 60
ATCTTTNANC TNTGGAAATT AGAAAGAAAG CTAGATCATT TGCTAAAGCA GCCATTGNGT 120
ANCAGTAATC AGCATTTAT 139

(2) INFORMATION FOR SEQ ID NO:719:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

GNAAGACCTG TAATGGTGGC TATCCTCCTN AAGCTTGGNA ACTCCTGGNC AAGAAAAGGC 60
CTGGTTNCTG GTGGCCTCTA TGAA 84

(2) INFORMATION FOR SEQ ID NO:720:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

GGNAGAGGNA GCCCACTCCT AATGATGTGG CCATATCCNA CCTCCCTCTG GCTCAAATGT 60
TTAANAGGAT TGTNCAGGCT GTTGTGTACA GCTGTGGAGC CAGAGTTGGA ATTCTTCCCA 120
AGGGGATATT CGGTTGCTGG CTGTACGNNA TGGAAGNCTT TGAAAGCCCN NATTGTITCC 180
CG 182

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

TTGGGGAGGA GATGAAGAGG CATGAAATTA TTNGACCCAA GTTGAAGTGA ACAAANTTTA 60
ANGGTATTAA ATNCGGTAC GGATTGNTTT TAAATTTAAT GGAAATCCTT TATTT 115

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

| | |
|---|-----|
| GGCAGNGAAG CAGTTGATCC TAAGACACGT TTA | 60 |
| CTTATGN ATAAAAATGGT CAACTCTGGA | |
| ATGTTGGAGA CAATCACTGG CTGTATTAGT ACAGGAAAGG | 120 |
| AGTCTGTTGT CTTTCATGCA | |
| TATGGGAGGG AGCATGGNGG ATNAAAAGGA AAGATAGTAA | 180 |
| AGTTATACCT ACAGAATGTG | |
| CCCATCAAGG TATTTAAAAC AACCCCTGAA TGNAATTTTA | 240 |
| AGGAATCGTG ACAAATATNT | |
| TGAAAGGTGG ATTTTCAGGT TTAAGATCG CTTTCAGTTA | 300 |
| AACTTANATC CACGTAAGGT | |
| CCATCCGCAT GTGGGGGCAG NAAAAGGAAT TGGCACANTT | 359 |
| TNGTCAAGTA TTGGCNGTG | |

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

| | |
|---|-----|
| GGCAGAGNAT TTAATGTAAG TATTATGGGA ACCTTCATAA | 60 |
| GGAAATNAAG ATTCNGAGAA | |
| ACAGGTAAAC TCTGGTCTTT CTAAAACAGA CCTGATGAAG | 120 |
| AGTAGAGAGT CATGGAGAGT | |
| TNTAATAGAG CAAAAGAGT GTGNATCTCA TGGTAATATA | 180 |
| GTAGGGGAAC TTAGCAAGGC | |
| CTGTTTATTC CAGATTCTTC CCTGGGGATC CTGTGTCTTC | 240 |
| AGAGATAAGG ATACTCGTTT | |
| TCCTCTGGGG TATGGGGGGT TGGGGGGGTA CCTCTNCACC | 300 |
| TGAGGGCCTT TTNGACCGNC | |
| TTNGGAGGAA GGTCCAGAAA ATCCTTNCCG GGGNGNTTAT | 360 |
| GAACCCGCTT TCATGGGGGG | |
| GAAGGTCAGA GGNAAGGTTT AGAGAGGAAC TTTNTTGCAC | 420 |
| ATGCNGTTCT CAAATTNCCT | |
| TTCCGGTTTC ATGGCAATNT | 440 |

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

| | |
|---|-----|
| GGCANAGGAA ATGGCCCTGA AAAAAGACAG GGAAAGCATG | 60 |
| GGAACACCGG TACATTGAGG | |
| TGTTCAAGTC CCACAGAACC GAGATGGGAT TGGGTGTTGA | 120 |
| AGCACAGTGG TCCCAACAGT | |

| | |
|---|-----|
| GCCCCGACAGC GCCAACAATG GCTTCGTGCG GCTTCGAGGA CTCCCATTG GNATGCACAA | 180 |
| AGGGAAGAAA TTGTTCCAGT TCTTCTCAGG GTTGGAAT NTGCCAAACG GGGTTCACAT | 240 |
| TGCCTGTGGG ACCCCGAAGN CAAGATTACA GGGGAAGCGT TTCGTGCCAT TTGCCTCGCA | 300 |
| GGAGTTTAGC TGGAGNAAGG CTCTAGGGGA AACACAAGGT GAGGTTTGGG GCACCAGGTT | 360 |
| ACATTTGAGN TGTTTTTAAG AGNCAGCCCA GAGGGAGNTT AAGNTCATAN TCAGATTCCC | 420 |
| | 420 |

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

| | |
|---|-----|
| GGCAGAGCTC ACCCAGTA ACCACACCCA CGGTGACCAC GCCCTCACTA CCCGCAGAGG | 60 |
| TGGGCTCNCC GCACTCAACC GAGGTGGACG AGTCCCTGTC GGTGTCCTTT GAAGCAGGTG | 120 |
| AGNNCCGCCA TCCGCCCCCA CCAGTGAAGG CTGGGNTGA AGCCTCCCGC TCGTGGGCCC | 180 |
| CCGGGCGACG GCGCTCGGTT TTCCCCACAC GAATGTGGAA CCTGTGNCCT GGTGTNACCC | 240 |
| TGTAAATTTN AAGCATCGCA AGGNGGTGCC AATGNGCACC AANNCTGATN TTCCCCCGGN | 300 |
| AGCTTCGNAA TGAANAGCAN TTGCCCCGTT CACAGGGAAC GGGCANGTTN GGCTNNGGGC | 360 |
| CCNAGNGAC GGNCANCCAC ATNCGGTTCA NGAAGTTCCT TGNNCCAANC TGTTTTNATT | 420 |
| TGGAATTCCG TGNCCTGGG GCCCCGTTN CGGGCAAATT CAAACGGNGA CACAAAGGGT | 480 |
| TTTGGN | 486 |

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

| | |
|---|-----|
| GGCANAGCGT GNATGAGGAG CTCNTCTACC ACAAAGTGAC GGCAGCCGAG CTCAGNACCT | 60 |
| TGTGTACCCG CCATGCAACT GGTGCTTTT TNTCAACACC ATCTTCTACC CCGTGAGAT | 120 |
| CAATGAAATC CNAGCCTATT GTGGTCTATG AACAAGGGAA TACCTTGAGC AGATCTCCAC | 180 |

| | |
|---|-----|
| TCTCATCAAC ACCACCGACA GATGCCTGCT CCAACAATA CATGATCTGG AACCTGGTGC | 240 |
| GGAAAACAAG CTCCTTCCTT GGACCAGCGC TTTCAGGACG CCGATGAGAA GTTCATNGAA | 300 |
| GTCATGTACG GGGACCAAGN NGACCTGTTT TTCCTGCGCT GGGAANTTTT GGGTTGATGA | 360 |
| ACACAGGAAA ACAACNTGGG TTTTGNTTTG GGGGCCCCAT GTTTTTTTCA AAGGAAACCT | 420 |
| TTGGNNCG | 428 |

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

| | |
|--|-----|
| GGCANAGTCA AATGNGAAGT GGTCAGTAA TCTAAAGGGA AAAAGGNGAT GAATGTCTTT | 60 |
| AATGGAGTCA TGGTTTGCAC TGNCCATCA CACCAATNCT CATTTACCTC TGGGAAAGCT | 120 |
| TGCCTGGGAA TTNGGAAAGT NTCAAAGGGA CAGT | 154 |

(2) INFORMATION FOR SEQ ID NO:728:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

| | |
|---|-----|
| AACATTCCTC TTCTCTGCCA CCATGACCAA GAAGGTTCAA AAATTTCAGC GAGCAGCTCT | 60 |
| GNAAGAATCC TGTGAAAATG TGCCGTTTCC TCTGAAATAC CAGACAGTTG GAAAAATTAC | 120 |
| AGCAATATTG ATGATTTTTG ATTCCCTCTG AAATTCAAGG NTACCTNACC TGGTTTATGA | 180 |
| TTCTGAAATG NAATTGGCTG GNAACTCCT TTATGGATAT TCTGCAGCAC CTGTGAATAA | 240 |
| TACCCAGTNG ANCAGCTTTG CTNACTGCGN AAATCTTGGG CTTGCACTGG CCATGCCCCC | 300 |
| TTCCATGGGN GCAA | 314 |

(2) INFORMATION FOR SEQ ID NO:729:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

| | |
|---|-----|
| GGCANAGCAA CTTGGTGACC TTTGTGGTAA TGGTGGTTCT CTATGCTCAC ATCTTTGGCT | 60 |
| ATGTNCGCCA TAGGNCTATG AGNATGTCTC GGCATAGTTC TGGACCCCGG CGGAATCNNA | 120 |
| NNTACCATGN ATGAGTCTTC TGAAGACTGT GGTCATTGTG CCTTGGGGCC TTTATCATCT | 180 |
| GCTGGACTCC TGGATTGGTT TTGTTACTTC TAGACGTGTG CTGTCCACAG TGNGACGTGC | 240 |
| TGGNCCTNAT GAGAAAATTT CTTTCCTTGC TGCCTTGGNT GAANTTCANC TCTGGNCATG | 300 |
| AACCCCATCC GTTTTACTGC TAANCGTGA CAAAGTTAAT GGAGCGGCCA CTTTT | 355 |

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

| | |
|---|-----|
| GGCAGAGCGG GAAAGGCGGG ATCGAGGTGG GCCTGAGCCC NNGGATTTGG AGCGAACATA | 60 |
| GATGAGAAAC ACTTCCCGAG GTCTCCAGGT NTTNTGGGGA GCCAGGAGGG AAGTAGGGGA | 120 |
| TGAGTCCATC TTCAAACGG AGGGGGAAGG TCTCCCCTTT TTTGGGCTGG GAACCCGGGG | 180 |
| GAAGGCAGTG GGCCGGNCTT CTGGAAAGGT CGGCCTGGGA AGGTCTGCCT GGGGTCTGGG | 240 |
| GGATGTTCCC GTGGGTTAGA CCCGGCGCGG CCCATGTTTC CTCCANTTAN CTAAGATTTT | 300 |
| CCCGGCCTTN AAACGTTGTG CTTTCNGTCA AAGANCCAGG GGGTTCCCCA AGGTTAC | 357 |

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

| | |
|--|-----|
| GGCAGAGCT GTACTCTGGG GCTCTTGGCG GCTGGGTCTT GCCCTGCTGT GCTCTGCCAT | 60 |
| TTAACAGCCC ANTTGACGAG GAGAATCTAA CCCAGGAGAA CNATGATCGA GGGACANACG | 120 |
| TNGACCTCGN ATTNAGTCCT GCGNCCAACG TGGNACTTCG CTTTCAGCCT GTACAAGCAG | 180 |
| TTAGTCCTGA AGGCCCCCTGA ATAAGAAATG TNNATCTTCT CCCCACTGAG CATCTCCACC | 240 |

GTTCTTGGCC TTCCTGTCTC TGGGGGNCCA TNAN

274

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

| | |
|---|-----|
| GGCANAGGNT GGGTTTNTGA ACTNCTGNGT TTTTGCTTGC TNCTCTGGAN ATGCAGCGTC | 60 |
| TCTTGNCTCC AGTGAAAGCG CATTCTGCAA CTGNACAAGA GNGGTGCAGG GAAACCTCCC | 120 |
| TTCACANCTG CTCGCCTGNT CCCAGTCAGC CCACCAAAGG TTTTCTACAG NATCTGNTGT | 180 |
| GCCCCCTGGC CAAAACAGAT ACTTGGCCAA AGGACGTGGG CATCCTNGCC CTGGGAGGTC | 240 |
| TACTTNCCAG CCAATATGT GGACCAAAC TACCTGGAGA NGTATAACAA TGTGGGAAGC | 300 |
| AGGTAAAGTA TACAGTGGGG TTGGGNCCAA ACCCGTATTG GGCTTTCTTG TTCCAATCCC | 360 |
| AAGAGGNCCA TCAAATNNCC TGTGGNC | 387 |

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

| | |
|---|-----|
| GGCAGANACT GGGTTGGTGA AGATTCCACA TACAAATTTT TTAAGGTTAT CCTCATTAAT | 60 |
| CCATTCCATA AAGCTATCAG AAAGAAATCC TGACACCCAG TGGGATCACC AANCAGTGCC | 120 |
| ACANGCNCAG GGAGTTNCGT GGGCTGACAT CTGCANG | 157 |

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

| | |
|---|----|
| CTCTCNTNTT CACCACCAGG TACCTGGACC TNTTCACCAA CTTNATCTCC ATCTACAACA | 60 |
|---|----|

| | |
|---|-----|
| CAGTAATGGA AGGTGGTTTT CNTCCTCTGT GCCCTATGAG AACAGTGTAC ATGAATGTNA | 120 |
| TGGGAAAATT CCGTGAAAAN TTTTGAGCAG TGAGGAATGA GCACATTCCG CCTGGNGTTT | 180 |
| CTNCTGGTCC CAGTGNATTG GCCTTTGCCT TCCTTGGAAG CTACAGTTTC ACTCTGCTGG | 240 |
| GGATCCGTGG GAATTTNN | 258 |

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

| | |
|---|-----|
| GGCAGAGCCC ATGCATCATG CCTCTGGTCA TGACACTCGT GGCCCTTCCT CACATGAAAT | 60 |
| GAGGGGAGGG CCATTAGGAG ATCCCAGACT GCTAATTGGA GAGCCCAGAG GCCCCATGNA | 120 |
| TAGATCAAAG GGGTCTACCT ATGGNTGGTA GAGGTGGTAG AGATTNTCGA GCGAATGGAG | 180 |
| ACTCGTGCCA TGGAAACTGA AGGTCTTAGA GACACGTGTA ATGGAGAGGA GAGGAATGGA | 240 |
| GACCTGTNCG ATGGAAACCA GAGGGATGGA AGCAAGGGGC ATGGTTGCAA GAGGATTGGA | 300 |
| GNTGAGGGGC CCTGTCCCCA GTTCAAGAGG CCCTATGATT GGTGGAATT TCANGGTCCT | 360 |
| GGTCCCATTA TTTTAGGGGC AGTTGGCCCT CCTTCAGGGA NCCCGACAGT TCCCGGGCAT | 420 |
| TTTAAGGGTT GGGGNATCTT GGAGGTGGTA TGCAGGTAC AGGNTNACAG GNACCGGTTT | 480 |
| TTAGGGGGCA GTTTTACAAG N | 501 |

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

| | |
|---|----|
| AANCCAACAN TAAAATCCCT TCCCTCCAAC ATATGCAAAG ACGTTNTNAC CGNACCTGGT | 60 |
| GATATGCTG | 69 |

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

| | |
|--|-----|
| GGCAGAGACG GTNCTCACAT TCTCCCCANA GGCCGANATG CGGGTAATGG CGCCCCGAGC | 60 |
| CCTCCTCCTG CTGCTCTCGG GANGGCCTGG CCCTGAACCG AAACCTGGGC CCTGGCTCCC | 120 |
| CACTNATNTG AGGTATTTCA ACACCGCCGT TCCCGGCCCCG GTNCGCGGAG AGCCCCGCTT | 180 |
| NATCTNANTG GGCTACGTGG ACGACAGTCA TTTGTGCGGT TTCGACAGGA ACGCCGNGAG | 240 |
| TTCCGAGAAG GGGAGCCGCG GGTCTCGTTG GGTGGGAGCA GGAGGGGNCG GAGTATTTGG | 300 |
| AANCNGGGAG GACAACAGNA GTTACAAGNG CCCAGGT | 337 |

(2) INFORMATION FOR SEQ ID NO:738:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

| | |
|---|----|
| GGAANAGAAT GGTCTGCACC ANTAAAACCA GGNGCACCCA CACCCTGGAA CCTCTCCANG | 60 |
| AAGACTCTCG | 70 |

(2) INFORMATION FOR SEQ ID NO:739:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

| | |
|---|-----|
| CAGCAAGACG TCCCAANTAA GTTTAAGTAT AAGGAAGGCA CTCTNAAGGT CGCGCCAGAC | 60 |
| TGGGCAAGAC CTCAAANAGG AGCATCCTGG GTCGGCTACA CTGCCCCCTT CCTTGAATNC | 120 |
| ACTCTGCCTG TTTANNAACC TGGGAGTGCT GGNCACCCTG CAGCAGTNCA GCGAATGGAG | 180 |
| CTTCATGCAG GCTCTATNCT GTGAACCTGT GAAGCCCTTT GCCTGGCCCA GGTNGACAGC | 240 |
| TTTANGTATT TGAAGGNTCA GGGGTGGAGT NAGGCTG | 277 |

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

| | |
|---|----|
| TGAGCCTAGG NGCTAGGTTG CAGTGAGCCA GATGGCCCAT TGCACTCTAG CCGGGCAGCA | 60 |
| GGCNGACC | 68 |

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

| | |
|--|-----|
| AGGAGCTGTC GGGAAGATCA GAAGCCAGTN AGGATGACCA GCGCGACCTT ATCTCCANCA | 60 |
| ATNAGCAACT GCCATGCTGG CCGGCGCCTG GGGCCCGGAA GAGCAAGTCC AGCGCGGANCA | 120 |
| CTTGTACACA GCTTTTCCAN CTGGTGACTT NCTCTCGN | 158 |

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

| | |
|--|-----|
| GGCAGAGNCT TGCTCTNCCC AAATTAAATT TGCAGTTTTT AACTCTTNAT GACTACCTGC | 60 |
| TAAGTGA CTT TAACCTCTTC CGCTTAGAAT CAACTTATGA AATTCGTCAG GACATTGAAG | 120 |
| ATAGTGTCAG CAGAATGAAG CCATGGCAAT CTGAAATATG GCGGTGTAGT GTTTGGTGGT | 180 |
| TGGGCGCGAA TGGCCCAGCC CATTGTGGCT TTNACTGTCTG TAGNAAGTGG CCAAACCCAA | 240 |
| CATAGGTGAA AACTGGCCAA CCCGAGTTCG TGCCAGATGT TACCATAAAT CTCCAATGTC | 300 |
| CAGAGATCCA CATCAAAGNT GANTGGGAAG GNCTTCGTNA GCATGATGTA TGCTTTTAA | 360 |
| ATTACCGTAC GNTCCCACAA AACCTT | 386 |

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

| | |
|--|-----|
| GGCANAGGET TGCTGCTGGG GAAGATCTGG AGGTCCAAGT GCTGCANGGC ATCTCTGGGA | 60 |
| AGAGCCAGAT CCTGTTTGCT CTCGTCTTCA CCACCAGGTA CCTGGACCTG TTCACCAACT | 120 |
| TCATCTCCAT CTACAACACA GTAATGAAGG TGGTTTTTCT CCTCTGTGNC CTATGTTACA | 180 |
| GTGTACATGA ATATATGGGN AAATTCGTA AAACTTTTGT ACAGTGNAGA ATGAACACAT | 240 |
| TCCGCCTGGG AGTTTCTTCT GGTCCCAGTT CATTGGCCTT TTCCTTCCTT GAAAACTACA | 300 |
| GTTTTCACCTC TGCTGGGAGA TTCCTCTGGA CTTTTTCTAN GCTATNNGGG AATTCATGGG | 360 |
| NNATCCTGTC CCCAG | 375 |

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

| | |
|--|-----|
| TCGGACGAGT CATGGGCTCC CGNAACAAAC GTGAGGNCTG NCAGNGTCAA ATTTACCCTN | 60 |
| GTCCAAGATC CGCAAGTCCG CCCGATGAAC TGA CTGACGC TTGATGAGGA AGGNCCCACG | 120 |
| GCGTCTNGTC GAANGCAACG GCCTGTCTAN CGGAGGG | 157 |

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

| | |
|---|-----|
| GGCANAGCTA CAACCAGCTG AGCCGTGCCG TGCCTAACTG GCGCGGCNCT TGCCCAACCT | 60 |
| GCCCGAACGC AACCAGTTCC GCGTGCCNCT TCGGCCGGCT GCTGGACAAG CTGTATGCTC | 120 |
| TCGGCTTGGT GCCCACGCGC GGTTGCTGG AGCTCTGCAC TTTNCGTNAC GGCCTCGTCC | 180 |
| TTCTGCCGCC GNCGGCTCCC CACCGTGCTC CTNAAGCTGC GCATGGGGAA CNCTTTCAGG | 240 |

GCTGCCGTGG CCTTTTTGGG AGCAAGGGCA CGTAACGTTT TGGGGCCCTG AACGTGGGTT 300
TACCGAACCN CGGNNTTTTC CTTGTTNAAG GGGGNAAAT 339

(2) INFORMATION FOR SEQ ID NO:746:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

AGGCCTGTAC TACCACCGGT ACCTCCAGGA GGTCAATCGAT GTACTGGAAG ACGGATGGGC 60
ATTTCCAAGA GAAGCTGCAG GCTGCGCAAT GCGGAGGAAC ATCANGAAGC GGGAAAGCTG 120
AGCCGAGAGC TGGNACTTTN TNAGCCACCA CGTCCGCACC AAGCTGGNAT GAGCTTCAAG 180
CGANCAGGTA GGTGTTACAG GACTGCGGAT GTTTGCTTCA AGGCCAAGNA TGGACGCCGA 240
GCAGGGATCC CAATGTGACA GGTGGNATTC ATCTGGAATC TGCCTGGAAA CAGTTTTGGA 300
ACACCTGGNA CCCTTCAGGA ACCAGCATAC ATTTTCGAGNG CCCGNGAACC TGGNAGTT 358

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

GGCAGAGCTC AGACATGCAA GANGTCATTG GCTCANCCAT TGCTATCAAT CTCCTGTCTG 60
NAGGAAGAAT TCCTCTGTGG GGTGGCGTTC TCATCACCAT TGCAGATACT TTTGTATTTC 120
TCTNCTTGGA CAAATATGGC TTGCGGGAAG TAAGNNAGCA TTTTTTGGCT TTCTCATCAC 180
TATTATGGCC CTCACATTTG GNATATGAAG TATGTTACAG TGAAACCCAG CCAGAGCCAG 240
GTTACTTCAA GGGNCATGTT CCGTNACCAG GCTGTTTCAG GCTGTTTCGNA ATTCCACAGA 300
TTGNAN 306

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

| | |
|--|-----|
| GGCANAGCCA CTGTCTCCTT TACCACAGGG AATATGTCAG TGGATTTGGA AAAGCTATGA | 60 |
| GGATGCCCCAT GTGGAGTTCA TACACAGTCC CCCAGTTGGG AGACACATCG CCTCTGCCTC | 120 |
| CCACTGTCCC AGACTGTCTG CGGGCTGATG TCAGGGTTCC TCCTTCTGAG AGCCAAAAAT | 180 |
| GTTCTTCTA TTTAGCAGAC AAGAATATCA CCCACGGCTT CCTCTATCCT CCTGCCAGCA | 240 |
| ATAGAACATC AGATAGCCAA TATGGTGCTT TAATTACTAG CAATTTGGTA CCTATGTATG | 300 |
| AAGAATTTC AAAAAATGTG GGACTACTTC CACAGTGGTN CNTNTTGANA AAACATGGCC | 360 |
| ACAGAAAGGA AATGGNGTTA AATGTGGGTT TAGTGGGACC ATNATTTGGG TTNTAATTAT | 420 |
| GATGGGNCNT TTGGTGTTCC AGTGAATTTA CCAA | 454 |

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

| | |
|--|-----|
| GGCAGGAGCC GCCTGCAGGG AGGAGAATGT ACCCCACTGG NACCTGNAGC TCCTGGTCCC | 60 |
| TCAGCCAAGA CCTGAANGNG TCCCCAGCCA GCCTGCTGCT GGGGACCCTG TGGCTTGCTG | 120 |
| TCAGTGATG GGGCCTCTTG GCCTTCCCCCT GGGGAAGTTC ACCCNTGTTA CCCCAGCTTG | 180 |
| CCTTGCCCCCT GGGNCCTTTT NCTGGGCCCC AGTGNCTTCC TGCCTTTGAC ATNAGAACTT | 240 |
| G | 241 |

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

| | |
|---|-----|
| CCACCTGGTN CTGCAAGGAC CAAGNGGTCT GTCCATTCAA GGAATGCCCC GAATGCCAGN | 60 |
| AGAAAAAGGA GAGAAAGGAG NTACTGGNCT TCCAGGTCCA CAGGGTATCC CAGGAGGCGT | 120 |
| TGGTTCACCA GGNACGTGAT NGGCTCACCA | 150 |

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

| | |
|---|-----|
| GGCAGAGGTA CACGTGCCTC GAGCTGCCAC CTCCGGAGTG GGGCTGGAGA ACGGCATCCC | 60 |
| ACGGGGACCT GATCCGGGGC ACGGTGCTCA CCTACCAGTG CGAGCNTGGC TACNAGCTGC | 120 |
| TAGGCTCCGA CATTCTCACT TGCCAGTGGG ACCTGTNTTG GAAGCGCCGG CCGCCCCGNT | 180 |
| GCCAAAAGAT CATGAACTTG TGCTGACCCT GGCGAGATTN CCAACGGGCA CCCCACNGCC | 240 |
| TTCGGAACGC CGGCTTCCCC GTTGGNTCCC ACGTTNCAGT ACCGCTGCCT GCCAAGGTTA | 300 |
| CAGCCTTCGA GGGGGCAGCC ATGTTACCT GNTTACAGCC GGGGACAAAG GCACANCCAA | 360 |
| TGGNAGNATT AGGGTTCCCC AATGGGGCTT TGAATAAGGA GCCTNGCCTT AAACCGGGGG | 420 |
| TTNCGAGAAT GGTACCAAA GTTTTANAGA ACATTACCAG GGGGGGATTT TTGGGTTTTT | 480 |
| NTGNTATTAG GGTTTTAG | 498 |

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

| | |
|---|-----|
| GGCAGAGGNN NNCACCCACA TTACCTGCTT TCTTCTTGGG TAGCTTGTCC ATCAGCTCCA | 60 |
| CCCCTTGTGA ACACCTTTCT GAAAGCTGGA GGGCTGGGAG AAGGGGGTTG TATTCATCAA | 120 |
| TGGCCAGAAC CTTGGACGTT ACTGGAACAT TGGACCCAG AAGACGCTTT ACCTCCCAGG | 180 |
| TCNNCTGGTT GAGCAGCGGG AATCAACCAG GTGCATCGTT TTTGAAGGAG ACGATGGCGG | 240 |
| GGCCCTGCAT TACAGTTCAC GGGAAACCCC CCACCTGGGG CAGGAACCAG TACATTAAAG | 300 |
| TGNAGCGGTG GCACCCCTC CTGCTGGTGC CCATGGGAGA CTGCCGGCTN CTNTTGACCT | 360 |
| GAAAGNCTGG TTGGTTGTTG CCCCAACCTT CATTGCAAAA GCATTTNCTT AANTAGNAAC | 420 |
| TTCAGGGATT GGGGGTTAAA ATTTGCCCTG TTTTAGTTNA AAACCTAAGC TTN | 473 |

(2) INFORMATION FOR SEQ ID NO:753:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

| | |
|--|-----|
| GCACCCCAAC ATCGACACGG CCAGTTTNTT CCGCTGGCGG CATCAGGCCC GGGTGAACG | 60 |
| CATGGNGCAG TTCCAGAAGG AGAAGGAGGA ACTGGACAGG GGCTGCCCGG AGTNCAAGCG | 120 |
| CAAGGTGGCC GAGTGCCAGA GGAAACTNAA GGAGCTGGAG GTNGCCGAGG GCGGCAAGGC | 180 |
| AGAGCTGGAG CGCCTGCAGG CCGAGGTACA GCAGCTNCGC AAGGTGGAGC GGNGTGGGNA | 240 |
| GCAGAAAGCT GNNAGGAGAT TGC GCAAGAT AGGNGNAAGT AGCATGCCCT GGTAACGTGG | 300 |
| GACANGCTTC NGCAAAGACG GCTTTCAGCA AAGAGCCATG GTTAAATTAC CAAGCCCCNG | 360 |
| TAAGTACGGT GGTAGGNATT CAAAGGTGGT NTAGGGTAGC CAGAAACACA AGGACTTTCT | 420 |
| TGGNAAANAT TACG | 434 |

(2) INFORMATION FOR SEQ ID NO:754:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 375 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

| | |
|--|-----|
| GGCANAGGNA CTGTAAAAAT GAAAGTCCTA ATGGGAAACC CTCTTCTCCC CACACCCCAG | 60 |
| TTGTTGGGCT CAAGTCTGCT CTGNAGTCCT GATCTCCCTT GAATTGAGTC TCAGCATCTT | 120 |
| CNNGTTGCCT CCACCTGCTC GTCTGTNAAT CCCATTCCCT GCAGACAGTG GAACAAAGTC | 180 |
| ACTGGTAATC TTCCTCAT TG CCCTGGGACT GCTCCCAGAC ACAGCTATTT GGGACCCAGA | 240 |
| TCTTCCCCAC CAAGCCATGG GCGANATCTT GTTGAGTAAG AGTTTCAGTC CTGGGGTCTT | 300 |
| ATTTCCCCCA AACGTGGTAG GGGATCTTGG ACCCNATGT CTCTGNTTTT TTCCTAAGGN | 360 |
| CACAGAGGNT GTGGG | 375 |

(2) INFORMATION FOR SEQ ID NO:755:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

| | |
|--|-----|
| GGCAGAGCAG AGTTTGACAG GGAGATAGAC CGGGGATCCN GGANCCCTTN TNAACAGCTG | 60 |
| TTTGAGAAAG ATGGTCAGTG GCATGTACTT GGGAAGAGCT GGTTCGACTG ATCCTAGTCA | 120 |
| AGATGGCCAA GGAAGGGCCT CTTATTTGAA AGGGCGGATN ACCCCGGAGC TGCTCACCCG | 180 |
| AGGGNNAGTT TAACACCAGT GAATGTGTCA GCCATCGAAA AGAATNAAGG NAGGCCTCCA | 240 |
| CAATGCCAAA GAAATCCTGG ACCCINNCTGG GAAGTTGGAG CCNTTCCGAT TGATGGACTG | 300 |
| T | 301 |

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

| | |
|---|-----|
| ACCCTCCTTT CCTGCAGCTC CAGCTTTNTG CTCTGCCTCT NAAGGAGACC ATGGCCCAGC | 60 |
| ATCTAANTAC CCTGNCTGCT CCTGCTGGCC ACCCTAGCTG TGGCCCTGGC CTGGNAGCCC | 120 |
| CAAGGAGGAA GATAGGATAA TCCTGGGTGG NCATCTATAA ACGGCGAACC TNCAATGAAT | 180 |
| GAGTGGGTAC AGCGTGCCCT TGNACTTCGC CATCAGCNAG TNATGAACAA GGNCACCAA | 240 |
| AGATGGACTT ACTNACAGAC GTCCGNTTGC GGGTTACTTA AGAGCCAGGC AACAGACCGT | 300 |
| TGGGGGGGGT GAATTAATTN TTCGACGTGG AGGTNGGCCG AACCTATGTT ACCAATTCCC | 360 |
| ANNCCAATTG GGACAANGTG | 380 |

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

| | |
|---|-----|
| TTTTGCCCCG TTGGGATTGT NATGGGTTGC CCATTGAAAT AAAAGTATTA TCAGAACTTG | 60 |
| GTAGAGAAGC TCAGAACTT TCAGCTATGG AAATTAGANN GAAAGCTAGA TCATTTGCTA | 120 |
| AAGCAGCCAT TGAGAAACAG AAATCAGCAT TTATTCGTTG GGAATAATG GCAGATTGGG | 180 |

| | |
|---|-----|
| AATAATTGGC TACTATGACA TTTGAATGGG NAAGTNTGAA GCCAAACAGT TGAGAAACTT | 240 |
| TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGTTCTTA CAAACCTGTN TTTTGGNCTC | 300 |
| CGTNCATCTA GGACGNCATN GGCTGAAGCA GAACT | 335 |

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

| | |
|---|-----|
| AGTAGAAAAA TCAACAGAAC AAAGGAAGAG TATGGCTCCT GAACCTACAC AGAGCTCTAC | 60 |
| AGTAGTCGCA TCTGCCCAGC AAGTGAAGAC AACGCAAAC TCAATGCTC CTGAATGTAA | 120 |
| ATGAATGCAA TTNTGAAACT GATTCCAATG AATTTTGAAT GTTAAGGGAA ACCTCCCATC | 180 |
| CATTTAGTGG ATTTCTNCAT CTAGATCTAC ACATATGTGA ATGACATTGC ATGGCTAAAA | 240 |
| GAAAAAGAGT CCAAACAGAC GTATTACTGG AGGGGCCAAT GCCAACTTNT CTTTNNACAC | 300 |
| AGCTAACTAT AGGNTTATTT NTNCCTTATC C | 331 |

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

| | |
|---|-----|
| ACTGTGGACA TGATGTATGG TGGCATGAGA GGCATGAAGG GATTGGTCTA TGAAACATCA | 60 |
| GTTCTTGATC CTGAATGAGG GCATNCGTTT CCGAGGCTTT AGTATCCCTG AATGCCAGAA | 120 |
| ACTGCTACCC AAGGCTAAGG GTGGGGAAGA ACCCCTGCCT GAGGGCTTAT TTTGGGCTGC | 180 |
| TGGTTAACTG GGACATATCC CAACAGAGGA TNAGGTATCT TGGGCTCTTC AAAAGAGTGG | 240 |
| GCAAAGAGGG CAGCTCTGCC TTNCCATGTG GTNNACCATG NTGGGACAAC TTTCCCACCC | 300 |
| AATCTACACC CCATGTTTTT AGCTCAGTGT CAGTGTTTAC ANCCCCTTCA ACATGGAAAG | 360 |
| TTAACTTTNN CCCGNGCATT ATGGCACCAG GGN | 393 |

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

| | |
|--|-----|
| GGCANAGGAT TTTGTGCCCCG GCTGGGATTG TCATGGGTTG CCCATTGAAA TAAAAGTATT | 60 |
| ATCAGAACTT GGTAGAGAAG CTCAGAATCT TTCAGCTATG GAAATTAGAA AGAAAGCTAG | 120 |
| ATCATTTGCT AAAGCAGCCA TTGAGGAAAC AGAAATCAGC ATTTATTCGT TGGGGAATAA | 180 |
| TGGCAGATTG GGAATNAATT GCTACTATAC ATTTGATGGG GAAGTATGAA GCCAAACAGT | 240 |
| TGAGNAACTT TTTACCAAAT GTATGATAAG GGCTTGGTTT ATCGNTCTTN ACAAACCTGT | 300 |
| GTTTTTGGTC TCCGTGCATC TNAGGGACTG CCATTGGGCT GGAAGCAGAA CTTGNATTTN | 360 |
| ATCC | 364 |

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

| | |
|--|-----|
| AAAGCTATGA GGATGCCCCAT GTGGAGTTCN TACACAGTCC CCCAGTTGGG AAGACACATC | 60 |
| GCCTCTGCCT CCCACTGTCC CAGACTGTNT GCGGGCTGAT GTCAGGGTTC CTCCTTCTGA | 120 |
| GAGCCAAAAA TGTTCTTCTT ATTTAGCAGA CAAGAATATC ACCCACGGCT TCCTCTATCC | 180 |
| TCCTGCCAGC AATAGAACAT CAGATAGCCA ATATGAATGC TTTAATTACT AGCAATTTGG | 240 |
| TACCTATGTA TGAGGAATTC AGAAAAATGT GGGACTACTT CCACAGTGTT CTTCTTATAA | 300 |
| AACATGCCAC AGAAAGAATG GNGTAAATGT GGTTAGTGGA CCATATTTGN TTATAATTAT | 360 |
| GGTGGGCCAT TTGNNGCTCC CGATGGAATT ACCCAACCTT TGGGCCAACA NGGTGTT | 417 |

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

| | |
|---|-----|
| TTAAGAGTTC CCAGAAATAC ATTTGCCACC AACAGAGTAG CCAAATTTAT AAGGAAAAAT | 60 |
| GATTCCCAAT GGATATTTGA TGTTTGAGGA TGAAAATTTT ATTGNGTCTT CTGTTGCCAA | 120 |
| ATTAAATGCC CTGAGGAAAA GTGGCCAGTT CTGTGAATGT TCGACTTCAG GTCTGTGGCC | 180 |
| ATGAANGTTA GCACACAGAG CAGTGCTAGC TTGCTGCAGT CCCTATTTAT TTGGAAATCT | 240 |
| TTAATAGTGA TAGTGGTCCT CATGGAATTT CTCACGTTGA AATTTTGATG ATCTCAATCC | 300 |
| CAGANGCTNG TTGGAAGTCT TGGTTGGNAT TNTGGCCTAC ACTGNTCCAG TT | 352 |

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

| | |
|--|-----|
| GGCANAGCTC GGCATGTGNC GGGAACCTGA GGGACTTGTC GGGCCTCAAT NATCTGCTCA | 60 |
| ACGTGCTGCA GAGCCTGCTG CTCCCGTTTCG CCGTGCTGCC CATCCTCACG TTCACCAGCA | 120 |
| TGCCCCACCT CATGCAGGAG TTTGCCAATG GCCTGCTGAA CAAGGTCGTC ACCTCTTCCA | 180 |
| TCATGGTGCT AGTCTGCGCC ATCAACCTCT TACTTCGTGG TCAGCTATCT GCCCAGCCTG | 240 |
| CCCCACCCTG GNCTACTTCG GCCTTGCAGC CTTGCTGGCC GCAGNNTACC TGGGCCTTAG | 300 |
| NACCTNACCT GGT | 313 |

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

| | |
|---|-----|
| GGCACGAGAG AGAAAATCAT CAAAGAAGAT TCTTTGGGGA TCCTCTTCCC TTTTAGAGAC | 60 |
| CGGGGTAAAT TTAAAAACAC TGCTTGTAAC ATTTGTGGCA AAACATTTGC TTGTNAGAGT | 120 |
| GCCTTGGNAC ATTCACTATA GAAGTCATAC CAAAGAGAGA CCATTTATTT GGCACAGTTT | 180 |
| GCAATCGTGG CTTTTCCACA AAGGGTAATT TGAAGCAGCA CATGTTGACA CATCAGATGC | 240 |
| GAGGTNCTGC CATCCCAGCT CTTTGAGCCC AGTTCCAACC TTGGCCCCAN TCAGAACTTC | 300 |
| AGCGGTGATT TCCCGNCAAN TCGTTGTTCA TCTCTTCATT CAAGACAGAG GGTCCAACGG | 360 |

GNTTTCGTGG CCAGTTTTTT TCCNCCAGGG CCCGTTAAAG GGCCANCCCC CA

412

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

| | |
|---|-----|
| TTGTGCCCCG CTGGGATTGT NATGGGTTGC CCATTGAAAT AAAAGTATTA TCAGAACTTG | 60 |
| GTAGAGAAGC TCAGAATCTT TCAGCTATGG AAATTAGAAA GAAAGCTAGG ATCATTTGCT | 120 |
| AAAGCAGCCA TTGAGAAACA GAAATCAGCA TTTATTCGTT GGGGAATAAT GGCAGATTGG | 180 |
| GAATGAATTG CTACTATACA TTTGAATGGG AAGTATGAAG CCAAACAGTT GAGAACTTTT | 240 |
| TACCAAATGT GATGATAAGG GCTTGGTTTT ATCGATCTTG ACAAACCTGT GTTTTGGNTC | 300 |
| TCCGTTTCATC TGAGGACTGN CATTGGGCTG GAAGCCAGGA ACTNGNAATN | 350 |

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

| | |
|--|-----|
| GGCACGAGCC AAAGGCCATG TACTCTGCGG GCAGGATGTG GAGAGGGGCA CATTTCAGTNA | 60 |
| CCGGCACCAT GTTCTCCATG ACCAGGAGGT TGACCGCAGA CGTGTGTNCC TATAANTCAT | 120 |
| CTCTGGCCTG ACCAGGCCCC GTACACCGTG TGCAANAGCT CCCTCTCGGA GTACGGAGTC | 180 |
| CTGGGCTTTA AGCTGGGCTA TGCCATGGCC AGCCCCAATG CCCTGGTCCT CTGGNAGGCC | 240 |
| CAGTTTGGGG ACTTCCACAA CACGGCCCAG TGCATCATCG ACCATTTCATC AGCACCGGCC | 300 |
| AGGCCAATGG GTGCGGCATA ATGGCATTTGT GCTGCTGTTG CCCCCTGGGA TGGAAGGCAT | 360 |
| GGGCCCAGNG CATTTTTNAN GAAGGCCNNA AGTTTCTGCA GT | 402 |

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

| | |
|--|-----|
| GGCAGAGCCT CTCCGCACCA CCTCAGCGGG CAGGAGGTCC CACCATGTGN ACAGACATAG | 60 |
| CCCAAGGAGG CACCACAGGT CTATGTGTGC TGGGGGATGT NAGGTGCCAC CCAACGCTGT | 120 |
| CCTGGTGGTA TTTACAATGA ACATCCTCCT CCTCCATCAC TCCAGGGGTG GTGTCTCGGC | 180 |
| CGCCCCCTACC AGCTGGCTGA GCCCCCTGGC CTCCTGCGNT TCCCTCACTT CCCTCAGTTC | 240 |
| CCAAAGCTGC CCAGTCCATG GGGGACAGAA CCGTNACTCA GANTCCACAT TCAAGTGTGG | 300 |
| CCCACCCTGC AGTCTTCATC CTTTCATTCAG CTGCTGCCTT NTGGAGGTGN CTTTGGGGCC | 360 |
| ACATGTGCTG TGGTGTGTTGT TTTCTNGGA CAGGAGNCTT TTCCANCAGN AGGTTGGGTT | 420 |
| CCANGGGTGC GTTTGAAATT CTTCTTTGG GANCTTGGTT TTCCGGNGAA CTTTCTTTGG | 480 |
| GGCCTGTTTA AGAAGGTGGT GCNG | 504 |

(2) INFORMATION FOR SEQ ID NO:768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

| | |
|---|-----|
| GGCANAGCAA AGAGAGAAGG TCGGGTACTT CAAGAAGAAA TGAAAGAAGG GACAGACATG | 60 |
| TTCATCATCA AGGCTGTNCT GCCTGTTGCT GAANCTTTGG TTTTCCTGAT GAAATCAGNA | 120 |
| AGAGGACAAG TGGCCTGGCC AGCCCACAAC TAGTATTCAG CCATTGGGAG ATCATTCCCA | 180 |
| GTGAACCCCT TCTGGGTGCC AANNACTGAG GAGGAATACT TGCACTTTGG GGAGAAGGCT | 240 |
| GACTCTGAGA ACCAAGCCCG GAAGTACATG AACGCATACG GAAAGCGGAA GGGGNTTTTA | 300 |
| TGTTGGAAGA AAAGNTTTTG GGGCATNCCA GAAAAAGCCA GGGGNCCCTT NGGCAAAATT | 360 |

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

| | |
|---|-----|
| GGCAGAGGCT CCAACGGCTT CTCAGACCCC TACGTCAAGA TCTACCTGCT GCCTGACCGC | 60 |
| AAGAAAAAGT TTCAGACCAA GGTGCACAGG AAGACCCTGA ACCCCGTNTT CAATGAGACG | 120 |
| TTTCAATTCT CGGTGCCCCT GGCCGAGCTG GCCCAACGCA AACTGCACTT CAGCGTCTAT | 180 |
| GAACTTTGAA CCGCTTCTCG CGNCAGGACC TCATCGGNCA GGTGGTGCTG GACAACCTCC | 240 |
| TGGAGCTGGT CCGAGCAGCC CCCTGACCGN CCGNTCTGGA GGGGACATCG TGGAGGGCGG | 300 |
| CTTCGGGAAA AAGCAGATCT TGGGGAGCTT CNNCTTNTGC ACTNTGGTTA CCTNCCCAAG | 360 |
| GGCCGGGGGG CTTCACCTGG A | 381 |

(2) INFORMATION FOR SEQ ID NO:770:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

| | |
|--|-----|
| GGCAGAGNAG CAGGCACTGG NGGAGGGGGC TTNAAGGAGG GAGTGCCCCC TCAAACCTCCC | 60 |
| TGCTTCCCTG GANCTTCAGG NAAGCTCAGC CTCAGCCTTC AGGCCTGAGC AAGTGCAGGG | 120 |
| CGGANTAACC AGCCCAGGTT CAGATGTTGG GGTGTGAAAG CCTCAAGTGA ACTCAGCCTG | 180 |
| GTTGGAGAAC TGCCCCACCC AGTATCTTCT GTGCCATGGT TCCCACATTC GCACTCCATG | 240 |
| GCCTCCTGTC CTGGNACCCC ACGTTTTGNA ANGTAACCCC TAGGNACCAT GGGATTACCT | 300 |
| CTGTGAATTC ACGNTTGAGC CCAAGTTCCC CACAATGGAA AACTGGGGAA ATGGCCAGTT | 360 |
| GTGTGTTCCC AGGAATTNCT TCCCTTANTG TTNCCTTGAA GTGCCCAGC ATGTAGGGCA | 420 |
| AGAAGGAAGG TTGAAGCGTT TTCCTAGNG GAATTTTTCC TTCAGGGGGG CTCNATTTTT | 480 |
| GNCCAT | 486 |

(2) INFORMATION FOR SEQ ID NO:771:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

| | |
|---|-----|
| GGCAGAGNCA ACGNGNGNCT TCCTGGAGAG CAGCAACAGC ACGGACTACA TTGCCATGCA | 60 |
| CGACGTTGAC CTGCTCCCTC TNANCGAGGA GNTGGACTAT GGCTTTCCTG AGGCTGGGNC | 120 |

| | |
|--|-----|
| CTTTCACGTG GCCTTCCCGG AGCTCNACCC TCTCTACCAC TACAAGACCT ATGTCGGCGG | 180 |
| CATCCTGCTG CTCTCCAAGC AGACTNACCG GCTGTGCAAT GGGATGTCCA ACCGCTTCTG | 240 |
| GGGCTGGGGC CGCGAAGGAC GGACGAGTTC TACCGGGGGC ATTAAAGGGA GCTGGGNTTC | 300 |
| AGCTTTTTTTT CCGCCCCTCG GGGAATTCAC AACTGGGTNA CAAGACATTT TCGCCAACTG | 360 |
| NCACGANCCA GNCTGNTGGA AGAGGGACCA GAAGCGCATT GNAGTTCAAA AACAGGNGCA | 420 |
| GTTTCAAGGT GGACAGGTNG GGAAGGCTGA ACATNTTAAG TTACCATGTT GGTTTTCCGG | 480 |
| ATTGCCTGTT | 490 |

(2) INFORMATION FOR SEQ ID NO:772:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

| | |
|---|-----|
| GTGTGGGGTG CCGNGGTGAC CGNAGNCAAA NAGGNGGTTG TGGCTCAGTG CATCCACTCT | 60 |
| GGGAGAGCGT GGACCTGGTT CCTGGGGGCG ATCGACAGTC ACNMNTNAAC ATTCCGTGGA | 120 |
| GGGACAGTGT TTATGATCCC GGCTTAAAC CACTGACCAT CTCTTATGAC CCNGCCACGT | 180 |
| GCCTCCACGT CTGGAATAAT GGGTACTCTT TCCTCGTGGA ATTTGAAGAT TCTACAGATA | 240 |
| AATCAGCTGC ACTTAGTGNA TTGGAACGCA NCAAAATTGA AAACTTTGAG GATGCAGCAC | 300 |
| TGGAAGAAAA TGGTTTGGCT GTGATAGGAG TATTTTAA GATTTCGGGA AACTTCTGGC | 360 |
| AGCCAGTGT CTACTGGAAG GCCCAAGCCG NTTGCCAGAA AGTGGGGCCC GCCCAAAAAG | 420 |
| ACTGGGTTTT GCAGTCCAGG CCTTNCTNAG TTNCCAGTNC CAGGGAA | 467 |

(2) INFORMATION FOR SEQ ID NO:773:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

| | |
|--|----|
| AGGCACGCAG CCTACTAGGT GTGGCGGCGA CCCTGGCCCC GGGTCCCGT GGCTACCNGG | 60 |
| NGCGGCNGCN CCCN | 74 |

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

| | |
|---|-----|
| ANACCACCTG TGGTCTCACT AACCCCAAAA CTGCGCTCNA CCCGGCTGCN TCCAGGGTCT | 60 |
| CTAGTCCCCC CACTAGAGAC TGANAAGTTG CCTCGCAAAC NAGCAGGGGC CCCATTTGGT | 120 |
| GGGAGTCCTG GGCTGGCAAA GCGGGGCCGC CTACAGCCCC CAANTCCCCT GGGGCCTGAG | 180 |
| GGTTCANTAG AGGAGTNTNA GGCTGAAGCC TTAGGTGAGT TAGGAGGAAG GGGATGGGAC | 240 |
| CCCACGGCCG ACNTCCTGGC CCCCGNCGGC TTGTTGGGAC CACCAACCAA GGGGACCAGC | 300 |
| GNATCCTTGG CAGAAGNCC CTTCTTCCT TGGTTGNCC TGTTTTTAAN TCAAAAGGGG | 360 |
| CCNAAGGCAA | 370 |

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

| | |
|---|-----|
| GGCAGAGCGA ATTTGTATGA NATTAGCCGG CCGTGGATTC ANAATCGCTC TTTGTGTGAT | 60 |
| GGGTCCCAGG GGTTCCTTTT NACCACAGAG CCAGCCTGAA ACTACCCACG GGTGCTGTGG | 120 |
| ACCCCTTGAA TCATGGCGGG ATGGAAATGG GCTGTGCCTN CAGCCGGGNA CTCAGGACTG | 180 |
| NAGCATGTNT GGGCAGCAGC CTGGTAAGCT GGCCAGCCTC GCGCCCTTG GGGACAGCCC | 240 |
| TTGAANACTC TGGCTTCGGT GCCCTGAGTG AGGGGGCGCC ACCCTGGGCT TCCCTGGGAT | 300 |
| GCGAGCAAGA CCCAAGNCAG GNTGNTGGAA CCGGGACAAT TCGNGTCATG TTGCTGTTGT | 360 |
| NCCCTTCCTG | 370 |

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 521 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

| | |
|---|-----|
| ATCCCCCGGG NCTGCAGGAA TTCGGNACGA GAGTTAAACA CTTNATTTCC TCCCAACAAC | 60 |
| ACTAGAGCGT TGGCNATNAT AACCCCCATT TAATGGATTA GGAAACCAAG GAACCATGAA | 120 |
| ATTAAAAAAC TTGCCCCAGG ACATACAGCT AGGTTTTCCC AGGTCCTGCT GCAAGGAGGC | 180 |
| GGCCAGGTCC TGCTCGGTTG GACACTCCAT TACTTCCCGT TTTTCCTGAT GGGCCGGGTC | 240 |
| CTCTACTTCC ACCACTACTT CCCAGCCATG CTCTTTTCAA AGCATGTTGA CAGGNCTTCT | 300 |
| TTGGGNACAC CCTCCTGAGG GCTCTTTGCC CTGGNGCTT GGNCTCCATG GGCCCCTGGG | 360 |
| CGAAGGGGGC ATTNACANTG GCGGGGGGAN TCCTGANGCC NGNTTCCTGG GGGAAGTNC | 420 |
| CTNACAGTTT TTAAACNTTT TNCCAACCTT TGGGTTTTAN GGGGATGGTT TGGTNCCCTG | 480 |
| GGGCCCAGGA CCCCCCAAAT TCCCATGGGN AGGACTAAGG T | 521 |

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

| | |
|---|-----|
| TATCCATAGA TTCAGTGCAA TTCCAATAAA ATCCAGCAG GCATTGTTGA AGAAAATGAA | 60 |
| CAAGCTTATT TNCAAATTCA CGTGGAAATG CAAAGAAGCC AAATTAGTCA AAACGGATTT | 120 |
| GAAAAAAAC AAAGTAGTGA CTTAACGTTT ACCTGACTTT AAGNATATAT TATNAAACCT | 180 |
| ACCTTACTCA AAACAGTATA GTAGTCATAT AAAAGATAAT GGGAACAGNN TTAGAGAACC | 240 |
| TAGAGGTAGG ACCCGGCACA ATTATGGACA ACTGCTTTTC CAACAAGGGT GCCAAAGGCA | 300 |
| TTCCGTGGGA AAAAGGAAAG TTTTTTCCAA CAATGGGTNT TCCTNTGTAA AATGGACNTT | 360 |
| AAATTCCTTC CCCTGTNTTT TNGGCCAAAT TGNCCTTACT GGGGTTTTCG GTCTAATGTA | 420 |
| AACCNCAATT TTAAGTTCCT TGGGGAAAGG AACGTNGGGG AACCTTGTTN CCCGGGNTTG | 480 |
| GGGNACGTTT TAGGTTTGGG TCCA | 504 |

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

| | |
|---|-----|
| AGGGGCTTGT TTTTATAT AGTGTGTTT GGGGAGGGG GACGCGGGAG GNTGCATGTT | 60 |
| TTGGGAAAAG GGGGTGACAG ACAACTTTTA AAAGGGCAGC ANACTCCCTC AGCCATGAGA | 120 |
| AACCAGCTTT GGGGAGGAAG GCCGGGAAAT CAAAGCGAAG TCCAGTTAAT CTCCCCTGAA | 180 |
| CANTTTGGGA AGTTCATTTT NCCCTCANTG CCAGCCAAAT CCGGGCANGA CCCTCGAAAG | 240 |
| AAGNACCGAG GGTCCCAAAG GACCAATGCT ACAACCAGCA AATGCTGCCA CATCTTTNNN | 300 |
| CTGATTGGGG GGTNGGGGAT GGGTTGGGG GGATTGGGAC TNGGGGCCAA AGGGTTCCTGG | 360 |
| GGTGGGGCCA TTTTAAAC TTTGGNGGN CTTTCCATT TTTTGGTTN AGGGCCAT | 418 |

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

| | |
|---|-----|
| GGGCACACGT GGAGCTNAAC TTAANGCCAG CGGGGAGNCG GGGAGGCACT GCCCTCATTN | 60 |
| TTGCANTNCC TTNATTCTTT TGAGGGCACT GCCAGCCCGG GAACCACTCA ATCTNCTTNT | 120 |
| GGTTGAAAGG TTTGGTTCAG GAAGGNTGGT CTCCTGGTTC CCNTTGGGGT GCTTAATGAT | 180 |
| GCACTTNAGG GGCTTGCNAG GGGTGAAAGT CCTTGNAGGC CCTGATNGGT CCAGCTTNTC | 240 |
| CACAGGGTGA TNNTTGTTGT AGTCNAGCCG GGTCAGCAAN GTTNAGAGGC AGCAGGCCCT | 300 |
| GTTTTTTNCA GGTGTTCT CTGGATCCT GGCAAAGNTT TTTGGGTGAT TGATGGCCCC | 360 |
| GGCCCCAAG TTGGCGAGNT TCAAAGCTG TATGTTCCCG GTTTNGAAAC CTTGNCCTAA | 420 |
| TTTGGTTTC CAATNACCAN CCACTGATGC CAGTTTTTTT TAATAACGGG G | 471 |

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

| | |
|---|-----|
| TTCCCGNTGT GGAGCGAGTG GACTCCTGCC CCTCCATGTA CAGCCGCTCC ATCCAGGGCC | 60 |
| ACCATGTCTG CCTCCTGGTG AAAAAGGGTG AGAACTCTGT CTNAGTCGAC GGGAAGTGCC | 120 |

| | |
|--|-----|
| AGTGAAGCTCC ACGCTNACTG AAGCAACTTG TTAGNAAGAG AATGAAGGCG AACGCTGGCC | 180 |
| AAGTGTGAA AGCTGCCTGC AAGCCCCGCA CCACCCGAG GAGCAGTNA CCCAGGGAAC | 240 |
| CGCAGCCCTG ACGTGTCTCG CCTCTCCTGN AGTCGTGTGT ACTGTTACCC ANGCCTGNNG | 300 |
| TGTTTAATTT NAACTCTAAT GTTTGTNCCG NCGTTGTTNG GACATCCGAG GGTCCATTNG | 360 |
| TTNGGGGTTT GAAATTATTC TGGAACNTC CTTTTTTAAC GTGGAATTNT TANCCCTTTC | 420 |
| TTTTTNGGGG CAAGAAGTTC CCTTTTTTGG NGCCCCAAAA CCAG | 464 |

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

| | |
|---|-----|
| AAAACGGGNA GTAAGGCAGT GGTGGAGATG GAGAGCCCTG AGCNTCCACT NTCCTGGCCC | 60 |
| CCAGTNTTCC TACATAAGGC CACGGCCCCG NTAATGGCGG GGCNAGCCC CA | 112 |

(2) INFORMATION FOR SEQ ID NO:782:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

| | |
|---|-----|
| CGNATGGCCC TGTCTNAAA ACGGGGAGTA AGGCAGTGGT GGAGATGGAG AGCCCTGAGC | 60 |
| NTCCACTNTC CTGGCCCCCA GTNTTCCTAC ATAAGGCCAC GGCCCGGNTA ATGGCGGGGG | 120 |
| CNAGCCCCA | 129 |

(2) INFORMATION FOR SEQ ID NO:783:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

| | |
|---|----|
| GGCAGGAGCA GGCACGGAGC CTNAGCCCAT CGCNATGCTG GTCCTAAGGG GCTCGTCCTN | 60 |
|---|----|

| | |
|---|-----|
| GAGGGGTCCT GATGCTGGGT GCCTGAAANA AGAGCTCGGG GAGCCCGCTG CAACCNAAG | 120 |
| GCCTGCCCAG CCGGGAAGCT GCCAACCCCC TGGTGGTGGG AAGCCGTGGC CCTCCTGGGA | 180 |
| CCTCAGCCTG GAATTCCTGT TCTCCCAGCT CCTNACCTGA GGCTANTTCC TGGCCTGGTT | 240 |
| CTGGCTTTGG TTGCNTGCCT CTTNACCCTT TTGAACCTGC CTTTTTTTTC TTCTCCTNTT | 300 |
| CCTGGGTGTN TTTTTTCCCA | 320 |

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

| | |
|--|-----|
| GGCACGAGTG GCAGCAAGCC TCTCCTGCCC TTCCAAATTA GCCCATCGAA TGGTAAGGTT | 60 |
| CCTNAACTTT GGGCAGGTNA AGANCTGTGA AGGTGGAGCA GGTAAAGGGG GTCACCTACT | 120 |
| CCCTGGAAAGT CGTTCCTGGG CCCGCTTATG TGCCACAGAG GACCTGCCCT TCCCACCAGC | 180 |
| CGNGTCGTGT GAACTCCTTC AAGAACCAGC TGGTCACCCG GGAAAGGGGA ATGAAGCCTC | 240 |
| TATTNACTGT NTTTCATCTTA CCTGGGCCCC TGGGGGACTA CCACTGGTTT NACTNCCCC | 300 |
| ACCGGACTGG NACTGTNTCC CACCGGGGGG NCAATTTTCC AGGGTTCCTG ATGTTTCANTG | 360 |
| AAAANCCTGG GNATGGGTTG GTTGGTTTCA AAGAGGTTTT TTTGNCCATA AAGGAGGNGG | 420 |
| GTTGGGTTCT T | 431 |

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

| | |
|---|-----|
| GGNANAGNCG TNAAACTAC CCCTAAAAGC CAAAATGGGA AAGGAAAAAG ACTCATATCA | 60 |
| ACATTGTCGT CATTGGNCAC GTTGTNTTCG GGCAANTCCA CCANTACTGG NCCATCTAAT | 120 |
| CT | 122 |

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

| | |
|--|-----|
| GGCACGAGAG AAGATAAAAA AGTGAGGTGG ATTAAAGGGC CCATAGAGGA AGCCACCTGA | 60 |
| ACCCCCGGCC TGGCCTCCTT NTCGGCTCTT CCTCTCCGGG GGCCCAATAG GGCTGTGCGT | 120 |
| TTAANAGGCA GTTGGGAGAC CCTGGTGGCC GGTTTTGGTC GGTCACCTGGG CACGCGGCTG | 180 |
| GAGCCAATCA GAATCTCCCG GCAGTTGGTT CCCGGGAGGC AGAATCTGTT NAACTGACA | 240 |
| AAGCCACAGT TTCCGGGTCC CTGTTTCGGG GAGTCGGGGA CTNATTGGGT CACCCCGGGT | 300 |
| TAGTTCGAGA CTTTAGACTN GAGCTGTTTT NGGTNCACTC AGGGAGGCNA GTT | 353 |

(2) INFORMATION FOR SEQ ID NO:787:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

| | |
|---|-----|
| CACGCATNCA ACAAGGGCCC CTCGTACGN CTGTCGGCCG AGGTCAAGAA CCGGCTCCTG | 60 |
| TCCAAATATG ACCCCCAGAN GGAGGCAGAG CTCCGCACCT NGTATCGNGG GANCTCACCG | 120 |
| | 120 |

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

| | |
|---|-----|
| GGCANAGAAA AGCCAAAATN GGAAAGGAAA AGACTCANAT CAACATTGGT CGTCATTGGA | 60 |
| CACGTAGATN CGGGCAAGTC CACCACTAAC TGGCCATCTN ATCTATAAAT N | 111 |

(2) INFORMATION FOR SEQ ID NO:789:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

| | |
|---|----|
| ACGATTCACA CCGTAGCCCT GGGGNAGACA NTGATTTGAT TACAAAACCA CCCAGACCTT | 60 |
| CCGGCTTGCC ATCATGNNTG TG | 82 |

(2) INFORMATION FOR SEQ ID NO:790:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

| | |
|---|-----|
| CATTCGTACG CGGGTGTGGT GTCAGTACAG CCACAGCCAG ATNCAGGAGC ACGTGANGCC | 60 |
| TGCNCANCCC AGCATCCGNG AACGTGCAGG AGCTCAAGGA AGCCATCAAG AGCCTGCATT | 120 |
| GGAT | 124 |

(2) INFORMATION FOR SEQ ID NO:791:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

| | |
|---|-----|
| GGCANAGTGA GTGACCGGCC TTTNAAGTGC GGCTACTGTG GTCGTGCCTT TGCCGGGGCC | 60 |
| ACCACCCTCA ACAACCACAT CCGAACCCAC ACTGGAGAAA AGCCCTTCAA GTGCGAGAGG | 120 |
| TGTGAGAGGA GCTTCACGCN GGCCACCCAG CTGAGCCGAC ACCAGCGGAT GCCCAATGAG | 180 |
| TGCAAGCCAN TAACTGAGAA GCCCAGAATC AATCGAAGTG GGATTAACGG GNTTGACTGG | 240 |
| TTGGNATTAA AACTGCAGGA GAAGTCCATG NTTNAA | 276 |

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

| | |
|---|-----|
| AAGACCGGNC TTCNTAATAA NCTTAATTAA TTCCCCCGGN AATGTGGATT TTTCCTNGGA | 60 |
| AGGACGAGCA GGAGCTTTGC ATCACCATCA AGTAAACTGC AATCTCCTTT TTTTANGAAN | 120 |
| NTCTGGGAGG AATGAATTTG AACTTAATNA AGCAGNACAC G | 161 |

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

| | |
|---|-----|
| GGAGAACCAC GTGGNACAGC ACCATGAACA TTTTGGGCGG GGNAGGCAGT NCTGGCCGGT | 60 |
| AAGCCCCTCA AGTCGGGTAT GAAGGAGCTG GCCGTNTTCC GGAAGAAGG TCACTGAGCC | 120 |
| AGCACCGGCA GATGGGCCAA GGNTGGCAAG CATCACCTTG GCCTGGAGNT AGCCCAANAA | 180 |
| GCTNCGAACC ACCCCCTGCN AGGACTCCCT GGCCAACAGG GAACTGG | 227 |

(2) INFORMATION FOR SEQ ID NO:794:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

| | |
|---|-----|
| GGCANAGCTG AAACGGGCAG AAGACAAAGC AAAGCTAAAA GAGCTGGAGA AACACAAAAT | 60 |
| CCAGCTGGAG CAGGTGCAGG ANTGGAAGAG CAAAATGCAG GAGCAGCAGG CCGACCTGCA | 120 |
| GCGNCGCCTC AAGGAGGCAG GAAAGGTAAG CCAAGGNAGG CGCTGGAGGC AAAGGAAACG | 180 |
| CTATATGGAG GAGATGGCTG GATACTNGCT GATGCCATTG AGAATGGCCC ACTTTGGGAC | 240 |
| AAGGGAGATT GGCTTGAAGA GCGGGGTNGA GTTCCCTNGC ANGCAAGGGA GGTGGGAGGG | 300 |
| CACTTNN | 307 |

(2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

| | |
|---|-----|
| GGCAGANNCT TTGGATGACA ACGTCTGCAT GGCCTTTCCA GGTCTNCACC GCCGATGCAA | 60 |
| GGNTAGTNAT CAACAGGGCC CGGGTGGAGT NCCAGACCCA CCGGCTGACT GTGGAGGACC | 120 |
| CGGTCACTGT GGAGTACATC ACCCGNTACA TCGCCAGTTT GAAGCAGCGT TATACGCAGA | 180 |
| GCAATGGGCG CAGGCCGTTT GGNATCTNTG CCCCTCATCG TGGGTTTCGA ACTTTGAATG | 240 |
| GCGCTCCTAG GCTTNTATNA GACTGACCCC TTCGGGGCAC ATAACCATGC NTGGTAAGCC | 300 |
| ANATGCCATA GGCCGGGGGG TGCCAAGTTC AGTGCGTGAG TTNCCTGGNN GAAGGAATTA | 360 |
| TAT | 363 |

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

| | |
|---|-----|
| GGCANAGNCT CAAACAGTGC AAGATGTCTC TAAACGGGCA GCGTGGNGGA GTNCTGGTGT | 60 |
| GTAAACCCCA ACACCGGGGA AGCTGATCCA GGGAGCCCCC ACCATCCGGG GGGACCCAAG | 120 |
| ATNTNAATCT CTTCTACAAT GAAGGCAGCA GGTGGCTCGC GGGGTGCACA CCCAGCGGNA | 180 |
| TGCAGTAGAA CCGCAGCCAN CCGGTGCCTG GNGCCCCTNA NCCCC | 225 |

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

| | |
|---|-----|
| AGGCACACAG GACCATAAAG GTNCTTCTCC TNAAAGGGCT GGGGGCCCTT TNCTTNCGCC | 60 |
| TATAATTGGN ATGANAACTT CAACCCGNGT AAGCACCTGG AGTTGAAGGG AGGNAGAAAC | 120 |
| CGGGCCAGCT GTCCTGTCCT CCGCCCANAG TGACCACCCC GGNTATGGCC AGCNAGCCTC | 180 |
| CNGGGAGCGA GAGTCCTGCT GAAAGGGGCC ANGNTGGTTT TGGTGAGNAG CTGGCCTATC | 240 |
| ATTAGGGNGT TTGGGCTTCC ANCTGGTNGT NAATGCCCAA CTTAGGGGTT TCCTT | 295 |

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

| | |
|--|-----|
| GGNANAGTGG ACAAATTCGN GGAGACCGCA TCAATTAAAA TCCAGATCAT TAACCGTCCG | 60 |
| GNTCCACCCC AAATTNTGAA AGATTAAAGGA TGTCTGGGGA GAAAATNTCG CTCTCANATG | 120 |
| GGNCTCCACC AAAGGAATGA TGGNAAATGC CTGCTTATCA NAGGCTTTTN CCATTNAAAA | 180 |
| GGCTGACAAA AGAGGCTGGA ATGGTTTTAC TGTNNATTGA AGCTTTNTTC AT | 232 |

(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

| | |
|--|-----|
| GGCAGAGNAT CAAATATTAT TTTATTATTT ATTTAATTAT TAATCAAATG TTTGTGTAGG | 60 |
| TCTATTTCTG GGATCTCTGT TCTATTTTCAT TAATCTTGTG TCTGCTCCTC TACCAATACC | 120 |
| ACACTGTCTT TATTACCGTC GCTATATGGT AAGCCCTGAC ATCATGGAAT TTNCTTCTNT | 180 |
| TTCATACGTT TTGGCTATTC TAGTGTCTTT CCCTTTCCAT ATAAATTTTA AAATAAGCTT | 240 |
| GTCTATGTCT ACAAAAAAAT CTTTGCTGNG NATTTTGGGG NAAGGAATTG GCATTTAAAG | 300 |
| CATCNCGGGT CATGGTGGGC TTCACGGCTG TAAATCACAG CACTTTNGGA GGGCTGAGGG | 360 |
| CAGGNAGGGT TGTTTGTGGG GCCAGGTGGG TNNTGGAACT CCCGGNT | 407 |

(2) INFORMATION FOR SEQ ID NO:800:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

| | |
|---|----|
| GGCAGAGCAA AAAGCAGGTC AGACAGGGCC AGGTTCAAGA GGTATACATC TTTAATGCTC | 60 |
|---|----|

| | |
|--|-----|
| CTCANCTTCT TGCAGACCAC AAGGACCAGG ATGACCAGGC TGTTCCTCCNG AAGATTGANT | 120 |
| ACAAACAGGA GGCAATAAAA GACAGCAAGG NGCAACTTGC CATTTNTTTG ATTAAGTNCC | 180 |
| GCATCACAGG GGCTTGAGAA AGATATCAGG GTAGTAGTAG TCGGTCCTG TTGTCACACT | 240 |
| GAGGTCAAGT GTATAATCCA TCAAGGCAGC GGGACCTGGT CACNGAGGAC ACATAAAAGA | 300 |
| CATTCCACTC CTTAAAAACA TTTTTTTTTT TTAAAAATTA GGGGGATGTT ATGGGACTGA | 360 |
| ACTGTGTNCC TCCCAATTC CAGTTTTGAG GTGCTCAACC TCCGGTGTGG GTGTGACCAT | 420 |
| TGGGGTGGGN NNGACTATTT NGGNCCTTA AAGTTGTAAT TAAGGTAA T | 471 |

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

| | |
|--|-----|
| CTGGTGGGGN TGCTGGAGAT GCCTTTGAAT GGCTTTGAAT TTTGGGNGTT GATCCTNGTG | 60 |
| ACCAGTTTTT CCCATCCCAT NNTGGCATGC GGTTCAAGTTC CTGGGACCAT GACCNTGGTA | 120 |
| AGTTTGAGGG C | 131 |

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

| | |
|---|-----|
| CTGGAATTTT AGGCCANTNA GCCCAGGGTC TGGNAACGCA AGGCCTAACA ACCCAAATTG | 60 |
| GGGCACATTT TAAGGAGGTN TNAGGAATTT TAAGTCCCGG GGACAAGGGG GGGTTACCNC | 120 |
| ACGGAAAAAT TGGTCNNTT | 139 |

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

| | |
|---|-----|
| CAATTCTCCT ACCGCCAGTG GTNTGACCAA AACGCGATTC CCAAAANTTG CGCCATGATT | 60 |
| NTCGCCGCCG ATGNANTTCA TTCCTGGCAA CGGTATTCCG GTCGATAGCN TGGTTATTGA | 120 |
| CCGCAAAATC AATCCGCTAC AGATCAAACA AGACGGTGGC AAAGNCTTNA AAACNCTGG | 180 |
| TGCTGTGGCG TAGTGATGAA GATGCGCAAA CGTNTGGTTA TGGTGAAAGA NTTCAACGAA | 240 |
| CTGTGCCACT CACACGGTCT GGTAAGCATC ATTGAGCCAT NCGTCCGTCC ACCGNGTCGT | 300 |
| GGCGATNAAT TTCGATCGGN AACAAGCGAT CATTCGATGN CCGCCAAAAA GTT | 353 |

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

| | |
|---|----|
| GGCAGAGCA GCCCCAATT TTTCCCTCCG GCCTGGGCGG CCCCTGGTCC NGGNGGCNAA | 60 |
| TGGAAGANCA AGGGACCTGC CCGGGGNC | 88 |

(2) INFORMATION FOR SEQ ID NO:805:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

| | |
|---|-----|
| TGTTGTTTTG TNGTTTCATT TTTTAAGACT CCCAGNTGGA CATNTTAATT GCTTTGCAAA | 60 |
| TNACCTGCTT CAAGGATGTG GGAATTCCT AATTNTNCT GTGAACCCTT TTNAATTCCC | 120 |
| CCACCATGCG TNTNGTGAAC ACCTTCACCA ATAACATAGT CATGTATTTC CCTGCTGCCA | 180 |
| TATTTGGTTT TTTTCCACC TCGGGGATC CTTTTTNTN ACTATNAAAA TNGGNTTCCT | 240 |
| CCATTCTGAA GGGT | 254 |

(2) INFORMATION FOR SEQ ID NO:806:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

| | |
|---|-----|
| TGGTGGCCAT CNTAGACCCC CACATCAAGG TGGACTNCGG CTACCGANTT CACGAGGAGC | 60 |
| TGNGGAACCT GGGGCTGTAT GTAAAAACCC GGAATGGCT CTAACATAA GGGCTGGTGC | 120 |
| TGGCCAGGCT CAGCTGGTTA CCCTGAACTT CACTAATCCN ACGATGAGGG CCTNGTTGGN | 180 |
| TAACATGTTN CAGNTAATG | 199 |

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

| | |
|---|-----|
| CCCANGGTGT NANCACATT GAGGAGGGTT TATTAAGTGN CCGTGGTCAT CGACCCCTTG | 60 |
| AACAAGAAGA GAGANGTGGC TCACGGCCTG AGGCCTAACC NACCGACCNT CAGTGGAGGT | 120 |
| GGCTATCGGG NTCGTCC | 137 |

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

| | |
|---|-----|
| CTCTTCAGCN TCGAGGTCAC CTCCACCTTC TTTGCAGTGC GGGNACTACT NGCGGGGGCT | 60 |
| TCTTNGGTTG CCCCCTTCAG TGGCCTTNCA TCTTCCGGGT TTTTGGGCGT CTNGGG | 116 |

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

| | |
|---|----|
| TTACCAACNT GANGCTGATT GAGTATTGNG GGAGCTTTGG TTCGGAGACA GGCAAAGGAG | 60 |
|---|----|

NCATGTTTGG TGAGNTTGGT TTTTCAGTAC TTCCAGAACC GNGANTGATT ATGGAAAGGA 120
CCTNATGGAG AAGGT 135

(2) INFORMATION FOR SEQ ID NO:810:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GGNAGAGGGC AAAGGTGCTA TTAACCACTA CGTAANACCT GTAAAGCCTG GCCGCCTTGT 60
TGTAGAGATG GGTGGNCGTT GTAAATTTAA AGAAGTNCAA GGTTTCCTTA ACCAGGTTGC 120
CCACAANTTG CCCTTCGCAG CAAAGGCTGT NAAGCCGCGG GAANTCTAGA GAAGATGCGA 180
AAAGATCAAG AGGAAAGAGA AACGTTAACA NCCAGAACCC CTGGNACATT TNAGCCGATT 240
TAGCCACTGC CCAACATNCT GGGGCTTACG GGAAAGTTAC TTGGGCCCCAT ATGAATTTGA 300
CCCACAAGGG GGAANTACTG GGGGCAAGTT NCTTACATGC CCCAAANGTG TGTAGTGNGT 360
TTTAGGGGGT TAANTGT 377

(2) INFORMATION FOR SEQ ID NO:811:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

AGGTGAAATG GATGANAATT CANTNTCCCC AAAGGCTTGT AACGANTTTA AGATCANTGG 60
CTACCCCAAA CGGGGNCAGN AAACGGAGAA GCACAAACNA AACTNAATGC NTCCAATATC 120
GAGGATCANT NTGAGANCAG AAGCCAATGT NAGTTTTGCA AGTTGGGATG TTGAGAAAGA 180
CAGCCATCTT TGNCTTTCAA TATTTCCAC GTCAGAAACA AGGTTGCGATT CCTAGGAACT 240
CCTTCCAGCT CTTACAACTN TGAACGGTTT CACAACAGAT ACTTGATCGN TTCTGGAAAT 300
GAAAGNTGGC TTCTTTAAAA TCCAACCAAA GNGGGGGGTC CGCTACCTCC ACTTTCACAA 360
GGAGGAGCCC GTGGGTGGNA NCCC 384

(2) INFORMATION FOR SEQ ID NO:812:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

| | |
|---|-----|
| CTGGGAAAAG ATTGTCAGGN CATTGCCATT AGGGAGCTAA ACAGAGCGGG CTTTACTTTN | 60 |
| TTNAACCCCTC TGNGAGATTN ACCGGCATT C TTAGTCTACT GTGAAATTCG NTGGGTCTGG | 120 |
| G | 121 |

(2) INFORMATION FOR SEQ ID NO:813:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

| | |
|--|-----|
| GGGGGCCTGA TGTGCTCACA GCNACAGTTA GTGGGAAGCT GCCTACACAG AGCATNACTT | 60 |
| TCCAAACGGA GTCCAGTGTG GCAGAGCAGG AGGCGGAGTT CCAGAGCCCC AAGTATATCT | 120 |
| TCCACAACCTT CATGGAGAGG CTCTGGGNCA TACCTGAACT ATCCAGCAGC TGCTGGAGNC | 180 |
| AAACTGTTTC CGCATCCAAT GCTGATCCAG CAGGCCCTCC GGNAACCAAG CGCTGNAATT | 240 |
| TNTCCACTTG CCTACAGCTT TGTNACGGCT CTTNACATCT TTGGTTAGTT CACCAAACCC | 300 |
| GGTTGACCCA AGAGGCAGTT TTCAAGTTTG NTTGNNGAAG GCCC | 344 |

(2) INFORMATION FOR SEQ ID NO:814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

| | |
|--|-----|
| ACCTGACTTA ATTCGTTTCGN ATACCACCTG TTTCTGTNCT TCATTTAACA CAGGAGGTCG | 60 |
| ACCAAAACGT TTCCCTGCGC CGCGGGCTCT NACTATCCCG GAATGAGTGC GTTCAAGTAA | 120 |
| AAGGTCTCGT TCAAATTCAG CGACTGCTGA AAATTACTTG CATCATCATT TTTCCTGTNG | 180 |
| GGNCTTGGTC AGGTCAATGC CCACCCCAAT GGTTAAGGCA AATGCACTGN NGATNACC | 238 |

(2) INFORMATION FOR SEQ ID NO:815:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

```
GGCANAGGGA AATNAGTTTT TGGCTAAACT TGGAACGTGC GTNATACCGC ATCCAGGAGA      60
AACGGGAGAG CCCGGAAGTT CTCCTGACTC TGGATATCTT GNAAACATGG CAAGCGCCTT      120
CCATGCCACC GTNAGTTTGT AACACTGAAC ACAGGTCTAA AACAGGCTTT GGGAAACTGT      180
GAAATGAACT ACAATCCTCT GAATGAAAGN TTTCCCTCTG AAATGGATTT GCTGTCTGCC      240
ACGGGGCTGN NACAAANTAA GACAGGCGCT TGTGTCATT TTCACACATT TNAGG          295
```

(2) INFORMATION FOR SEQ ID NO:816:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```
GGCAGANAAG GTTCTGTGGG CTGCNTTGCT GGTCACATTC CTGGNAGGAT GCACTCNAAG      60
GTGGAGCAAG CGGTGGAGAC AGAGCCGGAG CCCGAGCCTG CGCCANAACN CGNAGTGGCA      120
GAGCGGCCAG GCTGGGNAAC TGGCACTGGG TCGCTTTTGG GAATTACCTG CGNTGGGTGC      180
AGACACTGTN TNAGCCAGGT GCAGGAGGAG CTGCTTCAGC TCCCCAGGTT CACCCAGGTA      240
ACTGAGGGGC GCTGATGGGA CGNGAACCAT GTAAGGAGTT TNGAGAACCA AGTCTNNAAC      300
CAACATGGTG GAAATTCCCC GTTTTTTTAT NA          332
```

(2) INFORMATION FOR SEQ ID NO:817:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```
GGCACAGCTT GGCCTCCCAA AGTNCTGGGA TTGCGGGCTG GCTGCACGGG GGCAGGAGCC      60
TGNCTTGAT TCAAAGGTTT CTGAGAGACT CGGTCTCTGG GGCAGAGGCC TGNGCAAGGG      120
```

GACCTCGCTG GGGTGTCTCT NTTTTAGCCA CGCTNCGGTG TTTCTGGGTC CTGTAACCCA 180
CGTTTAAGCA GCCTGTGGTG CTGGTGGCAC AGGNGAAGGA AACCGAGGTC AGGGNAGCCT 240
TTGGGGGCTG CTTTGNAGGG NACAGGCAGN TCCT 274

(2) INFORMATION FOR SEQ ID NO:818:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GGCACGAGGC GGCAAGAGCT TCANCCACAG CTCGCACCTN ACCGCGCACC AGGCATNCCA 60
CCGTGGCGTG CGGCCCTACC ACTGCCTCGA CTGCGGCAAG AGCTTCAGCC GGCTGAGCCA 120
GTTCGAACCC CGGNATGCAG CTCCGCNAGA CCCCAGTTCC CACGGAGCCC CAGGNAGTTA 180
CCGTNTCCCG GAGAAAGCCC AACGAAGGAG GAGAAGGGCG CCCCGBAAGA GTNCGAGGA 240
GGGCCTGGNC CCTNAANAGT NAAGGTGGGG CAGGAAGAGC TTACCGGT 288

(2) INFORMATION FOR SEQ ID NO:819:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

GGGGCTGGAC GCANGTGCAC TAANCATGGG TGAACCCAG GGATCCATGC GGGNTCTAGT 60
GACAGGGGGT CTNGGCTTGT AGGCAAAGNC ATCCCAAAGG T 101

(2) INFORMATION FOR SEQ ID NO:820:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

CATTGNATGT GGTTACCACC TTTNGTNNAT CCACTCATCC ATCGATGGNC ACGTGGGTTG 60
NTTCCACCTT NAANCTGCTG TGAAATAGTG CAGTGTACCC TNTAAACATG GGTGTACTGA 120

AGAGCTCTTA TCAAGTGCCT TGANAACATC ACTGGAAAAT GTCCATGGGA CTCTGAAAGG 180
TTGCCANAAG AATGGCNGA GGCTCTATNA CGA 213

(2) INFORMATION FOR SEQ ID NO:821:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

GGCAGAGNCA CCCTTTCACC CTTCCCCCTA TCCAGGACAG TTTCACCGAA ACCCCGGNGC 60
CCCGGNGGTA TCCTTGAGCG GAGAGGGCGG GCGGGGAGCA GGAAGGCCGC GCTGTCGGGA 120
AGGGGCGGGG ACCTGCCCCN TTGGCCCAGG TTTTGGACAC CTGGGCGCCC CTGGCCCTTC 180
GGCAGAACAC GGTGCCGGAC AGTAAGAGGT CCAGCGGTTA GTGGGCGCGG NCGGCGGCAC 240
GTAAGGCTGG AGCCGCCTGC ATTTTCCAGC AATGAACGGC GCCCTTTTCC CCTTGCCCGC 300
AAAGGGTCTT TNCAGGNCAA CTTTCGAGGC CCTNAATGGT GGGTTTTCCC TGGTTGNTTG 360
GGGTTTNCCT GGG 373

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GGCANAGACG CGGAGAATNA GGAGGAGGAT GACGTTCTTG AAATNAACAG CAGCTTTACA 60
GCCGTTACTG GTGAACAAGA GGAGCACACT CTCCAAGAAA CAGCATTACC ACCTGTGAAA 120
TAGTAGCATC ATCGCTGCTC CCATCACGGA CCCTTCTCAG AAGTTCCCTC AATACCTACC 180
TCTTTCTGCA GAGGATAATT TAGGTCTCTT ACCTGAAAAC TGGGAGATGG CCTATACTGA 240
AAATGGAGAA GTCTATTTTA TAGAGTAAAA GTATNACCAT TATTTNTACC TNAAATCTCT 300
NCTACTCTTT GTTTTANCCT TGC 323

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

| | |
|---|-----|
| GGCANAGNCA GACGATCATC CACTCTGGAT GTCATCCAAA TGGCTTTCCA TGANTGTTTT | 60 |
| AATGCTAGAT GAAAAACGTG TTATGGTGGA TGCCAATGAA AGTTCCAATT CAAAANATGT | 120 |
| TTGAAAANGT GGGTATCACT ACCATTAAAG TTAACATTCG TAATGCCAAT TCCCTGGGAG | 180 |
| GAGGCTTCCA TTGCTGGACC TCGAATGTC CGGCGNNGNG GCACCTTACA GTCCTACTTG | 240 |
| GACTGAACAG GCCTGATGGA GCTTNTGGCT GGCCTCAGAT ACACCTNAGN AAGCTTAGGG | 300 |
| GCAAGGTTCA TTCTNTGCTT TNAAAAAGTG GCATGGAACT GTAGTGGCTT T | 351 |

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

| | |
|---|-----|
| GGCAGAGNCA AGAGCGAGTA CTCAGTCTCA AAATAAAAAA AAAAGGGTGA ATTTTGCCTG | 60 |
| ACTCTTATGG CTGTGGTTTA AAAGAATCAG AGTTTAGNTC GGGCATGGTG GCTCANCCCT | 120 |
| GGATAATCCC AGCACTTTGG GAAGGCCGAG GTGGGAAGAG CAAAACTCCG TCAAAAAAAA | 180 |
| AAAAAGGGAA AAAAAAACC CNGGNNCCNG GAAAAA | 216 |

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

| | |
|---|-----|
| AGGNNAACCC TTCGAGCAGA CCAAGTACCT GGNGGGCCCG GAGCGCGCCT TNNTCGCCTA | 60 |
| CTCGCTGGGC ATGACCGAAA GCCAGGTGAA GGTCTGGTTC CAGAACCGCC GGACCAAGTG | 120 |
| CGCAAGNGN CATNTTNGGN AGAATGGCGT CGGCCAAGAA GAAGCAGGTA NTCGGAACGC | 180 |
| CGAGAAAGCT GAAGGTGGGN GGCTCNGNAC GCGGNAGGAA CGACGGACGN AATTACAACC | 240 |
| GGCCCCCTGGN ACCCCAACCTT CGGNACGGAC GAGAAAGATT CACGCGGGCT GCTNCAGGAA | 300 |

AGCACAAAAC CCTTCGAAAC TTGGGCGCTG GTTCANCCCC TTCGGNCGGC GGTGCGGGGG 360
GNACGCCTTT NTTTAGGTAC CC 382

(2) INFORMATION FOR SEQ ID NO:826:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAAGGAAGCN GGGGACAGGN TGAAAGCAAC AACACCTTTN CAGACAGTNG ACCGGCCCCAA 60
GGACTGGTAC AAGANGATGT TTAAGCAAAT TCACATGGTG CACAAGCNGG ATGATGACAC 120
AGACATGTAT AATANTCCTT ATACATACAA TGCAGGTTTG TNCAACCCAC CCTACAGTGC 180
TTCAGTCACA CCCTGCTTGC AAAAGACCCA AAACCTNCAG GCCTTTTTTTT CAAAAAGGC 240
CANTTCCGGN CAACAGNCCC CAATTGNTTT TTTAAGGGTT 280

(2) INFORMATION FOR SEQ ID NO:827:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GGCANAGGGA AAGAAGGCAA TGATGTAGAT GAGGCTTCCG ATCAGAGCTG CAATGTTGGT 60
GTTGTTGAAG AAGACACTGA TAAGATAGCT CATGGCAATA ACCGAGAAGC TGTAGTCCGA 120
AAAATACAGG AACAAAATGA ACCCATTTNT TTTAGGGAAG AATATTGCCA AACTTGAGTA 180
TAATGATGAG GATCACGATG GTAACCAGTN AAAAATCCAA CACTCTCTAT AAGCCAGGCA 240
AAGAAATGGC TGCAGGAGTT CACACCCATC ATCTTTCATG TACTGTAGGA AGGAAAAATG 300
TGAGGCACTT GTTATGCTGA TATTCTTCCC AATTAAAATT ATTTCCCGTG TTGTGTTCAA 360
AATGTNCNGT TAGTCCTCCG TATATGGANN AGGGCTTTTT NATTATTTTG 410

(2) INFORMATION FOR SEQ ID NO:828:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

| | |
|---|-----|
| GGCANAGCGG CACGAGCGTN AAGGTGACCC TCCGACTGGA CACCCACCCT GCCATGGTCA | 60 |
| CCGTGCTGGA GATGGGGGCT GCCCGCCACT TCCTGCGCAT GCACAGCTGG CCAAGACCCG | 120 |
| GAAGGAGCGC GCACAGCTGC CTGCAGCCCA CGCTGGNAGA TCAACCCCAG GGCACGCGCT | 180 |
| TCATCCAAGA AAGCTGAATG CAGCTGCGCG CAANAAGGCC TGGGCCTGGT TCCAGCTGCT | 240 |
| GGTGGTTCCA NATATACGAG AAACGCCATG GATTGCTGCT GGGACTTGTT GGACGGACCC | 300 |
| TNGGGGCCAT GGTGGGGCCC TTTGNANTGA GCTGCTTTGT TCAAGGGCCN TGGGAGNGGA | 360 |
| CAATG | 365 |

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

| | |
|---|-----|
| GGCACGAGCT CGTCNANGGA ATCGGCGTTT ACTGGGGGCC AGGCCGTNGT TTAAATGTAG | 60 |
| GCATTAGACT TCTTGGGCGG CNGACAGACC AAAGAGCGGA AATTCATCCT GCAAAGCCAT | 120 |
| TGNAACAAGC AAAGACTCAA AACATCAATA AACTGGTTCT GTATACAGAC AGTATGTTTA | 180 |
| CGAATAAATG GTATTAAGT AACTGGGTTC AAGGTTGGAA GAAAAATGGG TGGTANGACA | 240 |
| AGTGCCAGGG AAAGAGGTGA TCCAACAAAG AGGACTTTGT GGGCACTGGN GGAGGCTTTA | 300 |
| CCNNGGGGTT GGACATTTNG TGGATGCCNG TTCCTGGTCC TTTCGGG | 347 |

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

| | |
|---|-----|
| ATGAAGTCCA GCGGCTTCCT CCGAAAAATT CTGTACANAA GGGTGGCTGT TTGGGGCANC | 60 |
| AAGTAATGCG TTNAAGGGNA GGCAGGTGGG NGTGAAGGAG | 100 |

(2) INFORMATION FOR SEQ ID NO:831:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

| | |
|---|-----|
| AGGTATGGTC AANCTGACGG CGGANTGGAT AGAGCAGGAG GCGCAGTGCA CCAACGCGGT | 60 |
| GCGCAACCGG GAAGCTGGAC CTCCGGGGGT ATAAAATTCC CGTNATTGAA AATCTCAGGT | 120 |
| GCTACGTTAG ACCANTTTGA ATGCTATTGA ATTTTNCTGN ACAATGAAGA TCANGGAAAC | 180 |
| TNGGATGGTT TTCCTTTGTT GAGAAAGACT GTAAAAACAT TGTT | 224 |

(2) INFORMATION FOR SEQ ID NO:832:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

| | |
|---|-----|
| GGCACAGCTC AGTACAACAC TGAAATTAAA CTGCCTTGTT CATGCTTTCA TGTCTCAAAT | 60 |
| CAAGGCCTAA ATGAGTAAAA AGATGATTAC AGATTACCTA AAACCCTTAA CCAGTTTTGG | 120 |
| TTTTTGAATT ATGCATATGC TGTTGGCTTG CAATTGAGGT TTTTAAGTTT CTGTTTATGT | 180 |
| GAACTTGTTT GAAAACATTG GATTCGTCTT CTCTCCACA GTTTCTACTT GNANCCTTAG | 240 |
| TTAGCTTTTT NNNGGGGG | 258 |

(2) INFORMATION FOR SEQ ID NO:833:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

| | |
|---|-----|
| TTTTCAATAT CAGACCTGAC CTATAAGAGA TGCTAAGGGG AGCTCNTTAA TCTGAAAGGA | 60 |
| AAGGACATGA GTNAGCAATA NGAAATCATC CAAAGGTACA AACTCACTG GTATCAGTGA | 120 |
| AGTNCACAAG ANCAGATTGG CTTGACACAC TAATTGCCGT GTGTAAGCCA TATTTTGAGT | 180 |
| AGGAAGACTA CAAAGCCTAT CAAAANTTAT NATTNCAATT TTTTAAGCGN TNAATATAAA | 240 |

ANGNTNAAAT AGGAAACATT GGCCGGGCCA CGGTGGCTCA CACCTGTTAA TCCCAGCANT 300
TGGGAGGCTG AGGCAGGTGG TTTCANGAGG TCCAGTNCGA GAACCANCCT GGGTTAACAC 360
GGTGAACNTC CGTTCTCCA 379

(2) INFORMATION FOR SEQ ID NO:834:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

TGAAATCACA GGCGCNTTGC TGGCCAAATT CATCAAAACC ACCATGCCTA AAACAGTGTC 60
ACACTGTNTT TCAACTTGAN TCCTTGTAAG ATAGTGATTT TTTTTTTTNN TTTTTTTTTT 120
TTTTTCCCCT TAGAAAGCAG CCTGGGCGCG GNGGCTCAGG CCTGTNAANC CTAGCGTNTT 180
GGGAGGCCNA GGTGGGCAGT TTGTTTGAGC TCAGGGGTTC GAGACCNGCC TGGGTAAACNT 240
GGGCAAAACC CCANCTTTAC TAAAAATACA AAAATTGGCC GGGCGTGGTG GCGCTGTCCG 300
TNANACCC 308

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GGCACGAGCT CGTCCNTNCA ACGACTGCAA TATGGCGCGT CAGTGCGAGG CAGCATCCTC 60
AGCCTCTCGC TCTTGCGGGC GCCTAAAGCC CCGGACGCTA CTGCTGACAC GGGGCGCCAC 120
GAGTTCACCT ATGCACTGAT GCCGCACAAG GGCTCTTTCC AGGATGCTGG CGTTATCCAA 180
GCTGCCTACA GCCTTAAACT TCCCCCTGTT GGCTCTGCCA GCCCCAGCC CAGCGCCCGC 240
CACCTCCTGG GAGTGCCTTT TCCGTGTCTT CACCCGCGGT CGTATTGGAG ACCGTCAAGC 300
AGGCGGAGAG CAGCCCCCAG CGGCCGTTTC TTGGTCCTGA GGNTGTTATG AGGNCCAAGG 360
GCAACCAAGT TGGGATTNGT TGGGNTGNAA 390

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

| | |
|---|-----|
| GGCACGAGCC TACACAGAGT GCTGCTGCCT GTATNGAGAG GCCTNNGGCA TGGNCTGCGC | 60 |
| CCTCTGCCCT GCGCAGGACT CAGATGACTT CGAGGCCCTG TGCAATGTGC TACGCCCCC | 120 |
| CGCATATAGC CCCCCGCGAC CAGGTGGCTT TGGACTCCCC TACGAGTACG GCCCAGACTT | 180 |
| AGGTCCACCT TACCAGGGCC TCCCATATGG GGCTNAGTTG TACCCACCAC CTGCGCTACC | 240 |
| CTACGACCCC TACCNACCGC CACCTGGGNC CTTGNC CGGAGGNTC CTTATGGGGC | 300 |
| AACCCGNTTC GACATTGCCA GACTTTGAGG ACGATGGT | 338 |

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

| | |
|---|-----|
| GGCACGAGAA AAAAAGATAC CCAGATTCCA AGGACCTCAC GATGGTGCTG AAAACCTATG | 60 |
| ACACCAGCTT CCTGGACTTT CTCAGAAGGT GTTTGGTATG GGAACCTTCT CTTGCGATGA | 120 |
| CCCCGGACCA GGCCCTCAAG CATGCTTGA TTCATCAGTC TCGGAACCTC AAGCCACAGC | 180 |
| CCAGGCCCCA GACCCTGAGG AAATCCAATT CCTTTTCCC CTCTGAGACA AGGAAGGACA | 240 |
| AGGTTCAAGG CTGTCATCAC TCGAGCAGAA AAGCAGATGA GATCACCAA GAGACTACAG | 300 |
| AGAAAACAAA AGATTAGCCC CACGAAGCAT GTTCAGCATT CAGGTGATCA GCAGGACTGT | 360 |
| TTCCAGCACG GAGCTTGACA CTGTTNAGCT GCCTCAACTT GGTAGACGGT CCAAGGAAG | 420 |
| TCAGAGGCAG TTGTCGGGGG CGGAGGTGT NCATGACCTT CCCAGGGCAG NGCAAAAATT | 480 |
| TTTCCTTCAA GGACACA | 497 |

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

| | |
|---|-----|
| GGCACGAGGC AGGGTGCCTG TNATTCACTG TGTTATTTGG TTTAAATCAA AGTGATTCTG | 60 |
| GGGGAAGCTA TGCTCTTTCA GTGGATAATA AAATTGGTAA CTCTATTGTA AAACATGTCA | 120 |
| ATGGTGTGTG AAGAAAAATC AACCAATCTG TAGGTGTTGA TAACTAGACA GTACTGTGTA | 180 |
| TGTNACGTGC CTGTNTGGGA TGTNCACTTC CAGCATGGTA TGTGTTAGCG ATGTGGNTCA | 240 |
| TGCCCAGAGN TCGTAGATCC TGTTTTGGGG TTGTCACATG GATCGTATGT TAAGCTNTTT | 300 |
| NCTTTTNCAT TAAATGAATT TT | 322 |

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

| | |
|---|-----|
| AGTACATTCA AATGTGGGCA NCTCANGGCC AGAAATTCCT GTTCNCCCTG AGCCAGCATA | 60 |
| TCAACTGGGT NCGCTGTGCC AAGTTCTNCC CCGACGGCGG CTCATCGGGT CTGCCATTAA | 120 |
| TGACAGGNCT GTTAANGCTG TGGGGACAAG AGCCAGCCGG GAAATTTTTC CACTGGNNTT | 180 |
| NTAGGCATGG GGG | 193 |

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

| | |
|---|-----|
| GGCAGAGAAG ACTTCAACTC TNTCGGATGC TCAACCTCAC TGACCGGCAA GTNAAAATCT | 60 |
| GGTTCCAGAA TCGCAGGATG AAAGAAAAGA AACTGAACAG AGACCGTCTG CAGTATTTCA | 120 |
| CTGGGAAACC CCTTATTTTG AAGAGCTCCA GGTAAGCGCC CTCACCCAG CCCCCTCAC | 180 |
| CCACCCTCCT TCCCACCAGC CTGCTCTCCG CAGCCCCACT GTCCCTTGGG TTTAATGAAC | 240 |
| GTCTCTTCTT CTGTGGGAAT TTCACGATTC CTTCCCACGG TCAACTCGGG GACCTTCCCA | 300 |
| GCGNACCATT GCAGCCTGCG GGANGAGGCC GGGGANTTGG CCGAGNNGGG TTCNTANTAA | 360 |
| GGGGGGAAAA TTGGGGGCCT GGGAGATTCC ACAAGGAGGG GCGGGGTTNA AGNTTNCCAA | 420 |

AAGNCCGGGT TTTTNANCCA ANAGNCCGG GTTACCTTTT TTTTNCCAA AATGGGTTTT 480
TNATTAGGGG G 491

(2) INFORMATION FOR SEQ ID NO:841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

CGGAAANTNT GGGTNCCCCG GGNCTGCAGG AATTCGGCAN AGGGGTACTG AACGCGGTTC 60
TGGGAGCAGC AAGCCCACGG GTAGCAGCCG AGGCCCCAGA ATGGCCAAGT TTCTTTCCCA 120
AGACCAAATT AATGAGTACA AGGAATGCTT CTCCCTGTAT GACAAGCAGC AGAGGGGGAA 180
GATAAAAGCC ACCGNCCTCA TGGTGGCCAT GAGGTGCCTG GGGGCCAGCC CGACGCCAAG 240
GGAGGTGCAG CGGCACTGGC AGACCCACGG GNATTAGACG GAAATGGAGA GCTGGGATTT 300
NTCCACTTTT CTGTACCATT ATGCACATGG CAAATANAAC AAGAAGACCC AAAGGAAAGA 360
AATTNTTCT AGGCCCATGT TTTGGATGGG TGGGGACCAA GGGAGGAAGG ANAAGGGTTT 420
AACGGTTCAT GGGNGTTCC GAACCCTGGC GGNTTCCAAA AAANACTTNA ACGGGGGTTC 480
TTTGGGGGG 489

(2) INFORMATION FOR SEQ ID NO:842:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GGCAGAGNAA GGAGCCCACC TGGAATTCT GGAAGTACCT AGTAGCCCCA GATGGAAAGG 60
TGGTAGGGGC TTGGGACCCA ACTGTGTCAG TGGAGGAGGT CAGACCCAG ATCACAGCGC 120
TCGTGAAGGT AAGCTCATCC TACTGAAGCG AAGAAGACTT ATNAACCACC GCGTCTCCTC 180
CTCCACCACC TTCATCCCGC CCACCTGTGT GGGGCTGGAC CAATGGCAAA CTTCAAATGG 240
GTGCTTTCAA AGGGGAGGAG ACCCACTGGA CTCTCCTTTC CTTGACTTC TTNATGGCCA 300
TTGGGTCCC CATNATTTCT TTGTGGGGGG GAAAAATTC TTAGTNATTT TTGGATTNAA 360
TTTTTGAAA TTCTTTTAAC CAGGCAAACC AAAATTAGGG GGAAACTTNC CCTNGGGGGN 420

CCCAAT

426

(2) INFORMATION FOR SEQ ID NO:843:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

| | |
|---|-----|
| GGCAGAGGNN ACATCTCCGC CAGCAAGATG GAGAAGGCGG CACANCGNAG GGCCAGGGCC | 60 |
| ACGGCATCCA AAGCCACACG CTGCATCAGC CTGGGCTCTG GGACCTGAGG GGGCATGAAA | 120 |
| CCCGTGGGGA TGTCGCCAGC CACGCTCGAG CCAAAGNGCT TGTGGAGCTG NCCGAAGTGC | 180 |
| GACACGAGTN TGGCCACCAC GATNTACCAG CAGCTCCGTG GGNAGCGGCA CCCTCAGGCG | 240 |
| GTGTCGGTAG CGGTCTGAGA GCTTCTTCGC GGCTNGCAGC ACCGCCAGCA CACCGTGNTG | 300 |
| GTGGACCACG TCGCACAAGT TGGCCTGCCC GGTGCCNGCA AAAGTTTCAG CCATGTNAAG | 360 |
| GACCACCATG NCGGGNCCTT GTTGCC | 386 |

(2) INFORMATION FOR SEQ ID NO:844:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

| | |
|---|-----|
| TGGCACGNAA NTGGAGAGCC GGCAGCCAGG CAAGGCCACT GAATTGCCNG GGAGCCGGGG | 60 |
| NCCAATTCCA CNAACACCAG CCCAACTGA AAGTCCCTCT TCCTTCCCCT GNCTGGNGCT | 120 |
| GCTCCGCCCT | 130 |

(2) INFORMATION FOR SEQ ID NO:845:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

| | |
|---|----|
| GGCACANTGA ATGATCCTGG GGGAGCNTTT GNCCACCCAG GGCCCTTATA ATTTTGGNTC | 60 |
|---|----|

GGGGGAAACG GCCCGCGGCA TACAGGACCT CATCCCGGTC CTGCTGCGGC ACNGTCTGTT 120
TCCCCACCC AAGGAGACCT ATGCCCTGCA CCGNAAGCNG GCAGGGGCTT TCNTGGCCTN 180
T 181

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GGCTGNGTAG GGAACAGAGG AGGCCGAAAT CCCTCCCCCA TGATTCCTCA ACCNTTGTTG 60
GNCAANGGCA TCTTTNATGG GTACAAGGGA GAGGCTTCTG GAAGAAGCTC CCTGNACACA 120
NTACAGGTGC CCTTTTCCAA GGGCAAGAGN ANTTTGGGCT TCCATGG 167

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GGCANAGCTC GAGGCTGTGA ATGCTCACAC AGCGCCTGGG AAAGGGGATN AACTCAGAGN 60
TGCCTTTTTG GGTACTTTT GTNCTGAGGT AAGAGAGGGC AGCAAGTGA CCCCATGGG 120
CTGCAGAAGC CGGTTCCGAN CAGGGACTGN TTACATAAGT TTTGGCAGTG AACCCCGGTG 180
AAGTNTGGTG TTCCTTATGA AACCTGCTT TCCACAGTTG AGCAGAAGAC ACCACAAATN 240
AAGNAGGGNA GCCCTCCCT TCACTGNAGT GGGAGTNTTC AATGGGGACG TTTGTGAACT 300
CTGCCCTTGG GGACAATTTG TGACTGCTTT T 331

(2) INFORMATION FOR SEQ ID NO:848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

| | |
|---|-----|
| TTAGAGTAGA GATGTAGCTT GANATTTTGA GAGGCTGAGG TGGAAGGATT NCTTGAGCTC | 60 |
| AGGANTTTAA AACCAGCCTG GGCAACATAG TGAGATGTTG TCTNNANTAA AAAAAAAAAA | 120 |
| AAAAAAAAAA AAAA | 134 |

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

| | |
|--|-----|
| GAGCCCTTNA ATCTAACTTC GAAGCCCTCG GACTACGCTC TGGACCTNAG CACTTTCCTC | 60 |
| CAGCAACACC CGGNGCCTT CTAACTGTG AACTCCCCGC ACTCCCCAAA AAGANTCCGA | 120 |
| AAAAACCACA AAGNAAACAC CAGGGCGTAC CTGNTCGCCG AAGAGCTAAT GCCCCAAC TG | 180 |
| GGAACTTCCG AGGTCAACTT GNAACTN | 207 |

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

| | |
|--|-----|
| GGCANAGGAG AAAGCAGCAT CAGGTAGACT ACATTCTTAA AACCTGGACC CCTCCTNAGG | 60 |
| TCCTTAAGGA TTACTACGCG GNAGGCTGGC ATCATCACGA CAAAGAATGG GCGGCCCCCTC | 120 |
| TACGTGCTCA GGCTGGGGCA GATGGACACC AAAGGCTTGG TGAGAAGCGC CTCGGGGAGG | 180 |
| TAAGCCCTGC TGAGAATTAC GTTCTCTCCA TAAATGAAAG AAGGGGCTAA GGCGAATGCG | 240 |
| AAAGAGGAAT TACAAAANTT TTTGGTCGGC CTATTCAGCT TCATGGGACC TGCCTGGTGG | 300 |
| GACTTGGGAA GGGCTGAACA TGCGCCCACT TTTGGGAGGA CCTGGTTTNA AAAGNCCTNT | 360 |
| TGGGGATTCA TCNNGGTT | 378 |

(2) INFORMATION FOR SEQ ID NO:851:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

| | |
|---|-----|
| TCTAGTGCTG ACTGGTCCCC AANGTCCCC TGGNTCTACT GGTGCTCCTG GCAAAGAATG | 60 |
| GNCTCAACGG TCTCCCTGGT CNCCATTGGG CCNCCTGGTC CTCGCGGTAG CACTGGATGA | 120 |
| TGCNGGTCCT GTTGGTCCCC CNGGGACCTA NTGGACCTGC TNGTCCCCTG GTCCTCCCGG | 180 |
| AGATGGTTTC GACTTNAG | 198 |

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

| | |
|--|-----|
| TTCATTGCCT TTGCCCAGAA CTGGTGCATC AAGCGGCGGT CGCAGTCCAT CTACCTGCAG | 60 |
| GTGCTGACTG ANAAGCATGC CCCTGAGCAC TACAGGGTGC TGGGCAGTGT GTGCCAGTTT | 120 |
| AAGGAGTTTG GCCGGGCTTT CCACTGTCCC AAGGACTTCA CCCATGNAAC CCTGCCCCACA | 180 |
| AGTGTTCCGT GTGGTGAGCC TGGCTGCCCC CCTGCACGCC CCCACTGCCC CCGCACGAAT | 240 |
| NACCTCCTGG TGGCTACCGG GGCAGGCATG CAACCGGTGC CAGNCCCGTT TTNGGGNACC | 300 |
| ACCTGNTTTT CCAGCCCTTN CAGANCCGGT NCCNCTGNTG GCCCTTGAAT TTAAGAGGGG | 360 |
| CTNGGAAGCA GGTTAAGGTT GGGATTTTGG GGGGGTTTTN AGGGGAATTT AATGGGGTTC | 420 |
| CNAATTTTTG TTTTAAGGGG GCCAGANCTT TTGCAAAGTT GGNTTTTAAG GGGCCCAN | 478 |

(2) INFORMATION FOR SEQ ID NO:853:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

| | |
|---|-----|
| GGNAGAGGTA TCCGAGTGT NCTGGAACGG CCCTGTCTTG AGCAACATTA ACCGGATTGG | 60 |
| AGCAGACCAT GTCCAGAGCC TCCTCCTGAA ACACTGTGCC TCCTGTNCTG GCAAAGCTGC | 120 |
| GCCACCGCC TGAAAAATNA GGAACGCCTA TCGGGCAGAA TTCGGGTCCC TTGGGCCCCT | 180 |
| GCCTCTGCCT CCCNAGGTGG TCAAGGCTCG GGCCCCAGGC TGCTCTGCAG NCTNCAGCAG | 240 |

GTNAACAGGA CCACTCTGAA CCATN

265

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

| | |
|---|-----|
| AAGTCGGACA GGGGCCATGA CAAGTCGGAC CGCAGCCATG AGAAACTAGA CAGGGGCCAC | 60 |
| GACAAGTNAG ACCGGGGCCA CGACAAGTTT GACAGGGATC GAGAAGCGTG GCTATGAACA | 120 |
| AGGTAGACAG AGAGAGAGAT NTAGACAGGG AACGGGAATC GGGAACCGCG GGTATGAACA | 180 |
| AGGCAGACCG GGNAAGAGGG CAAAGTAACG GCGCCACCAT CGCCGGGNAG GAGCTGGCTC | 240 |
| CCTTATTCCC AAGAGCCAAG ATGGCAGTTA GNCGANAAGN TTGAAAGAGT TTAGACCCCA | 300 |
| TGGACCCTAG CTTCATACTT CAGACGGCCC CCCGGGGCAC GTNGTTCAAA CAGGANTCCC | 360 |
| CAAGCGGNAT TTAGGCCCAG NTTTGGGGGT TGACACCACA GCAGTTGGNC CCTTTT | 416 |

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

| | |
|---|-----|
| GGCACCATAA AGGTTGTCCA ACTAATCTTN AAAGCTGAAT TTCCATTGGG AAGGGAATTC | 60 |
| TTTCCCGAGT TCATAAGTNG CCTTTCATC TTCCCATCGA GTATTTGGNA ACTCTCTNAA | 120 |
| GGTTCCTCC ACTTTCCCAG GCTTTTCCAA TCTGGTCGGC GTATACCTTC TCCTTTGGAT | 180 |
| TTCCAAAAAT TGCTTCATAT ACAGCCTCTA GTGTGTATGT NGGGAAGATT TAATTGTGCC | 240 |
| TTGTNAATTA CATGGATACA AGTGGAATG TATTCCTTGCC CNTGAACTTC TGACAGCCGT | 300 |
| TNATATCGCC TNTTCC | 316 |

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

| | |
|---|-----|
| GAAGGCTTCG GNCACGCAAC GAAANTACAA GGTAGTGGNT CCTTCCTTGC CCACCCCCAA | 60 |
| NTCCAACAGG CGGCCCCCTTT ACCGCTTGAA AANTTTTTTCG CCCTAATCCA TGTGGTCNCC | 120 |
| AAGTCCCGNT TCTGAGTACT TTNTATCTAA TTTNAAAGAA GATGAAGAAG TTTTCAGGGG | 180 |
| NGATTNTTTT ACTGTGGGGC ANGTNTTTTG AGAAAGTCCC CCTGGGGGTG AAAGAACTTC | 240 |
| GGGATCTGGG NTGGCTATGA TTNCGGGGAG GGGGNACCCA CACTTGTTCG CGGGNATTAC | 300 |
| GGGGACCTT | 309 |

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

| | |
|--|-----|
| AAACTAGTG GATCCCCCGG GCTGCAGGAA TTCNGCAGAA GTTTTACTCN CCAACTTNAT | 60 |
| CATCCAAATG CAAGTGANCA AANAGGCCCC CAGCTCTGGC CATCACGTAT AGCATCACCT | 120 |
| TCCTCCTCTT CCTCCTNATC CTTTTTGTCT GCTTCTAAAA GGACCTGAAT GAGGTGTGTC | 180 |
| CTGAAGGCCC CANGAATGCT GCACTGGCTG CCTGCACTGT NTGGCCTGGT GGCCACACGA | 240 |
| ACCAGGACTG AGAATAGCCT TGGGCACCGN CACCATCCTC CTTGTNTTTTG GCCATGGGCC | 300 |
| ATTAACCAGN CTGTNCTTTT TTNCC | 325 |

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

| | |
|---|-----|
| GACCTATTGC TTTAANAACA AGGCCCTCTA TNANATCTCC TTCCCCACTC TAAAGCTAAC | 60 |
| CACACCAACC TACGGGGAAT CTGAANCCAC CTTTTTTNAG CNACCATGAA NTGGTGTNAA | 120 |
| CCNCTGNCTT CCTTTTCCTT GGCCAGCTCC AATGCTGACC TCCGCAAGTN GGNCAGTNAA | 180 |
| CATGGTCCCC TTCCNACGTT TCCATTTTTT TATGCCTGGT TTTGCCCTT TAAACCAGCC | 240 |

GTGGNAGCCA GCAGTTATCG AGGNTCTCAN AGTGGCCGGN AACTTNACCC AGCCAGGTTT 300
TTCGAATGGC CCAGGAACAT GATGGGCTGN TCTGTGAACC CCGGG 345

(2) INFORMATION FOR SEQ ID NO:859:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

ATCCCTCTTT GTCTACAGAG TTGTNGAATG CTCCACCGGG ANGGGGTGGG CAGTTNTCCC 60
CTTTGGGGAT GTTGNGNTTG TGGGGAAACC ACTTCCCCGT TTGCTGGACT TAGGGGCTGG 120
TTTGGGNGAA ATTTTTTGT 139

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

ANAGCAAAGA GCAGGTGGCC AACTNACCTT TTTTGGAGCA ATTCCGNAAA CGGGGCTTCA 60
AGGTGGTATA TATGAACCGN GCCCCATTGN ACGATTACTG TTTGCAGCAG CTNCAAGGGA 120
ATTTNANTGG GGAAGAGCCT GGGNCTGCAN TTAACCAAGG AAGGGTCTGG GAGCTGGCCT 180
GAAGGATGAG G 191

(2) INFORMATION FOR SEQ ID NO:861:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

TTTAAAAACA AGAAGAGGGT CCTNCTGGGA AGAACTGGC AAGGNAGAAG CTCNCGCGGT 60
ACTACAAGAN CATCGGTNTG GGCCTTCAAG ACACCCAAGG GGGCTATTAA GGGCACCTAC 120
ATTGAACAAG AAATGCCCCT TCANTGGTAA TGTTTCCATT CGAGGGCCGG ATCCTCTTTG 180

| | |
|---|-----|
| GCGTGGTGAC CAAGAATGAA GATGCCAGAG GACCATTGTG AATCCGCCGA GACTNATCTG | 240 |
| CACTTACATC CGCAAGTGAC AACCGCTTCG AGAAAGGGCN CACAAGAACC NGTTTGTTAC | 300 |
| ACCTGTNCCC CCTGNTTTC | 319 |

(2) INFORMATION FOR SEQ ID NO:862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

| | |
|---|-----|
| GGCAGAGCA GAAGTGGGTG CGGGANAGNG CCCANAGCAC CCACTTCCCC GGNTCAAGTA | 60 |
| CACACATNAC CAGCTCTTNT TCATTGCNTT TCCCCAGAAC TGGTGATCA AGCGGCGGTC | 120 |
| GCAGTCTNC TACCTGCAGG TGCTGACTGA NAAGCATGCC CCTAAGCACT ACAGGGTGCT | 180 |
| GGGCAGTNTN TCCCAGTTTA AGGAGTTTGG CCGGGCTTTC CACTGTCCCA AGGACTCACC | 240 |
| CATGAACCTT GCCCACAAGT TTTCCGTGTG GTGAGCCTGG NTGCCCCGNT GCACGCCCCC | 300 |
| ACTGCCCCCG NACGANTNAC CTCCTGCTGG NTTACCGGGG NAGGNATGCA CCCGGTGCCA | 360 |
| GNCCCGTTTT GGGNACNACC TGTTTTCCAG CCCTTCCAGG ACCGGTCCCC TTGTNGCCCT | 420 |
| AATTTNAGGA GGGGCTGGAG NAGGNTNAGG TGGATTGGG GGGTTTAAGG GAATATAATG | 480 |
| GGGT | 484 |

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

| | |
|---|-----|
| GGCAGACCTT GANCCCAGGA GTTTAAGGCT GCAGTNAGCT ATANTNATGC CACTCCACTC | 60 |
| CAGCATGGGT GAACAGANCA ANACCCCATC TTTAAACAC ACACACAGAT CATTATCAGA | 120 |
| ATGTACANTA AACTGAATG TTTTTGAAA CTCTGTTCCT TGTTTTATAT TGGCTGCTTC | 180 |
| TGGCATATTC ACTATTTTCC CATGAGNATC CAGTATTGAT GAACTNTAT TTTTGGTAAG | 240 |
| TGAGATGAAC GATGTNAAGA TTGTGCCATA GAGGCGGGGC ATGGCGGCTC TGGCACTTG | 300 |
| GGAAGGCTGA GGCGGGTGAN CTGCCTGNCG NCTGANTTCG | 340 |

(2) INFORMATION FOR SEQ ID NO:864:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

| | |
|---|-----|
| AATNACCGCG GACGATCAAC AGCAGGTCGT NATGCAGAAG TCCGGTGAGT GTAANAAGTT | 60 |
| GCTCATTGAT CGCCGCATTC GGTCCGTTTT TTGGTAACAA CNGCAATAGC GTTTNTGGAC | 120 |
| TGGCAAACAG ACTCATAGCC TGGNATAACG AAAAGATCGC ATTCCAGTNA GTNNTGGGAT | 180 |
| NAATGGAAAA AGTGTGGTGT TCTTCGAATC CTTGTGCCCG CAGTTACCTG NACGGAACAG | 240 |
| CGTCCTGNTT NNTTCCTGGC AATAACAGAG GNTCGTTTAC CAAGTAAAAA G | 291 |

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

| | |
|---|-----|
| GCTGATGGAA GTAAATGGGA ATACAGCCAN TTNTTGACG GNCGCACCTA CGATGTAATG | 60 |
| GTGTTCCGGTG CGGCAGGGAT TATTNCCTG GTCGTTAAGC GCCTGCTGAC GCTAANGATN | 120 |
| CGTNTGAANC GACCGCAAAG NTGGACATTC GAACGGCGAA ATTAATGTGG CTGCGTACAT | 180 |
| TCGCCGGGGG GTTTTGT | 197 |

(2) INFORMATION FOR SEQ ID NO:866:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

| | |
|---|-----|
| GGCAGAGNCT GAAATAAAG ACAAGAAAGC CAGGTCTACT TTAAATAGT CTTAAGCCAC | 60 |
| TATTATTATA TTTTNAAGT TTAGCCAATA ACTTCTAACT AGAAGCAAAA ATAATAACAC | 120 |
| ACGATCTAAT AAAAATACTT GGGAAAACAA AAAGATGAAA TACTTGAAAA CGGACAAACA | 180 |

GAATTGTGCT TCATATGCAA AAAAATCTAA GTCACTTCCC CATACTGGAA AATCTTAATA 240
GGAACAAAGG AACAGCACCA NGCATTTACT AAGGCCATAC CACGTGGGCA TTAACAATGG 300
AGGCCGTTTA TTGNTTGACC GTTTGNTTGA CTGAGNTGGN GTCTCGNTCT GTTCACACGG 360
TTGGGGT 367

(2) INFORMATION FOR SEQ ID NO:867:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

TGGNAGGCCA AGGCGGGCGG ATCTCCTGGG GTTGGNAGTT CACGACCAGC CTNACCAACA 60
TGGNAGAAAT CCCGTCTCTA CTAAAAA AAAA AAAA AAANCNCGG GGGGGCCCCC 120
T 121

(2) INFORMATION FOR SEQ ID NO:868:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

TGGA AAAACT GTATCAGGCG CAGNGCTNTA GCCAACAAGA AAGNCACCAN CTGTTT TNAG 60
GNTGNTGCGT GGCGAGCTGA AGCCGGAACA ACTGGCGGCG GCGCTGGTGA AGCATGAAAA 120
TTCGCGGTGA GCACCCGANC GAAATCGCCG GGGCAGCAAC CGCGCTACTG GGAAAACGCA 180
ACGCCGTTCC CGCGCCCGGT TTATCTGTTT GCTGATATCG TCGGTACTGG CCGTGNAGGC 240
AGCAANCAGT ATCAATATTT TTNACCGCCA TGCCTTTTTC GCCGCGGCCT GTGGGCTTGA 300
ANTGGGCGAA ACACGGCAAC CGTAGCGTTT TCCATAAATT TGGTTCNTTC CGTTCTGCTG 360
GCGGCGTTCG GTATTAATCT TTGATNTTGA ACGNCNNTTA ATCGGGCCAG G 411

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

| | |
|---|-----|
| CACTACCGGT ATCCAGCACC TTAAGCNTGA CGTGTTCCTG ATCCACTTCG GCGCTTAGGT | 60 |
| GNATGCAACC GCTCTCGGGG GTAAATCGA TGGCGTTATC CAGTAAATTT CCCAGCGCCT | 120 |
| GCTCCAGTGA ACGCCGGTTC AGCAGCAACG TTAACCTCGG TGGGCGTAAC ATGCAGAGTG | 180 |
| ATTTTTTTTT CTGCCAACTG CACGGTGCGC GCTTCGCTGA CGCGGCGGGA ATNAATGCCG | 240 |
| CCACATNCAA CAGCAGTNCA GAACGACTTC CTGGACGATT CTCCAGTNTT GCCTGGNGTA | 300 |
| GTAACGTTTC TACCAATGCC TGCAAACGNG CATTTTGNGT CAAAAGTTGT TCATGAAANG | 360 |
| GGCCACCATT TTCGGTGGNG GACCTTCGGG TAAAATTTNC GNCGTTCAG AATTCGCCGC | 420 |
| CATGGGGTTT TTTAGCTCCT GAGTTAATGC GTAAAACATT C | 461 |

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

| | |
|---|-----|
| TTGGCACGGA CTTTACCGTT AACCTGCACC ACGACCAGCG TGNAGTCTTN CACCATCGCT | 60 |
| TTTTCGTCAG CAACCGGCCA CGGCGCGTTG TCGATATCGC CTTGCGCTTT NAGTTCCTGC | 120 |
| CACAGCGTGA AGCAGATGTN CGGGGTGAAC GGGTTAAGCA TACGGACAAC GGCCAGCAGT | 180 |
| GCTTCCTNGC ATCAAAGCGC GATCCTGCTC GCCATCGGTT GGTGCTTTCG CCAGTTTGTT | 240 |
| CATCAGCTNN NNNNNCGNCG CAATTGCGGT GGTGTGAAAG GTCTGACGAC GGCCGATATC | 300 |
| ATCGGTCACT TTAGCGGNTC GTTTTATGCA CATCGGAGGG GGGGGCCCGG TNACCCANTN | 360 |
| CGNCCTTAT | 369 |

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

| | |
|--|----|
| TTTTTTNTGC CATTAAC TTC GGTATGCCTG CNGGACTGGC TTCGCTGGTG TTACAGGCAC | 60 |
|--|----|

| | |
|---|-----|
| AGGCGTTTTT AACTATCATG CTTGGCGCGT TTACTTTCGG GGAGCGACTG CATGGCAAAC | 120 |
| AATTGGCGGG GATCGCTTAG CGATTTTGG CGTACTGGTG TTAATCGAAG ATAGTNTGAA | 180 |
| CGGTCAGCAT GTGGCGATGC TCGGCTTAT GTTGACCCTG GCGGCACATT TAGTTGGGCG | 240 |
| TGTGGCAACA TCTTCAATAA AAAGAATCAT GTCGCACTCA ACGCGTCCGG CGGTGATGTC | 300 |
| GCTGGTAAAT CTGGAGCGCT TTTAATCCCA ATCATTCCCT TCTTTGGTNG CCTCGCTGNN | 360 |
| TCNTCGGATG GGTTCGCAA CCAGGNTTCA CA | 392 |

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

| | |
|---|-----|
| TTCCGGTCTN ATCCAACAAG CCTGCATTCC GCTGCGAATT GCCCCACCCA CGTNAGTGNA | 60 |
| GAATCGTCCC CAACATGTAA GATCTCGCCG ATCGGCACGT TGAGTTTTTC CGCAGCCAAA | 120 |
| AAGTACATAT CGCTGAACGG TTTTAAGCGC CCGTGCGGGC CAGCGCGCAN ACAAACTCA | 180 |
| AAATAATCCC CCAAACCAA CAGCTCCGGC TGGGNCGTTA CCGTTGGTGG ATCGCCACCA | 240 |
| GCGGCCATTT CTTCGCCAGC TGTTTTAAGG TGTCGTGAGT TTGCTGCGGG ACGTTCGAAT | 300 |
| TCGGCTGCGN CATTTGGCAA AAGTTGGATT CATTGGCTGC GTGTGGCNCC TTGNATGGGG | 360 |
| CTTTCTTTTCG GGGCANTCAG CCCGNNNGNN GNGCAATNG TTTGGTTTCA ATTCGGAACG | 420 |
| TAAAACGGCC AACGCGGTTT AAGGTCGTGA TNAAATTTTG GGGGTTTCCC GTTTTCCNNT | 480 |
| AACCGGCTGG NGGCAG | 496 |

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

| | |
|---|-----|
| ATGGTCTCGC CGATAGTCAG GTTAAAGTAC TCTTTGAACA GCCAGAAGCC CGGTTCGTTC | 60 |
| ACATGAGAGA AAATCACACT ACCGGAACCA ACCGCAATAA CCATCAGCTC CGGGNTAACA | 120 |
| CCCGTGTTG CCAATCAGCG GTGCCGCGAT ACCACCGCA GTGAATTNCC GCAACGNTTG | 180 |

| | |
|---|-----|
| CGGGAACCCA GCGCGATACG CATACGGNCA GCAATCGACC AGGCCATCAG CAGCGGGGGA | 240 |
| AATGTTGGTT TTCGTGGCAT CCATGGANGC AATGTTATTT TTTCCACGC CGTTNTNTN | 300 |
| CCCAGCAACC TGTTTTGAAA CGGNACCCG | 329 |

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

| | |
|---|-----|
| CTTNATGCAC AACGGCTTTT TCCTGTNCCG GCTTAACTCC TACAGTNAGA TCTTTTCCAG | 60 |
| TNAAGTCTCC GGCGTGGCGT TAAACGCTT CTTTAACTTT TNNATCCCGG CGAATGCTGG | 120 |
| TGGTCTACTT TCTGNGCCCA GGGACAGCAA AGNTNGGCTG TTATTTCTC GTNAGCACGG | 180 |
| TCGCCTTTGG CTTGGCTGAC TTANATGAAT TGTGNGGCGN GCACTNCGNC CCAATATCAT | 240 |
| CATCGCATTC GCTAATCTTC CTGTTTATTG GGCATTATTC GCGGGCTGGG ATTTCTTGT | 300 |
| GGGATGCNNG GNCNGCGGGC GGGCGTGCNT GGGGGATTTT TTGGGCA | 347 |

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

| | |
|---|-----|
| CGTTNTCGCG CAGGTTTTNA ACGCGCTAA NTAAATNAT GACCAGCTAT GTGGTTGGGC | 60 |
| AGGCGCTTAA GGCCGATAAG ATTAACTCA CCGATATGGT GACGGTCGGT AAAGATGCCT | 120 |
| GGGCGACGGG AAATCCGGCA CTGCNTGNTT TCATCGGTAA TGTTCCTCAA ACCGGGCGAT | 180 |
| CAGGTTTCGG TGGCAGACTT GAACAAAGGT GTGATTATCC AGTCCGGTNA ATGAACGCCT | 240 |
| GTATTGCGCC TGGCTGATTA CNTTGCCGGG NAGCCAGGAG TNCATTTTAT TGGTCTGATG | 300 |
| AATGGTTATG CCCAAAACT GGGTCTGNAC CAACATTACC TTCCAAACGG TGGCACGGGC | 360 |
| CTGGTTTGCG CCCGGGGCAT TTCAGNACCC GGCGGGAATT TTGGCATTNC TGGGTAAAAG | 420 |
| CNTTTTTCCC CGGTTTNCCC GNAGAGTACG CCTTTTT | 457 |

(2) INFORMATION FOR SEQ ID NO:876:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

| | |
|--|-----|
| ACTGGNTCTC GGCTGCCCTN TTGAAGANTT TAACGCATTT TGN NATGCCC ATCCCGATCG | 60 |
| GACTGTCGTC GTCTACGCCA ACACTTCTGC TGCGGTAAAA GCGCGCGCAT ATTGGNTGGN | 120 |
| AACTTCAAGC ATTGCCGTCG AACTTATTGA TCATCTTGAT AGTTTGGGNN GAAAAANCA | 180 |
| NCTGGGCACC CGACAAACAN CTGGGGCGTT ACGGGCAAAA ACAGACGGGT GGGAGACANT | 240 |
| CTATGCTNGT CAGGGTGCCT GTTTTNGTGN CATGGATGAA TTTAAAGTCT TCAGGCGTTG | 300 |
| AACCCNCTT | 309 |

(2) INFORMATION FOR SEQ ID NO:877:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

| | |
|--|-----|
| TATTTTGGCC GCATGCAAAG GTTTCATTAC ACTATTA ACT AACGGTGTGC TATCCGTTTC | 60 |
| TGGGAAAGTA AGAAATATTG TCAACATGAA GCCGGCGCAC CCATGGNAAG CTGAAGAATA | 120 |
| TTTGTGAACT GCCTGTACAT CAGTGAAAAG CCTGTTGAAG AAAAACTTA AGCAAGAGCA | 180 |
| AACGAACATT CTCACAGATT CTTT TAGATG CAAGAATGCA GCACGCAAAA AATTTGGTTA | 240 |
| CGCGTGGAAG GTTCCAGTNC AATAAAATTG CCGAACAATG TGGTTATGCC ATACATCTTA | 300 |
| TTTATTTTAT GCGTTCCGCA AACATTTCCG NAACATTC CG AGGGGNTTC TNAGGGGTTA | 360 |
| CCNTTGTTC AAGTCCCCCG GTTTGN TTA CGGGGCAAC | 399 |

(2) INFORMATION FOR SEQ ID NO:878:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

| | |
|---|-----|
| CATTGGCAAA GAAGAAGCCA ATCGGTGCGC CCAGCTGCGG AAAGGAGCCA TACAGTGCAC | 60 |
| GTTTGCCCGG TGGGGCGTTT TCAGTCGCCA GCAGCGCCGC GCCGCCCCAT TCACCGCCTA | 120 |
| AGCCCAGACC CTGACCAAAT CGAGCCAGCG CCACAGCAGC GGGGCGAAAA TACCAATCGT | 180 |
| GGCATAGCCC GGNCAGCAGA CCAATCACCA CGGTGAAAT CCCCATCGTT AGCAACGAGG | 240 |
| CGACCAGCGT CCCCATACG AACGGNTGTT CCCTCGTGNG GACGTTTTTC AANGACCGTT | 300 |
| GGNCNTGAAA TTGTGGGTTC AGCAAAAACG GCAGTTTG | 338 |

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

| | |
|---|-----|
| TCCTGGCAGA TGTCCGCGGA TATCCGCNAG CCCCAACANT TCGAAGAAAC TTTNCTAATG | 60 |
| CAGGCTCATT TNTTTNGCNC TGAGATAAGC CGGANTGCTT TCTCCGGCAT AGGTTCGCAG | 120 |
| CGTTCCAGGT TCCAGCCCGT AGTCAATNCG CATCGAGAAT CAACANATGG CTGGNGCTTT | 180 |
| CAANATACCC CAGCAAGTTC AGTCCCTNAN TACCGCCATC GACAATNTCC ACATACTCGG | 240 |
| GCCAGTGGTA ATGGGCATAC AGCCGTTCCG NCACCCGNAC GNCGAAGCCT TCATCGGCCC | 300 |
| ACAGCAGGTT GCCCAGCCCC ATGACCACCA CGGTTTTNNT CGNTTCATGA AACGGTTCCT | 360 |
| TGTTAAATTT ATTTTNNCCA AATTTTGGG | 390 |

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

| | |
|---|-----|
| CGTNAGCAGC CTGTNGCTTT ATACCGGGG GATTCTGGAA GCCAACCTGC TGCCACCGCC | 60 |
| GGAGCCGAAA GANAGCTGGC GTCGCATTAT GGATGAACTG TCAGTNATNN NCTGCNATGT | 120 |
| CTACCGCGGC TACGTACGTN AAAACAAAGA TTTTNTGCCT TACTTCCGCT CCGCTACGCC | 180 |
| GGAACAAGAA CTGGGCAAAC TTGCCGTTGG GTTCACGTCC GGCGGAAACG TCGCCCAACC | 240 |
| GGCGGCGTCG NAGTCACTTA CGGCGGCATT TCCGTGGNTT CTTTCGGCTG GGACGGCAAA | 300 |

AACCGTCTTG AANTGNTCCC CGNCTGGGNT TGGGGTGGCA GGTACGGGC GGNTTGCAAA 360
AAGTGGGTTC GAAGACGGGG CAAAACAGAG CGAG 394

(2) INFORMATION FOR SEQ ID NO:881:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

TCGAGTTTTT TTTTTTTTTT TTTAATTGA TGGGATGTTT CTAAACTTCA TCTGCTAATA 60
AATATTTGCC AAATTAAAAT GAGCCTAACT AAATTGAAGA CTAAAATTAT TCAGTGGAGG 120
ACCAGACCAT TTGCTTTATT TTCAGGGTGA AGAAGACCTG GNTTGCTCTA TTCAGGTCTC 180
TTAGAAAAAC AGGCATACAC ATGAGTTTCT AGTATCCTCA GCAACACACT ACATCATACC 240
TTACCCTGGG TAATCCTTCA GAGCACTGTC AGCAATCACC TCAAAATCCC TTCCCTAAAG 300
NCACATACAC TTGGGGGTTT ACTCTTATTC ACCTACTCCT CCCTACTCTT TAACATGGAA 360
TGMNCTCAAG GCTTTTGGGG GGGGNAAAAT TAAAGNATCT ATCCTTTTTT TTTTAAGGTT 420
CCNTTTCAAA AATTGCTTTG GGGGCCCCGT GGNCAGNAGG GGAAACAGGC ACTGTTNAAT 480
AGGTTCCCC 489

(2) INFORMATION FOR SEQ ID NO:882:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GTAAATTTAG CCGCGCCGGT GAACAGACCC AGAAATNAAC GTNCGCNTTA ATCCTCATGT 60
NATTCCTGGC ATGGTACAAG CTGAATCTAT AAGCTTTTTT ACCGGACTCA CCATGCGNTG 120
GTTCCGCAAT GCTTCTGTG CCGAAGAAAA ACTGATTGCG GAACGTTTAG GCATCGANAC 180
CTATACGCTG CTGGAAGAGA TGGCCATGGG GTGCCGCCTG GGTCTGTTGGG GCGTAAATNC 240
NGATCTTTTT NCGACAAAAT GCGGTTTTTA AAACNGGTAT CACGTTGGNG 290

(2) INFORMATION FOR SEQ ID NO:883:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

| | |
|---|-----|
| CACCAATGCG GCAGGCTCGC TCGTCCGGA AGTGGGGGCA GGCAGCCTGG TCGCATTGAA | 60 |
| AGANCATATC AACACCATGC CCGGTACGCC GATGGTGGGT CTTAACGATG ATCGTTTTNG | 120 |
| AGAGCNCTTC TNCTCACTGG CAAATNCCTA CNATGCGGAA TACCGCGCAC TGTTACAAAA | 180 |
| AGTGGCGAAA GAAGAGGGTT TCCCTCTGAC GGAGGGCGTG TNCGTNTCGT ATCCGGGGCC | 240 |
| GAATTTGAG ACTNCGGCGG AAATTCGCAT GGATGCAAAT TAATTGGTGG GGATGTTGTT | 300 |
| GGTATGTNTG TGGTGCCTGA NGTTATTTCA GNTCGCCATT GGGACCTTTA AAGTTCGTTN | 360 |
| GCGNTCTCT | 369 |

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

| | |
|---|-----|
| ACGCATTANA CCANTAAAAG CTTGAGCNT TTACCGACCG GAANTGGCAA TATCAGCAAT | 60 |
| CTGCTGAGAA CCAACCCTGC GGTACGTTGG TTTCAACGCA AAGTACCTCG TTAAACCAGG | 120 |
| GAGATATTCG CCCTGAGAAA NTNTCTTTTC ACGGTGCGTC GCCCTACCAN ATTGCCTATT | 180 |
| TAATTGAGGG GTATTAGTGC AACTAAATAA CCCTGAACCC CAGCGAATNA NTTNCCNATG | 240 |
| CCCAT | 245 |

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

| | |
|--|----|
| GGCACAGCTA GGCTGGACGN TACTCCGGAC GNAAAGNNGT CATCGTGTA GAACAT | 56 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:886:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```
GGCACGAGGA GGACAGCATT GCTGCTCCTT GCACCCCTGG NTGTGGCTAC AGGGCCAGCC      60
CTTACCCTGC GCCTGCCACG TGTGCACCAG CTCCAGCAAC TGCAAGCATT CTNTGGTCTG      120
CCCGGCCAGC TCTCGCTTCT GCAAGACCAC GAACACAGTG NNAGCCTCTG AGGGGGAATN      180
TGGTGAAGAA GGA CTGTNCG GAGTCGTGCA CACCCAGCTA CACCCTGCAA GGCCAGGTT      240
AGCAGNGGCA CCAGTTTCAA CCAGTGTTC CAGGNGGACT NTGCAATTGG GAAGTTGNAC      300
AACGTTGNAA C                                                                311
```

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```
GGCANAGAAA CAGCGCTCTG ACCTCTTTAA ACACCACAGA ATCCACACTG GGGAGAAGCC      60
CTATGGATGT TCCGTCTGTG GGAAACGCTT CANTCAGAGT GCAACCCTCA TTAAACACCT      120
NAGAATTCAC ACTGGGGNAA AAGCCTTACA AATGTNTTGN AATGTGGGGA AAGATTTAGA      180
CAAAGTACAC ACCTTATCCG ACACCAANNA ATTCATCAAA ATAAAGTGCT GTCGGCTGGG      240
CGTGGTGGCT CACGNCTNAT AATCCCAGCA CTTTGGAGG NCA                          283
```

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

```
GGCAGAGCAG GTGCGCCTNT TCCGCCCCTG GNTCAACATG GACCGGATGC TGCGCTCAGC      60
CATGCGCCTG TGCCCTGCCG AGTTTCGACA AGCTGGAGTT GCTGGAGTGC ATCCGCCGGC      120
```

S.n. 08/ 401, 881



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

**William A. HASELTINE, Craig A. ROSEN, Steven M. RUBIN, Patrick J. DILLON,
Haodong LI, and Julie EARLE-HUGHES**

Serial No.: Unassigned

Filed: Unassigned

For: HUMAN GENES, SEQUENCES AND EXPRESSION PRODUCTS-17

SEQUENCE LISTING

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| | |
|---|-----|
| TNCATCGNAN TGGGACAAGG ACTGGGTCCC CGATGCCGCC GGCACCAGCC TCTATGTGCG | 180 |
| GCCTGTGCTT CATTGGGAAC GAAGCCCTCG NTGGGTGTNA GCCAGCCCAG GNGCGCGCTC | 240 |
| CTGTTCGTNA TTCTCTGCCC AGTGGGTGCC TACTTTCCTT GGAGGCTCCG TGNACCCCGG | 300 |
| TTTG | 304 |

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

| | |
|--|----|
| AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGNGGGGG NGGCCCCGAT | 50 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

| | |
|---|-----|
| GGCAGGAGCG GCACGAGGAG AAACCCATA TATGTGAAGN AGTGTGGTAA GGCCTTCAGT | 60 |
| CTCCCCTCAA ATNTTCGAGT CCACCTGGGT GTTCACACAG GGNNAAACT CTTTGAAATG | 120 |
| TGATAGAGTG TGGTAAAGGC TTCAGTNCAG GAGTGCACGT TTTGGNAGCC CATCAAAGGG | 180 |
| TCCACACTNG GGGAAAAGCC NTACAA | 207 |

(2) INFORMATION FOR SEQ ID NO:891:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

| | |
|---|-----|
| GAAATCCCTC AGCTTTTGTT TGTNTGGAAG TCTTTATTTT TCTTTCATGT TTGAAGGTAT | 60 |
| TTTTGCAGAA TATACTATTC TAGCATGAAA GGATTTTNCC CTCAGCACTT GCAGTATGTC | 120 |
| GTACCATTCT CTCCTGGCCT GTAAGGTTTT CACTGAAAAG TCTTCTCCCA GACATATTGG | 180 |

AGCTTAATTG TGTGTNGTTT CTTTTCTCTT GCTGCTTTTA GGGATCCTTT CTTTNTTACA 240
GNCCAGTTTT TATCCTTGAC CTTTGGGAGT TTATTAAAT GCTTTGAGGG TACTTTTGGT 300
TTGGGGTTCC AATCTGCTTT GCTGGCTNCT ATAAACCCTC TNGTNACTNG GGNATTGG 358

(2) INFORMATION FOR SEQ ID NO:892:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

NTATNTNAAT AATGCTTTTG GCACTGATCA CAGAGCCCAA ANATACCATG GTAGGAGTCA 60
ATNTGCCACA GAAGGTTGGT GGGTTTTTAA TGACGAAGGC GCTGAACTAN CTTTNNCAAA 120
GGCCTTGAG CGCCCANAG NGACCCTTCC TGGCCATACC TGGGACGGA 169

(2) INFORMATION FOR SEQ ID NO:893:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

TTTTTTTTTT TTTTTTGGG NAACCCTTT TTTTTTTTTT TTTTNAANN ANGGCCT 57

(2) INFORMATION FOR SEQ ID NO:894:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GGCAGAGCCA CCATGATGCT GTNATCTTCC TGGCCGAGCA GCTCCCCGGA GCCCAGCGTT 60
GCCAGCACTA TAAGTTCCGT TACCACCAGC AGGGAGAGGG CCAGGAGGAG CCGCCCCCTGA 120
AATCCCCATG GGGNCTGCTC GGGCAGAGGT CTATCTCCGG AAGTGNACAC TTTGAACATG 180
TTCAACTTCC TGGCCTCCCA GCCACCGGGT GCTTCCCTGA GGGGGCCACC TGTNAATGAG 240
GAAGAGGATG AGGTGCAGCT TCAGGTTCAA CCAGACGTGN CCACCAGCCT GGGAGCTGCC 300

| | |
|--|-----|
| CCATGGCCAT GCNTTTTTCG TTCACCTTTA AGGAAGNACG TTCCAAAGAA AGTTGTTGGG | 360 |
| GTGTTTTTACA AGNTTCAGCC CATTNCAAGG GGGGGAGGNC TGGTTTCTTG TTAAGCGGCN | 420 |
| AAACATTCGA AGGCGGGGGG NAGATTGGTT CATTCGAGGT TAATTCTGGG GCAATTGTTN | 480 |
| ATNCCGTTCC GGT | 494 |

(2) INFORMATION FOR SEQ ID NO:895:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

| | |
|---|-----|
| GGCANAGGGA ATGACGTGCT CCACAGGTGT TTGCCACTGA AGGGGGGTAG CCAGTGGCNC | 60 |
| CAATGAAACC AGCTTACCTG GCCCAATTCC CACTTTGAAT GATGTCAGCC CCAGAAAGGA | 120 |
| TGAGCTCTTC TACCATCTCT CCTGTTACCA CATTCCCTGC CTGAGAACAG AGCAATTGAA | 180 |
| ATACAGCATC CTTAGGGCCA GAAACAGGAG GTCATGTATT GTTACGGTAT GCATGGACCA | 240 |
| GGACTTTCCA ACATTATTAC AANGAAAGGA TAACTAGGTC CCCTCTTACT GGGGCCCTCT | 300 |
| GNAGGGGTTT TNACANTAGC CACTTTTAGA GGAACCCTGN TTCCCTNACC CATTCCAACC | 360 |
| CAACAACCAA G | 371 |

(2) INFORMATION FOR SEQ ID NO:896:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

| | |
|---|-----|
| TGCAAAAAGG GAGCCAGNAA GAAAGTGGTT GNATCCATTT TCTAAGGAAG ATTGGNATNA | 60 |
| TGTGAAAGCA CCTGCTATGG TTCAATATAN GAAATATTGG GAAAG | 105 |

(2) INFORMATION FOR SEQ ID NO:897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

| | |
|---|-----|
| TACAGGGCTC CAAGTGTCTT ATGAGAGCAG GACTTGGGCT GACCATGTCT CTCTGCCCTC | 60 |
| ACCCATGCTC TGCTCTGAAT TTCAGATCCT AAGTGTGAAA CGAGAAAGTC CCCAGCCCTG | 120 |
| CTGCTGAGCC AGTTGCTGCC CTACATGGAG AACAGGAGGG GTGCTGTCAT CCTGGTCTCT | 180 |
| TCCATTGCAG CTTATAATCC AGTAGTGGCG CTGGGTGTCT ACAATGTNCA GCAAGACAGC | 240 |
| GCTGCTGGGG TCTACTAGA AACTGGCAT TGGAGCTGGC CCCAAGGAC ATCCGGGTGA | 300 |
| AACTGCGTGG TTCCAGGAAT TATTCAAAT GGACTTTCAC AAAGTGT TTT CNGGGGAATG | 360 |
| AAGTCTCNCT GGGAGAACT TTCAGGGACC NTCNTCAGTT GTCAN | 405 |

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

| | |
|--|-----|
| NAGTNTGCGA NCCTCTACTG GNGGGGTGAA GGAAACCTCA TTCGTTACAG GCCTGGTACT | 60 |
| GTGGCGCTCC GTGAANATTA GACGTTATCA GAGGTCCACT GAANCTTCTG ATTTCGCAACT | 120 |
| TCCCTTCCAG NGTCTNGTNC GAGAT | 145 |

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

| | |
|--|-----|
| GGCAGAGGTT GGATGAAGAT GTGGAGGAGA TGCTGCTGCA GATTGCTGNT GNTTTTATCG | 60 |
| AGAGTNTGGT GACAGCAGCC TGTCAGCTTG CNCGGCATCN AAGTTCTAGC ACCCTGGAGG | 120 |
| TGAAANATGT CCAGCTGCAT TTAGAGCGCC ATGNNACAT GTGGTTCCCA GGNATTTGGC | 180 |
| TCTGNAAGAA ATCCGACCCT ACAAAAAAGC TTGCACCACA GAAGCTTCAC AAACAGAGAA | 240 |
| TGGGCATTGA TCCGGAAAAC AACCAAGAAA TAACACACGG AAAGGTCCAG GGAATGGGAC | 300 |
| AGCAATGTAT TTGGGNGATA CTTGAGCTGA GGAAGTTCAG CCCATCTCAT CCTTGGNTTT | 360 |
| TTTTTTTTTAA ANGTTTTTTA CAGGGAGCNA TATTTTTTAA TTTAACATGC AGCAATTTTC | 420 |

TTAATGNCTG GAGGTTCTNN CCAAAGGNTA AAGCCTCTTA CCCAATTTTCG GNCCCTTTTC 480
CNGNCCTTTN AAGGG 495

(2) INFORMATION FOR SEQ ID NO:900:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GGCAGAGGTG TCTCACAATG CAGTCGAAAC TGGATACTTG AATTCAGTTT GCCAGAGTTT 60
GTTAGACAAT CTGGATTTGC TTCCTGGCAA CACTAGAACA AAAATTGGCT TCATAACATT 120
TGACAGTACA ATCCATTTCT ACGGTCTTCA GGAAAGTCTC TCTCAACCTC AGATGCTAAT 180
AGTTTCAGAT ATTGAAGATG TTTTATACC TATGCCAGAG AACTTATTAG TAAACTTNAA 240
ATGAGAAGTN AAAGAGCTCG TGCAAGGTTT ACTGAAAANT TTNGNCACAA ATGTTTG 297

(2) INFORMATION FOR SEQ ID NO:901:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GAATTCCACC CATGGNAAAT TCCATGGNAC CGTCAAGGNT GAGAAACGGG AAAGNTTGTT 60
AATCANTGGA AATCCCATCA CCATCTTCCA GGAGCAAAAT CCCTCCAAAT TNAAGTGGGG 120
CGATGCTGGC GCCTGNAGTG ACGTGCGTGG NAGTCCACTG GNGTTTTTCAC CACCATGGAA 180
GGAAGGCTGG GGGCTNCATT TNCCAGGGGG GNGCCAAAAG GNTNCATCAT CTNTGCNCCC 240
CTNCTGGTGG ATGCCCCCAN GTTCCGTAA TGGGNTGTTA AACCATGTGA AAGTTATGGA 300
CAACAGGTCT NCAAGGTGCA TTCAGCAATG GTCTNCCTGG AACCNCC 347

(2) INFORMATION FOR SEQ ID NO:902:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

| | |
|---|-----|
| AGNAGAGCTG AGATCACGCC ATTNCACTCT GGCCTGGGTG ACAGANTGGA GACCCTGTNT | 60 |
| CAAACAAAA AAAGTTTCTT TCCTTTNCTA GCTCAAAAGC CAAAANTTTC TGAAAAACGA | 120 |
| ACTTTGAAAG ATCTNTNGTN CCAATCAAGG CTTCTNCCTC CAGGTNTGAC AAGAAAGGGC | 180 |
| CAAANACCAT TGCAGAGATG AGGAAGCAGG ACCTGGCTAA AGACACGGGA CCCACTCAAG | 240 |
| NTGAAGNTCC TGGNCTGGAT TGAGGGCAAG GANGCGGAAC ATCCGGGGCC TTGCTGTTCC | 300 |
| ACGTTGNACA AANTGTTGTG GGGACGGGGA GAGGCCCTTG GACGNCCTGG GGNATGG | 357 |

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

| | |
|---|-----|
| GGNACAGGGA GATCTGGTGG CCTGGNTTGT NCCAAGAAGG CCGCTCAGCT GGGAAAGGAA | 60 |
| GGTNTCCGTG GTGGACTATG TGGAACCTTC TCCCCAAGGN ACCCGGTGGG GCCTTNGCGG | 120 |
| CACCTGCTTC AACGTGGGCT GCATCCCCAA AAAGCTGATG CACCAGAGCG GCACTGCTGG | 180 |
| GAAGGTCTGA TCCAAGATGC CCCCAACTNA TGGCTGGGAA GGTGGCCCAG CCCGTGNCCG | 240 |
| NCATGANNTG GGAGGTAAG | 259 |

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

| | |
|---|-----|
| GGCACGAGGN AGAAGCCGGT GTACAAGAAC TTACAGCTCT TTATGGAGAA CAAGGACCCC | 60 |
| CGGGACGACC TCTTCGACAG GCTGACCACG ACCAGCCTGA ACAAGCACCT CCAGGAGCTG | 120 |
| ATGGACGGGC TGACGGCCAA GGTGTTCCGG ACCTACAACG CCTCCATCAC TCTGCAGGAG | 180 |
| CAGCTGCGGG CCCTGACGCG CGCCGAGGAC AGCATAGCAG CTTAAGNATC TTATCCTACA | 240 |
| ACCGAGCCAA CCGAGTTCGT GGCCATTCTT TGCAACCATT CAGCGGAGCA ACCCCCAGTA | 300 |
| CGTTTCGGAG GAAGTCGATT GCAGAATTTT CCAGANGGAG GNTTCCAGGT CAAAGAAGGN | 360 |

| | |
|---|-----|
| NGCAGGTTGG TTGAGGCCAG GGCAGAGTTG AGGNGGGNNG AGGGTTTTAG CACAAGGCCC | 420 |
| AAGGGGTTGG CAANTCCAGG AGTTTTCTGG TGAAGANGAG TTGGTTCTTG G | 471 |

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

| | |
|---|-----|
| GGCACAGGTT TGCCGTGTNA GCAACCACAG TNACCTTGCA GTNAGGCTGG AATCTTGGGC | 60 |
| CACCCCAAAG TCCTTTNCTG AAGGATTTAN ACGGGGATGA AGTGCCCTCC AGCCTCAAAG | 120 |
| CTAGCCACAA AGCCCCCAGA GCTGAATTCA TTGAGTATTT GTGCCTAAGG GCTTGGGCTT | 180 |
| GTTTTGTTTT AATACCCGGN CCCCCGNCAG AAAATAGNTT TNGCTTGACA ACCCAGNCTA | 240 |
| ATTTCCCCGA TTCTTGGGGC TCCCTCTTGN ATTAATTTTT TGAAAATTTN CCAGTTGTTC | 300 |
| AGGNATCAAT GGGGGTTAAT TCCGGNA | 327 |

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

| | |
|---|-----|
| GGCACGAGCC CAGCTGTACC CCGTGTTAGG TGGGTGGCAG GTGGCAATTT GCCCTGACAT | 60 |
| GGCACAGCAG GGCTCTTGCA TGGCCCGCTG ATTGCTCCTC ACAGGCACCT ACGGGCTGAG | 120 |
| CAACGCGCTG CTGGAGACTC CCTGGAGGAA GCTGTGCTTT GGAAGCAGC TCTTCCTGGA | 180 |
| GGCTGTGGAA CGGAGCCAGG CGCTGCCCAA GGATGTNCTC ATCGCCAGCC TCNTGGATGT | 240 |
| NCTCAACAAT GNAAGAGGCG TGAGTGNGGC GGGTCCTGCT TGGGTGAGCC CCAGTNTCCC | 300 |
| GCNACCAGGG NCAGAGGGAA AGGCAGGCCC TGTTGCCACG GGGANGGCC ATGGAAATTG | 360 |
| GCCAAGGTTT GGAGACCATG NCTTTTGGGA AGCCCCATTT TNAGCAAGGC CNTNGTTTTT | 420 |
| TT | 422 |

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

| | |
|---|-----|
| GGCATCTGGG TACTTGGTGA GGTCGAAGGT CAGGACTTTG CTGATCACAC AGTCCNNTTG | 60 |
| CTCAGGATAG ACTCCAATNA GGCTCTCGGC CTTNGTGTAG AACTCCTNCT TGAGTGAGAT | 120 |
| GACGATGGCC TGGTAAGTTG CAAGTCGACT GNCTCCTTGG NTGTAA | 166 |

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

| | |
|---|-----|
| TAATCCCGTT GATCATCCAC ATCGCCGNTA CANCCCGCTC ACCGGGCAAT GGATTCTGGT | 60 |
| TTCACCGNAC CGGCTTAAGC CCNCTGGCA GGGGGNCGN GGAAACGGCA GCCAAACAGG | 120 |
| TGTTACCTGC GNCACGATCC AAATTGCTTC CTCTGCGCAG TTAATGTGCG GGTGAACAGG | 180 |
| CGATAAAAAC CCCGATTACA CCGGGGACTT ACGTTTTCAC TGAATGAACT TTGCGGCTTT | 240 |
| GAATGTCTGG ACACGTCCAG ATGCGCCAGN AAAGTNCACG ATNCNGCTGN ATG | 293 |

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

| | |
|---|-----|
| NGCCNCATGG GCCANATAGG TGGCCCAGGG GCCCTGGNAG CCCCAAGTCC CAAAGGTANA | 60 |
| TCGGAAGACT ACAAGGCCAC CCAGAAAAAT CGCCTTCTAC TGCCACANGA ACCATTCAAC | 120 |
| GTCCCCCTGC GACCGGGAAC CAGACCATCC GCTTCGNACC ACGTGAATGC ACCAGCATGA | 180 |
| AACAACAATT AATGAAGCCC CGCAGTGGTC AAGTTACACC TGTNAAGTCT CNCGGGTCTT | 240 |
| CTGACTAACT TNNACCTNAC CACGC | 265 |

(2) INFORMATION FOR SEQ ID NO:910:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

| | |
|---|-----|
| AAAAGAATTT CTACGANTTG AATATTGGGG AATATTCTGG AACACTGGAG ATTCCCTTCC | 60 |
| GGGGGAATTT NGATCCTGAA GGTGCAGTGG TGGGCTAGTC ACCAAAGAAT GAAATTCAGN | 120 |
| CACGTGGGAC AAAAATCATG AACAACATATG AAAGGGNAAC TCGCCNNAN GNAAGGATCC | 180 |
| AGTCTGGTCT GGTGGTTTAA CAGGTGTGCA CTCTGGCAAA CCTGTAATGG TGTATACTTA | 240 |
| CAGNGGGCCC CTTACACGGN TNAAAACAGN CANTGGGG | 278 |

(2) INFORMATION FOR SEQ ID NO:911:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

| | |
|---|-----|
| TGGAGAGCCT GGTNTCTCAG TACTTCCAGA CCGTGAAGTG ACTATNGCAA GGACCTGNAT | 60 |
| GGGAGNAAGG TCAAGNAGCC CAGAGCTTAC AGGCCGAGGT CAAGTTCTTA CTTTGNAAA | 119 |

(2) INFORMATION FOR SEQ ID NO:912:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

| | |
|---|-----|
| CTGTNTCAGG TTCAAGGTGA AGAACCCAG AGGNNACTTC CCTCTGTCAC GGTTCCGCTG | 60 |
| TGCCCCAAGG NTTCCAAGGN CTGATGGCTC CCACTGCTAA TGCCTTGTTT TTGTCACCAA | 120 |
| AATCCTGGGA CAGATGCAGA TCTGGNGTGC CAAAAGCGGG CCTGCTGGGA AACCTGGGTG | 180 |
| TGCTGGTGCT NCANTGGGGG TGNAGGGGTT CCNTGCGTG | 219 |

(2) INFORMATION FOR SEQ ID NO:913:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

| | |
|---|-----|
| GGCAGAGGTT TACTTCAAGG GCCTGTGGAA GTNAAAGTTC AGCCCTGAGA AACACAAGGN | 60 |
| AAGGAACTTG TCCTACAAGG CTGATGGAGA GTCGTGTTCA GCATCTATGA ATGTACCAGG | 120 |
| NAAGGCAAGT TCCCGTTAAT CGGCGNCGTG GCTGAAGGCA CCCAGGTGCT TGAATTTGCC | 180 |
| CTTCAAAGGT GATGACATCA CATGGTCCTC ATNTTGCCCA AGCCTGAGAA AGAGCCTGGC | 240 |
| CAAGGTGGGA GGAAGGAACT TCACCCCAGA GGTGCTTGCA GGAGTGGTTG GATGGAATTG | 300 |
| GGAGGAGATG GTGCTTGGTG GTNCCACATG NNCCGGTTTT CCGCANTN | 348 |

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

| | |
|---|-----|
| GGCAGAGGTT TTATAGTGCA AGGNATTGGG GTACAACTTT ATNATTTTCC TTGTGGATAT | 60 |
| CCATTGTCTG AGCAACATTT GTTGAAAAGA GTGTTNTTTT TCCATTGAAT TGTCTTGGTG | 120 |
| TCCTTTCTGA AAATCAACTG ACCATAAATT CAATGGTTTA TTCTTGACTC TCACTTTCAT | 180 |
| CTCATTTTTG TATATGTCTG TCGTTATGCC AGTACTACAC ATTTAATTAC TATAGCTTTG | 240 |
| TAATAAGTTT TATTTATTTA NTTATTTNAT TTTTGAGATG GAGTCTCGGT CTGTCGGCCA | 300 |
| GGTTGGAGTG CAATGGTGNC CATTTNGGTT CAATGCAGGN | 340 |

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

| | |
|---|-----|
| GGCANNGCGA CAGTGAAATC CCATCTNTAC TAAAAATACA NAAAATAGTT AGCTGGGTGT | 60 |
| GGTGGTACGC ATANTNTAAT CCCAGCTACT CGGCCTCCCA AAGTCCTGGG NATTACAGTC | 120 |

| | |
|---|-----|
| ATGGACCCAC GGNGCCTGGC CCTGAANCAG TTCTTTAAGG GGATGAGAAC TTGGCCCTCA | 180 |
| AGATCTGGGT TTCCATTACC CCTGCCATCG TCAAGGGTAA AGTNCCTGA ACCTCTGAGA | 240 |
| AAGGGGTCTC CCAACCAGG GGGATCACAG GATCTCCCAA CCAGGGNGGN TGCCCCGGA | 300 |
| GAGTGTGGTC AGGGTTTCAT GAATGTTTAC ACATTTTNAAGTTCTTTTG CAAGCTATTA | 360 |
| GTGAATAATT TCCAGNNAAA TGAANTGGGA TTATTAAATN TCTGTAAAAA TT | 412 |

(2) INFORMATION FOR SEQ ID NO:916:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

| | |
|---|-----|
| TTTGGCTCTG GGGACAGTTG GCATGCNAGG CCTGANTGCC TACTTTGGCC TACTTAAAAT | 60 |
| CTGTGGTGTG AAAGGGTGA GAAACAGTGA ATGGTTAATG CAGCAGCTGG AGCTGTGGGA | 120 |
| CTCAGTCGTG GGGCAGATTG CAAAGCTCAA GGGCTGCAAA GTTGTGGAG CAGTAGGGTC | 180 |
| TGATGAAAAG GTTGCCTACC TTCAAAGCT TGGTTTTGAA TGTCGTCTTT AACTACAAGA | 240 |
| CGGTAGAGTC TTTGGTAAGA AACCTGAAG AAAGCGTCTC CTGATGGTTA TGATTGTAA | 300 |
| TTTTGATAAT GTAGGTNGGA GAGTTTTTCA AACACTGGTT AATCGGCCCA GTTGNANGAA | 360 |
| ATTTGGNAGG GTTTGNCC | 378 |

(2) INFORMATION FOR SEQ ID NO:917:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

| | |
|---|-----|
| GGCAGAGACG GGTAGGAGCC CTGAGTGAGT NTCCATTCCA AGGGGACGAG TCCATCCACA | 60 |
| GTGCAGGTAA CACAGAGACT TGTTTGCTGA CATTGGACCA CGGGATCCTG TGGNGTTTGG | 120 |
| TGACTCCTGT GTTCTTGNAT CTCCCTCTCC CTTAAAACCC ATTCCTTTGG CTCACCTGTT | 180 |
| CCTAGGGTTT CTAACCTGTT ATTCCAAATC TGTCACCTGN ACTCCACAAT CTTNCANTAC | 240 |
| ACCCATCCGA GAAAAAAAGT NGNTCTAAGG | 270 |

(2) INFORMATION FOR SEQ ID NO:918:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

| | |
|---|-----|
| CTGTCTAGCT TNNCAAAGTT CACCAATACT TTAATGTAGA GCTTATCCAG CCTNGNAGCA | 60 |
| GTCAAGGTTC TACGCCTATT ACACCCTNGA GGCAAAGCTG TACCCGTTTT CTACCATCCG | 120 |
| GAAAANGNTA GGATGG | 136 |

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

| | |
|---|-----|
| TTCGGCACGA GGTCAGAAAC ACCANGNGT GGAGGTCAGN GTGTCACTTT TNTGTTTTCT | 60 |
| NTTTGAAAGA TCATTGAGA AACACGTCAC TGATCTCCCC TGCAACCATG TNTTCCATTA | 120 |
| AGATTGAGTG TGTTTTNCCA GAGAACTGCC GGTGTGGTGA GTCTCCAGTA TGGGAGGTAA | 180 |
| GTNTCCAAC CTNTGCTCTN NGTAGACATT CCTGTCAAAA AAGGTTTNCC GGTGGGATTC | 240 |
| ATTCACCAAG CAAGTTACAG CGAGTGNACC ATGGGATGCC CCAGTCAGCT CCGTGGGCTC | 300 |
| TTCGCCAGTG CGGGGAGGCT CATGTTGCCA CCATTGGGAA CAAAGTTCTG TGCTTTNAAC | 360 |
| TGGGAAAGAA CAATCAGCCA TTGTTCTTGG CCACGGTGGG TTAACGACAA GAAAAACANT | 420 |
| CGCTTTCAAT GATGGGGAAG GTGGNTTCCC CCCGAGGTN ANTTGCTGGC CAACCGCAAA | 480 |
| AGTGTTTTAC AAGNTAGGAA AAGGANGAAC AATTCCCANT TGGGANTTGG TATTGATGC | 539 |

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

| | |
|--|----|
| GGTCANCAGC GGCTGCAATA TGGTTGTACC TGGGTCAATA CCCATTTTCAT GCTGGTAAGT | 60 |
|--|----|

| | |
|---|-----|
| GAAATGCCGC ACGGTGGGCA GAAACTTTCT GGTACGGCA AGGATATGTC ACTTTATGGG | 120 |
| CTGGAGGATT ACACCGTCGT CCGCCACGTC ATGGTTAAAC ATTAAGGATA ATATTGCAGA | 180 |
| TCGTAAGAGT ATGAGATGAT CTTTCNTACT GTCAGAGCAC TGATTTCTCT GACAGTAGTG | 240 |
| CTGCGTGCAA AATCCACTAC ATCAAATAAA CCAGCCAAAT CTGCATAGNG GTNAAGAGTG | 300 |
| AAACAAACCA ACAGCAGCAA GAATTTNTNC ATANTACATT CTNANGGGAA ACNTNCTTTT | 360 |
| TGCCACCTTT NTNCNTGCCC NNTGTGTGTN AGTACGGGTT NAGGAAATTC CGCATNATNA | 420 |
| NTCNTCNGAG NTGGGTNAGG GCAGTNGCTG TTTGATGTTT TTNTTTCAAA NGGTGNAAAA | 480 |
| ANTGNTGGCA CGT | 493 |

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

| | |
|---|-----|
| AACTGGTCTT TCATTCACTG TCCAGCTTGC CAATGCAACG GCCACAGTAA ATGCATCANT | 60 |
| CAGAGCATCT NTAAGAAGTG TGAGAACCTG ACCACAGGCA AGCACTGCAA GACCTGCATA | 120 |
| TCTGGCTTCT ACGGTGATCC CACCAATGGA GGGAAATGTC AGCCATGCAA GTGCAATGGG | 180 |
| CACGCGTCTC TNTGCAACAC CAACACGGGC AAGTGCTTCT GCACCACCAA GGGCGTCAAG | 240 |
| GGGGACGAGT GCCAGCTATG TGAGGTAGAA AATCGATACC AAGGGAAACC NTNTCAGAGG | 300 |
| GAACATGTTN TTATNANTCT TCCTTATTGG ANTATNCATT CCACNTTtag TNTNTTCCCA | 360 |
| GGAAGTTGNT TCGTNATTTA CACAGTTATN CATTTTGTGG GTTATTCTTG GAGGAACAAA | 420 |
| ACAGGGGTTT GGGACNGTTN CNTCATGGCN TCCAGGATTT TCAACCTCAA CNTCACNGGG | 480 |
| GTGCCATTTT TC | 492 |

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

| | |
|---|----|
| GGCACGAGCT TGAACAAACC TGGACTGAAA TATAAACCAG TGAATAACCA GGTTGAGTGT | 60 |
|---|----|

| | |
|---|-----|
| CACCCATACC TCACGCAGGA GAAACTGATC CAGTACTGCC ACTCCAAGGG CATCACCGTT | 120 |
| ACGGCCTACA GCCCCCTGGG CTCTCCGGAT AGACCTTGGG CCAAGCCAGA AGACCCTTCC | 180 |
| CTGCTGGAGG ATCCCAAGAT TAAGGAGATT GCTGCAAANA CAAAAAACC GCAGCCCAGG | 240 |
| TTCTGATCCG TTTCCATATC CAGAGGAATG TGATTGTCAT CCCCAGTTC TGTGNACACC | 300 |
| AGCACGGCAT TGTGAGGAA CNTNCAGGTG TTTGGACTTT GAATTGAGTG NTGAGGAGAT | 360 |
| GGCAACCTNA TTCAGNTTTC AACAGAAATG GAGGGNCNGT GAACGTGTTG CATNCNNTNC | 420 |
| NTTGGGAGGA TTTTCCTTCG GTGCAGATNT TGAGGTTGAT CTCNGGTGNG TTNTACAGAG | 480 |
| TTCTNTTNTT CGTTGAGTGT GATTACTN | 508 |

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

| | |
|---|-----|
| GGCACGAGAA GAAAACTAAG CAAGNGGCAC CAGTACCACA TCCGTGCCTA TGAATCCCAA | 60 |
| GGGAGGCCTG GGACAATGCC CGACGTCTAA CTGGNNTTCC ATGAAACCTN CAACATNAAC | 120 |
| GAACTTTTCT NCTGGTGTAG CCAATACGTA GCGCCANATC ACGCCATTCC CCGGACTGTT | 180 |
| GGCCAGGAGA NGAAGGGTTA CTTTGAAAGA TCGTNGCCCC TCTGCCAACT GNGAACCCCT | 240 |
| TTTCGGTGNN CAGANGCCCT NCATNCGCAC GTNTTCTTAT TNAATGGNAA CCGGGGGATT | 300 |
| GAGGCCTTTA NCAGTGACAA AAATTAAGTG GGACTTAGAA CTTGCCAGCT TGTTTGNGGC | 360 |
| CNCTAGGCTT NGTTTCTTT GAAAACCNGA TT | 392 |

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

| | |
|---|-----|
| GGCACGAGTA GACATTNCCA GAGCTCTATG AGTTAGTGAA CAACTATCAG CCTGAGGTTC | 60 |
| TGTGGTCGGA TGGTGACGGA GGAGCACCGG AATCAATACT GGAACNTCAC AGGCTTCTTG | 120 |
| GCCTGGTTAT ATAATGTAAA GCCCAGTTCG GGGCACAGTA GTCACCAATG NATCGTTGGG | 180 |

| | |
|---|-----|
| GAGCTGTGTA GCATCTGTNA GACATGGTGG NCTTCTATAC CTGGCAGTGA ATCGTTATNA | 240 |
| ACCCAGGGCA TCTTTTNTGC ACATNAAATG GGGAAACTTG GATGNCAATA GACAAACTTT | 300 |
| TCCT | 304 |

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

| | |
|---|-----|
| GGCAGAGCCA GGGTGGCAGC CGGTGCCTTC CAGGGCCTGC GGCAGCTGGG AGATGCTGGA | 60 |
| NCTCTCCAAT AACTCACTGG CCAGCGTGCC CGAGGGGCTC TGGGNATCCC TAGGGCAGCC | 120 |
| AAACTGGGTA CATGCGGGAT GGCTTCGACA TCTCCGGTAA CCCCTGGATC TGTGAACCAG | 180 |
| AACCTGAAGC GAACCTCTAT CGTTGGCTTC AGGCCCAAAA AGACAAGATG TTTTCCCAGA | 240 |
| ATGAACACGC GCTGTGCTGG GGCCTGAAGC CGTGAAAGGG CCAAACGGTC CTGGCAGTGG | 300 |
| CCAAGTCCCA GTGAAGACCA GGGGCTTNGG TTNAGGCTGG GGGGTCTNGT TAGGAACANT | 360 |
| GCAACCCNTT TTAACAATGA TTCCTGGCTT TTGNNCNGGT GCGGGGGTTC AGGCTTAAAT | 420 |
| NCCAGCATTT TGGGAGGGCC AGTGGGGGGG ATCACGGGTT | 460 |

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

| | |
|---|-----|
| CCACCTGCAC ACGTTTGTA GNTCCCAGCC GGCAGCCTGG GACTTCCAGT GCTCAGAGGG | 60 |
| CGGGGAGAAT CTCAGCGTGG GNCAGAGGCA GCTCGTGTGC CTGGCCCGAN CCCTGCTCCG | 120 |
| NAAGACCCGC ATCCTGGTTT TAGACGAGGC CACAGCTGCC ATCGACCTGG AGACTGACAA | 180 |
| CCTCATNCAG GCTACCATCC GNACCCATTT GATACCTGCA TGTCCTGACC ATCGNACAAC | 240 |
| GGGTTAACAT ATCAGGGTAC AACAGGGNNG GTCCTGGACA AGGGTAGTNG TGANTTGATC | 300 |
| TCCA | 304 |

(2) INFORMATION FOR SEQ ID NO:927:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

| | |
|---|-----|
| TATATTATCT CCCCCGATTA CCGTCATCGG AGGAGATATA ACTNTNAGGC AAATATCGTC | 60 |
| ATCAAATAGG CGGCAAACAG TGCCAGATGC GCTGCGCCAT TGAGCACGTT ATACGTNCGG | 120 |
| TGGAGAAGGA GATATGGCAC AGCACTAAAG AGGCCACCAT CACCACCATT TCTGGCGCAC | 180 |
| CAAGTGCAAA CTNCAATTCTG TTACCCGTC TAAAGGCAAT TAGCGTNACG ACAGTACGGT | 240 |
| AAGCGNAATG GTTGCTAACA NGGACCAAAG NACAGATTCA TCGCGCGTNG TACCTGGTTG | 300 |
| TTCAACATGG TTTTAATGCA CNTAACCTTN CGGGGACAGA TCAACA | 346 |

(2) INFORMATION FOR SEQ ID NO:928:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

| | |
|---|-----|
| CCACCTGCAC ACGTTTGTA GNTCCCAGCC GGCAGCCTGG GACTTCCAGT GCTCAGAGGG | 60 |
| CGGGGAGAAT CTCAGCGTGG GNCAGAGGCA GCTCGTGTGC CTGGCCCGAG CCCTGCTCCG | 120 |
| CAAGAGCCGC ATCCTGGTTT TAGACGAGGC CACAGCTGCC ATCGACCTGG AGACTGACAA | 180 |
| CCTCATCCAG GCTACCATCC GCACCCAGTT TGATACCTGC ACTGTCCTGA CCATCGCACA | 240 |
| CCGGCTTAAC ACTATCATGG ANTACAACAG GGTCTGGTN CTGGACAAAG GANTAGTTGN | 300 |
| TGAGTTTGAT TTTCCAGCCA ACTCATTGCA GTAGAGGCNT TTTTACGGGT TGCCA | 355 |

(2) INFORMATION FOR SEQ ID NO:929:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

| | |
|---|----|
| GGCAGAGTTG TGGCCCACTT TCTTTNAGAG ACCCCTTGTA AGGAAAGCCT TTAAGAAGAC | 60 |
|---|----|

| | |
|--|-----|
| CCTCAAGGAC CTGAAGCTGA GCTATCTGGA CGTCTATCTT ATTCAGTGGC CACAGGAATT | 120 |
| CAAGTCTGGG GATGACCTTT TCCCCAAAGA TGATAAAGGT AATGNCATCG GTGGAAAAGC | 180 |
| AACGTTCTTG GATGCCTNGG AAGGCGATGG AGGAGNGGTG GATGAGGGGC TGGTGAAAGC | 240 |
| CTTGGGTCTG CATTTTCAGCA TTNCAGNCGA GAAGTCTTGA CAACTGGCTG AATATAACCA | 300 |
| TGANTACCAG TGGTGTCAAC TACTNAGNAG GG | 332 |

(2) INFORMATION FOR SEQ ID NO:930:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

| | |
|---|-----|
| GGCAGAGCAA CACTCATTTT GGGAGGAGGA GGCTATAACC TTGCCAACAC GGCTCGATGC | 60 |
| TGGACATACT TGACCGGGGT CATCCTAGGG AAAACACTAT CCTCTGAGAT CCCAGATCAT | 120 |
| GAGTTTTTCA CAGCATATGG TCCTGAATTA TGTGCCTGGG AAATNACGCC AAGCTGCCGG | 180 |
| CCAGACCGCA ATGAGCCCNA CCGAATCCAA CAAATCCTCA ACTACATCAA AGGGAATCTG | 240 |
| AAAGCATGTG GTCTAGTTGA CAGAAAGAGG TCCAGGTTTC CAGAGCTGAG GAGTGGTGCC | 300 |
| TATTAATGGA AGACAGCGTG TTTTATGCAA GCAGTTTGTT GGGATTTGTG GACTNCAGGA | 360 |
| AAATTTGGAA GGAAATTTAN TCCCGNAAAT TTCCAGGGGC ATCAGTGGGC ANTGGNTTCC | 420 |
| CGGGGTTAAG | 430 |

(2) INFORMATION FOR SEQ ID NO:931:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

| | |
|---|-----|
| ACGGTTNCGC TGTCCCAAAG GTTCCAAGGG CTATGGCTCC CACTGCCTAT GCCTTGTTTT | 60 |
| TGTGNANCAA AATCCTNGGA CAGATGCAGA TNTGGAGTAG CCANAAGCGG GCCCTATGGT | 120 |
| AA | 122 |

(2) INFORMATION FOR SEQ ID NO:932:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

| | |
|---|-----|
| GGCANAGAGA AGATAAACGA GGGGCTGGAA CACCTCGCCA AAGCAGAGAA ATACCTGAAA | 60 |
| ACTGGTTTTT TAAAATGGAA GCCAGATTAT GACAGTCCCG CTTCTGNAAT ATGGAAAAGC | 120 |
| AGCTGTTGCT TTTGAAAAAT GCCAAACAGT TTGAGCAAGC AAAAGATGCC TGCCTGAGGG | 180 |
| AAGCTGTTGC CCATGNAAAA TAATTAGGGC TCTTTTTCAT GCTGCCAAAG CTTATGGAGC | 240 |
| AAGCTGGGAA TGAATGTTGA AGGAGATGCC AGAACTTAC CAGAGGCCGT TCCAGCTTAA | 300 |
| TTGGGGAAGG CCAGCATGAT GTGATCTTAG GAAAACGGGC ACCCCAGACA CAGGCAGCCC | 360 |
| TGGGTTTTGG GGCGAGCNTG GGAAAGTTTT TGGGAAAATN TTGATCCCGN GAAGGCTGTT | 420 |
| ACATTTTTTT CACCGGNCAG TTAATGTGTT TTGAAATNGA NGGACCGTTT ACGGCCAGG | 479 |

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

| | |
|---|-----|
| GGGCCTGAAG GANTTGGGAA GAGCACATTT TAAGGATGAT TGTTTAGNTT TAAAAGTTAA | 60 |
| CAAATANTTT ANTGTAGAGC TTATNCAGCT TGGAGCAGTA AAGGT | 105 |

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

| | |
|---|-----|
| AGTAAAAGGC TCACTATGGA GGNTTCACTG TNCAGAATGA AGNCAAACAA ATACCAGATC | 60 |
| TCAGTGAACA AATACAGAGG NAACAGNCGG TAATGCCCTC | 100 |

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTNCCCCC CNNAANG 58

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GGCACGAGGT GACAACTGCC GGNAGGTGCA CCTCGANAAG CGGCGAGGGG AGGGCCTGGG 60
CGTGGCCCTG GTGGAGTCGG GCTGGGGCTC CCTGCTGCCC ACAGCCGTNA TCGCCAACCT 120
GCTGCACGGG GGGCCTGCTG AGCGCTCGNG GGCCCTCAGC ATCGGGNACC GCCTGACCGC 180
NATCAACGGG ACCAGCCTGG TGGGGCTGCC CCTGGCTGCN TGCNAGGCCG CTGTACGCAA 240
AAACGGAATC GCCAGACGTN CGGGTGAACA CTTNAGCATT CGTCCACTTG CCCTTCCCGT 300
TAACCACCGN CATCATTTCCA CCGGGCCCCC AAGGCCCGNA AAGCAAGTTG GGGTTTTTGC 360
GNTNGGAGGA CGGGATTNAT TTT 383

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

CGCGTGGTCG CATGAAAGAT CTGAAAGCCA GCTATGTNCT GAACAGCAGT GAATTGCATG 60
CGCCGCTGCA AAAGANTCAG GTCGTCGGAA CTATCAACTT CCAGCTTGAT GGCAAAACGA 120
TCGAGCAACG CCCGCTGGTT GTNTTGCAAG AAATCCCGGA AGGTAACCTC TTCGGCAAAA 180
TCATTGATTA CATTAATAA AATGTTCCAT CACTGGTTTG GTTAAAAATT AAACACTTGA 240
AAGTGTAATT TCCGTCCCCA TATACTAAGC ATCAGTAAAA AAACCTCCGC CTTCTGGGGG 300
TTGGCCTTNA TTTNAATTAC GTTAACGCCG GAGCTGACAT GGAAAACCAA ACTTAACGGA 360

CTGCTTGATT TNCCNCTACTC CTTTTACTTA CAAAGTTTTG GGGGCAGGCG TTACCGNGGN 420
TGGTTGATCA GNGGGTTGAA GTGGTACAGN GCCTGGCCAG GTGGCTACAC CCCACGGTNA 480
A 481

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

GGCAGAGTGA ATCATCAGAG AATTCACACA GGGGAGAAAC CCTTTNANTG TAATAAATGT 60
GGGAAAACTT TTGGCCAGAA ATCAAACCTC AGANTACATC AAAGGACTCA CAGTGGGGAG 120
AAATCTTATG AATTGCAATG ANTATGGGGA AATTATGTAA GAGAGTCTAC CCTAAGCTTT 180
ATACCAGAAA ATTCAGGGN GAGGGGGGAA TCCCTATTGA TGTATTA ACT NGGAAATNCC 240
TTTTGACCAA AGGGATTNCC CCNTTTGAT 269

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

CCCAAAATAA CCAGCTAGGG TGGCTGTGGG GCCANANCCG TGCCCTCTAT CCNAGCATCT 60
ACATGCCCCG NGTGCTGGAG GGCACAGGGA AGTNACAGAT GTATGTNCAA CACCGTGTGG 120
GCCGAGNGCA TTCCGTGTGN GCTGTGGGCT GCTGGTGAAC CCCAATNTTG CCGGTNGTTG 180
CCCTATTGTC CCAGATTTTN CTTATGNACA CGGACAAACC ATTTTTTTTG CCCCCTGGGA 240
TTGAGCTTGG GAGCAAAGNC TTGGGGGGGAG AGTNNGGGCC CAGGGGGG 288

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

| | |
|---|-----|
| TGGGGACCTC AAGGCCCGCG GGCTGACCCT NCAGTGGGTG TACTCGGCGC GGGGGGACTA | 60 |
| NATCCGGGCG GCGGAAAANC TGCGGCAGGA GATCTACAGC TCGGAGGAGA GAGACGAGCG | 120 |
| ACTNANACGC ATGTACAACG TGCGCATAAT GCGGGTGGAG TTCTACTTCC TTTCCCAGTA | 180 |
| CGTTTCGCCA GCCGACTCCC CGTTCCGCCA CATCTTCATG GGCCGTGGAG ACCACANGCT | 240 |
| NGGCGCCCTN CTGGACCACC TGCGGGCTGC TTGCGCTTCC CAACAGTTCC GGGNACCCCC | 300 |
| GGGGGNCCAA CTTTCTTNCA ATTGGGTTTT CCAAGGAAAA GCNTTTTNCC GGGTTCAAT | 359 |

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

| | |
|---|-----|
| TGCAGGATTN CGGCAGAGGG AAAANTTGTT TNNTTAGGTT TGGTTAATGC AGGCAAAACC | 60 |
| ACTTTCTTCC ACATGCNCAA AGATGACAGA TTGGGCCCAA CATGTNCCAA CANTACATCC | 120 |
| GACATCAGAA GAGCCTAACA TTTGCTGGGA ATGAACCTTT ACAACTTTTN NACCTTGGTG | 180 |
| GGCAGGAGCA AGCACGTCGC GTTTGGTAAA AATNATCTCC CAGCAATTNA ATGGGGATTT | 240 |
| TTNTNNTTGG TGGGACTGTG CCAGATCATT CTCGNCCTCG TGGGAATCCA AAGTTGTAGC | 300 |
| TTGAATGGCT TTANATGGAT TGGATGGAAA ACAATTATCC CAAATGNTGC CCAATCCCCT | 360 |
| NATTTTTGGG GGAANCAAN AT | 382 |

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

| | |
|--|-----|
| GGCACGAGCC AGGATTGGTG CCTTCTCTNA TGGCTCTGGT TTAGCAGCAA GTTCTTTTC | 60 |
| ATTTTCGAGTA TCCCAGGATG CTGCTCCAGG CTCTCCCCTG GACAAGTTGG TGTCCAGCAC | 120 |
| ATCANACCTG CCAAACGCC TAGCCTCCCG AAAGTGTGTG TCTCCTGAGG AGTTCACAGA | 180 |
| AATAATGAAC CAAAGAGGAG CAATTCTACC ATAAGGTGAA TTTNTCCCCA CCTGGTGACA | 240 |

| | |
|---|-----|
| CAAACAGCCT TTTCCCAGGT ACTTTGGTAC CTGGGAGGCG AAGTGGGACG GAGCCAGCAT | 300 |
| NGCCGGAANG TATTGCCCCG GGGGTCCNG TTTTNAAGG TGTTTTTTNG AAGTTCCATG | 360 |
| GGAAAGTTTC CTGGGGAAAC GTTTTTTTTG GCAGGGTTTT TTCCCCGNGA AATCANTNTT | 420 |
| TTTNAAGGG TCCCCANTTT TTAGGTTGGG AAAA | 454 |

(2) INFORMATION FOR SEQ ID NO:943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

| | |
|--|-----|
| GGCACGAGCG GCACGAGCAC CAAGCAGGCA GTGAGCATGT TTCTNGGAGC AGTGAAGAA | 60 |
| GCAAAGAAAG AAGGTGGCAC AGTGGTCTAT GGGGGCAAGG TTATGGATCG CCCTGGAAAT | 120 |
| TATGTAGAAC CGACAATTGT GACAGGTCTT GGCCACGATG CGTNCATTGC ANANANAGAG | 180 |
| ACTTTTNCCTC CGATTCTCTA TGTCTTTAAA TTCAAGAATG AAGAAGAGGT CTTTNCATGG | 240 |
| AATAATGAAG TAAACAGGG ACTTTCAAGT AGCATCTTTT ACCAAAGATC TTGGGCAGAA | 300 |
| TCTTTCCGCT GGCTTTNGAC CTAAAGGATC CGACTGTGGG CNTTGTAAN GTNCAACATT | 360 |
| NCCAACAAGT GGGGCT | 376 |

(2) INFORMATION FOR SEQ ID NO:944:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

| | |
|---|-----|
| GGCACGAGCC TGTATCAAAA AAAGGAGACC TGAGGAGGGC CTTGAGCAGA TACATCTCCT | 60 |
| CTCTCATCCA CTCAGGTGGC CACTAACACG GACACCAGCC GAAATGCCGG AAATGCGGTC | 120 |
| CTGTTTGAGA CAGTACTCAC CATCATGGAT ATCCGCTCTG CAGCTGGCCT ACGGGTTCTA | 180 |
| GCTGTCAACA TTCTTGGTCG CTTCTACTC AACAGTGACA GGAACATTAG GTATGTAGCC | 240 |
| CTGACATCAC TGCTTTGAC TGGTGCAGTT TTGATTCACA GTGCTTGTTG CAGCGGGNAT | 300 |
| TCGGGCCCCA CTNTGGGTGG GNAATGTTCT AAGGGGGAAA CTNGANTGCC T | 351 |

(2) INFORMATION FOR SEQ ID NO:945:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

| | |
|---|-----|
| GGCACGAGGT GTTAACTTCC AGATAAGGGA ATATNATTNA ATAATTNATN ATTTTNAAAA | 60 |
| TACTGTATTA TGAAGCCATG TTCATAAAGG TAAGAAAGGC AGATTCTACA ACTAGTCAGA | 120 |
| CAACTTAACA TTCATACTAA TGACAGCTTC ATTGAAATCA CTTTACTACT CCCCTAGTAA | 180 |
| TGGAGTCATT GCATTTATAT TATACATTAT TCTCTTTNCA GTTTTGCTAG CCACCCTAAT | 240 |
| TATCCATATT CAGATGAATA TTAAACATGG AGGAGCTTTG CCTGAGGTCT ACCCAGNAAG | 300 |
| CCCTGTGTGT GGGTGGTGAC GNCGAGGACG GTCTCTTTTG CCGGTGGACT GGACANATNA | 360 |
| CNC | 363 |

(2) INFORMATION FOR SEQ ID NO:946:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

| | |
|--|-----|
| GGCAGAGTTG AGCGGCGCAG GGACCGATAC TTGTAATCAG GGATCGCNAC CTCANANAGT | 60 |
| GCCAAGCCCC CGACGCACAA ATATGTCCGG GGAGAGAATG GCCCTGGGGG CTTTCATCGTG | 120 |
| CTCAAGTCGG CCAGTTAACC CCCGTNTTTG NACCTTTNTN TGGGNTCTTA ATACAGGTCT | 180 |
| | 180 |

(2) INFORMATION FOR SEQ ID NO:947:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

| | |
|---|-----|
| GGCAGAGCGG ATCACTGGAG CAAAACCTG TCCCAGTTTT TCCCTGAGGC CATTTCTTTC | 60 |
| ATAGATGAAG CCCGGGGCAA GAACTGTGGT GTCTTGGTAC ATTGCTTGGC TGGNCATTAG | 120 |

| | |
|---|-----|
| CCGCTGCAGT CACTGTGAAC TGTGGCTTAC CTTATGCNGA AGCTCAATCT GTCGATGNAA | 180 |
| CGATGCCTAT GAACATTGTC AAAATGGAAA AAATCCAACA TATCCCCTGA ACTTCAACTT | 240 |
| CATGGGTNCA GCTGCTGGAC TTCGAGAGGA CGCTGGGGAC TTCAGCAGCC CATGTGAACA | 300 |
| ACAGGGGTTT CCAGCACAGC AGCTGTATTT TTACCACCCT TTCCAACCAG AATGTGTTAC | 360 |
| CAGGTGGGAC TTTTGTCAAT CTAGGGNAAA GACCCACAC CCTCNTGNTG GGATGTTGTN | 420 |
| NGGCCTTCAG CAATTTTTTTT GGCAGC | 446 |

(2) INFORMATION FOR SEQ ID NO:948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

| | |
|---|-----|
| GGCAGGAGCC ATCATTCCCC AAGANCTTCA AAGATTTTAA AGGCCACCAT TTCCATGCAC | 60 |
| ATGTTTCTTG GCGTTGCTGC TGTTTACACT ATGTGGAAAG CTGGACACTC AGCCTGTTTC | 120 |
| GGGGGGACCC AGGCTAAAGG TTNTGCCCTA GGTGTGGTAA GTATCTATTG ATGCGTAGTG | 180 |
| TGGCTTGCAG GGAACACAG GGGCCACACA CCAACCATTA AGCACCAGGC CTAAGGCAGN | 240 |
| AAGCAGAGAG AAACCAACTT CAAGGTCAGA GGAGCCGCTG GGNAGGGAGA AAGGTGTNTN | 300 |
| GGTGGAGGNC TAACCAGA | 318 |

(2) INFORMATION FOR SEQ ID NO:949:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

| | |
|---|-----|
| ATGCCAAAGT NTTCGATGAA TTTAANCCTC TTGTGGAAGA GCCCTTCAAA ATTTAAATTC | 60 |
| AAACAAAATT GTGAAGNTTT TTGAAGNCAG NTTGGAGGAG TTACAAATTN CCAGTAATGA | 120 |
| GCCTATTAGT TCGTTAACAC CANGTA | 146 |

(2) INFORMATION FOR SEQ ID NO:950:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

| | |
|---|-----|
| AACCCATAAN TCCAAAAAGA AGATCAGAGA ATATTATAGA CTGCTGANCG TGGAGGAAGG | 60 |
| ATGCCCTGCA GATGAAAGTC AGGGNAATCT TTTCATAAGC TTGCCAAGCA ATATCATCCT | 120 |
| GAACAGTGGC TCTNAATACT GCTGATTCTG CCAACATTTA TAAAGGNTTG AAAAAGCTTA | 180 |
| TAGNAAAGGT GCTCTCCCAT GTGAATAGAN CAAACAAATG CCAGTCAAGN GTNAAAGGTG | 240 |
| AAGNAGGANG NAGATGTAGG AAAANTTCAA ATATNAAAAC ACCCCAACAC CGGCNTTATT | 300 |
| TAAGTTTTTG AAGGGTTNNT GGTTTTGGGG NCTCCAAATT CAAGGGGGGA AGGCTTTTTG | 360 |
| GGGNCANTTT TGGGGG | 376 |

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

| | |
|--|-----|
| TATTTAGGTT TCTTTAATTT TATTCAACAA TATTTTGTA TTTTCAGCAT ATAAGTCTAT | 60 |
| CACTGCATTG GTTAAATTTA TTCCTAAGTA TTTTACTGTT TTTAATGCTA TTCTAAATGG | 120 |
| ATTCTTTTTTA AAATTTCCCT TTCATATAGT TCATTGCTAA CCTATAGAAA TACAACTGAA | 180 |
| TTTCATCATG GGCAGTTTTT TTTCTACATC TTAAGGAAAT TAGTTTATTA GCTCTAAATG | 240 |
| GGGTTTTATT TGTGGATTCT TTAAAGGTTT TCTTCCATAT TAAGATCCAT GTCCATCTCT | 300 |
| AAAATAGGGG ATTAGTTTTA ATNTTTTCCA TTFNCCCATT TGGGCTGCCC TNAAANTTNC | 360 |
| NTTTCCTGCC CNAATGTTCC CGACCNGAAC TTCCGCAGGT ATTGGATAGA GTGGTGAAGC | 420 |
| AGGGANCTTG GCCCGGTTTT TAACCTAAGG GNAAAGGTTN CG | 462 |

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

| | |
|---|-----|
| GGCACGAGGT TTTCTCATGC TTTTNAAATC ACTCCATCCG TAGCCAAGAA GATTGCTGCT | 60 |
| GTACTIONAGG ATTCAATTTCC ATTGAAAGTT CGTGGCATCC ATTTGATAAA TGAACCAGTA | 120 |
| ATTTTCCATG CTGTCTTTTC CATGGATCAA ACCATTCTCTG GACTGAAAAA NTTAAGGAAC | 180 |
| GGACAGGGCC TCACTTTGTG NCAGTGGGCA CGATCTTGGG CTCACTGCAA CCTCCACCTC | 240 |
| CTGGGGCTTC AAGCAATCCT CCTGCCTTCA GCCCACCAAG TTATCTGGGG ACTTACAGTN | 300 |
| CCTGCACCAC CANGGCTGTN AAATCCCCGC ACNTTTGGGA GGGCCCNNGC GGGCGGGTTC | 360 |
| ACGGGGTTCA GGGGNTCGGG ACCCTTCCGG GTTAAAANGG TGGNAACCCG TTTTTTANTT | 420 |
| AAAATTCCAA AAAATTTGGC CGGGNGTATT TGCGGGGGGC TTTTAGTNCC CATTATTTGG | 480 |
| NGTTTTNGGC AGGGATGGGG GTTAN | 505 |

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

| | |
|---|-----|
| GGCACGNGCG CATCATAAGG GGCCGCTGG CGAAGGCTGG AAGTGGGGCG GCTGCAGCNA | 60 |
| GGACGCTGAC TTCGGCGTGT TAGTGTCAG GGAGTTCGCG GATGCNCGCN AGAACAGGCC | 120 |
| NGACGCGCGC TCGGCCATGA ACAAGCACAA CAACGAGGCG GGCCGCACGA CTATCCTGGA | 180 |
| CCACATGCAC CTCAAATNCA AGTNCCACGG GNTGTCTGGC AGCTTTNAGG TTGAAGACCT | 240 |
| GNTTGGTNGG GCGCAACTTG ANTTTCCGTT GCCATCGGTG ACTTTCTCAA GGACAAGTTA | 300 |
| TGACAGCGNC TTTGGGAGAT TGGTTAGTAG AAGAAGNAAC CCTTNNTT | 348 |

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

| | |
|---|-----|
| TTTCCTTTAA TCTTCCCGCC CTGTAAGTGT TTCCATGCTT TATGAGCAAC AGCCTGACGG | 60 |
| ACCGCGACAT AGACATGCGC CGGATGCACG GGTATTTTGC CAATATCTGC GCCATCAAGC | 120 |
| CCGATATCTC CTGTCAGTGC ACCTAATACA TTACCCGGGC GCATTTTGGC TTTTTCCTCG | 180 |

| | |
|---|-----|
| NCATCGATAC ACAACGTTGC CATTTCTGCT TCCAGCGTCG CAATGTGAAC TATTTAGCTG | 240 |
| GCGGCGTTTT GNCAGTNAAA GTTTTTATCT TGCAACATGT NCAGAAATGG ATATTGGGCC | 300 |
| CGCTGGTGGT TTNTTCCGG AGNCACAGT | 329 |

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

| | |
|---|-----|
| GGNAGAGCCA TGGNGGNGCT GGTGGATNAG GGNCTGGTGA AAGCCCTTNG GGTCTCCAAT | 60 |
| TTCAGGCACT TNCAGATCGA GAAGCTCTTG AACAAACCTN GACTGAATNN TAAACCACTA | 120 |
| ACTNNCCAGG TTGCAGTGTC ACCCATACCT CACGCANGAG AAACNTATC CAGTACTGCC | 180 |
| ACTCCAAGGG CATCACCGTT ACGGCCTACA GNCCCCTGGG TTCTTCCGGA TAGACCTTGG | 240 |
| GCCAAGCCAG AAGANCCTTC CCTGCTGGAG GGTNCNAAGC TTAAGGTAGA TTNTTGCAA | 299 |

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

| | |
|--|-----|
| ATCACTTTTG ACCTCAGTTT TAACAACCTGA GGAGGAGGAG CTCATCATGT ATCTGTTTAT | 60 |
| TCATTTACCA TATATTTATT AAGCACCCAC TCTATTCTGG GAAATAGTNT ACAGTAGTGA | 120 |
| ATACTAAAAT GCCGGGCTAA TATCTCTACC TTCATATAGC TCACATTCTA GTGGCAGGAA | 180 |
| GAGATAATAA GTAAGATAAN ATGAAGTACA ATATATAATA TGTTAGATAA ATGCTCCAGT | 240 |
| GGGAAAAAAT AAAGCGGGGA AGGAATACAG GGAATGCCTG CAGAGTTGAA TGGTTAAGGT | 300 |
| AGCTTGGGGA AATCCCTCAC TGGGGNNTCC GNGGAACCTC AACAAAGGGN CCCCCTGAGG | 360 |
| CTTGTCTGGG GGNCCAGAAA GCTCTGTCTG GGGGCCTGGG | 400 |

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

| | |
|--|-----|
| AGAAGAGCTA ACANTTGCTG GAATNACCTT TACAACCTTTT ANTCTTGGTG GGCACGAGCA | 60 |
| AGCACGTCGC GTTTGGAAAA ATTATCTCCC AGCAATTAAT GGGAATTNTT TTTNTGGTGG | 120 |
| ACTGTGCCAG ATCATTCTCG CCTCGTGGA ATCCAAAGTT GAAGCTTAAT GCTTTAATGA | 180 |
| ACTGATGAAA CAATATCCAA TGTGCCCAAT CCTTATCTTG GGTAACAAAA TTGAACAGAN | 240 |
| CAGATGCAAT CAGTGAAGA AAAACTCCGT GAGAATAATT TGGGCTTTAT GGGACAGACC | 300 |
| ACAGGTAAAG GGGGANTGTG AACCTGAAA GGAGCTGAAT GCTCGGCCCN GGAAGTNTTN | 360 |
| CAGTGCCATG TGGTTCAAGA GGCAAGTTAC GGCGAGGTTT NC | 402 |

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

| | |
|---|-----|
| CAGNAGGGAA ATNNTATTTT TAANTCCAGC ACGGGGTAC TGTTTTTTTA TCTCAAAGCC | 60 |
| AAAAGCCACA GGCATGGCCA CAGTTACTGT NCATCTCAGG GAATGTGAAA AGANTCAAGA | 120 |
| TCCAAGCAGC CACAGACTCA AAGGNACATC AGTGAAGTGC NTGGCCAAAG CATACCCACA | 180 |
| GTACTACAGA AAGCCGTNCA GTGGTCAAGC GGATGCCGGC CATGCTCACT GGACTCTNTC | 240 |
| AAGGTCTGTG GCACTCGGNC AGGTGGTGTT TACTAGTGNT CCTCATAAAA NTTAACCTCC | 300 |
| CTGGTGCGAA TTTCCAGTTC ACCTGGTGAT TGCGGACTGG GAATTCTTGA GNTTTTGNTT | 360 |
| AAGAGCTGTT GCTGTTGGCT GNAGTATGGG TTGTGTTATG TNNAAGGTG | 409 |

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

| | |
|---|----|
| TAAAGCTAAC CAGCAATTTT AAGTCTACTG TAAAATCAAT GGGTCTGGAA ATGGATGGNC | 60 |
|---|----|

| | |
|---|-----|
| TGTTTTTNAA AAGAGAACTT GNATGGCAGT TTAGATTTCA AGAAAACTG GTTTCATTAT | 120 |
| GAAAGNAAGG NTTTGGANCA TCTTTTTCCT NACTGGGCAC AACAAATTTT TGGCTGGGAA | 180 |
| AATGAGAAAG GTTCATTTGA ATAAAGGCNC ACAGTCTGCC ATCCCATATG CTTTNAGAGN | 240 |
| TGGGACTGGG AAGGACTGGG ATGGGCAGAN CCCNTACT | 278 |

(2) INFORMATION FOR SEQ ID NO:960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

| | |
|---|-----|
| CGCGTCGTTT TNACCTGTNA CGTTCACGCC CATTGCAGCG GCACAGTCAC GCAGACGTGC | 60 |
| AGCGGCGACT TTCCTGTTGA ATACCTGAAC GTGCGGCANA AAACGGCGTT ACATACACCG | 120 |
| TGTGGCAGGT TGTAGAAACC GCCCAGCTGG TGCGCCATCG CATGAACATA ACCCAGAGAA | 180 |
| GCATTATT | 188 |

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

| | |
|---|-----|
| TTAACCAAAA TCCTGGACAA ATGCAGATNT GGCCTGCAAA ANGCGGCCCT NTGGAAACCT | 60 |
| GGTGTNTGTC CTCATTGGGG CTTAAGGGNT CCTTCCGTTT CCTCCCTGGT TGAANAGCAT | 120 |
| TGGTTAACAN CTACTTCATA ACGTTTGGTT TGGGNCTCC | 159 |

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

| | |
|---|----|
| CCGCCTCAAG GACCCTCAGG TNTGGATGGA TGCGGGCACC CANNTCTNNT TCTCCTTTGC | 60 |
|---|----|

| | |
|---|-----|
| CATCTGCCAG GGGTGCCTGA AAGCCCTGGG CAGCTACAAC AAGTNTCACA ACAACTGCTA | 120 |
| CAAGGANTGC TTCGCCCTAT GCTTCCTGAA CAGTGCCACC AGCTTTTTTGG CTGGGTTTTTT | 180 |
| NGTCTAGATT TGGGACATAT CTCCTGGAAG GAGCTATTAG CCATGACCCA CAAAGGTCAG | 240 |
| AGATTAGGGT TGCTGGTATT TTGGTTTTGG CTGNTTAAAG AGGCCCTTAG GGACCANAAT | 300 |
| TTTTCCN | 307 |

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 423 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

| | |
|---|-----|
| CGTGGTGGNT CATGCCTGTA ATCCCAGCAC TTTGGGAGGC CAAGGCGGGT GGNTCACGAG | 60 |
| GTCAGGNGTT CAAGACCAGC CTGGCCAAGA TGGTGAAACC CCATCTCTAC TAAAAATACA | 120 |
| AAAATTAGCC AGGCGTGGTG GCAGGTGCCT GTAATTCCAG CTACTCGGGA GGCTGAGGCA | 180 |
| GAGAATTGCT TGAACCTGGG AGGCGGAGGT TGCAGTGAGC CGGGATCACG CCACTGCACT | 240 |
| TCAGCCTGGG CAACAGAGTG AGACTCCATC TCAAAAACCA AAACAAAACA AAAAAAATT | 300 |
| CTTGCTCATT CTGCGCTAAC NATGCTTTCC CTGTTACCGT CANAGTAAAT ATATCTTACT | 360 |
| GGGGCTGGNA TTATAATTTA CANAACATTT TTNACATATT TGAGTNTTTC CTCTTGAAAA | 420 |
| AAT | 423 |

(2) INFORMATION FOR SEQ ID NO:964:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

| | |
|---|-----|
| CGAAGNCCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT GTCATCATCA GAACTCAAAA | 60 |
| GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGNCANTTC TGAAGCCCTC | 120 |
| AAGCAAGAGA CTTTCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTCCACCATG | 180 |
| TAAAAAATA CCTCTTTAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT | 240 |
| ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA | 300 |

| | |
|---|-----|
| CCAAAGGCAA CAGAGTCTTA GTCATGGCC ACCAGACCAA AAGCATCCAG TTCTGTTGCA | 360 |
| CCTCCTGGAA AGCTNGCAGA GGCCCTGGAN TTTCCAGNTC ANCTNAGGGG AAAGGGTTGT | 420 |
| TT | 422 |

(2) INFORMATION FOR SEQ ID NO:965:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

| | |
|---|-----|
| CGAAGNCCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT NTCATCATCA GAACTCAAAA | 60 |
| GCCACAGCAC CTGAGACAGA AGGAGAAATT CTAGAGTTGA ATGACAATTC TGAAGCCCTC | 120 |
| AAGCAAGAGA CTTTCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCACCATG | 180 |
| TAAAAAATA CCTCTTTAAC CGGNTCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT | 240 |
| ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TGCTGTGGAG TGAAAAGCAA | 300 |
| CCAAAGGCAA CAGAGTCTTA GCTTCATGGC CACCAGACCA AAAGCATCCA GNTTCTGTGC | 360 |
| ACTTNCCTGGA AAGCTGGCAG AGGTCCTGGA TTNCCANTTC TACCTNGGGG | 410 |

(2) INFORMATION FOR SEQ ID NO:966:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

| | |
|---|-----|
| GGCACGAGCA AACTATAAAA AATGGTACCC ATGGTTAGGA CATAGCTACA CAAGCATTTG | 60 |
| TAGTTTAGAA TATATAATTC ATAAAAATTT GAAGTGAGAG GAATAGTTAA TATGTAATAG | 120 |
| AAGAAAAAGT ACTTGCTCAG GTAGTTGTAA CTCTTAATAA AACCAATGAC TAGAATACAA | 180 |
| GTGGAAGTAA AAAGGTGGAG ATAGATTAAT AGCCTAAATA ACGAGAGAAC CTTATGCCTT | 240 |
| TTTTAAAACA AAACAAAACC ATTGAGACAT TTTACTTAGT CCTAAAATCT AGCCTGGGNT | 300 |
| TTATGCTATA AATGGATATT CTATTTTTCA TGTAAATTG TACATTACNC AGAAATNATN | 360 |
| AATATTNTTA CTTT | 374 |

(2) INFORMATION FOR SEQ ID NO:967:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

```
CGAAGACCAT ACCTGATGGA GTCTCTGCCA AAATATTTTT NTCATCATCA GAACTCAAAA      60
GCCACAGCAC CTGAGACAGA AGGNGAAATT CTAGAGTTGA ATGACANTTC TGAAGCCCTC      120
AAGCAAGAGA CTTTCCCCCC GACATTACGA CACTGTATAG AGCGGCTTTA CTNCNCCATG      180
TAAAAAATA CCTCTTTAAC CGGATCGACA TTCCACCATA TGAGTCCTAT GAGAAGCTCT      240
ACGAGAAGCT GCTGACAGCC GTGGAGGAGA CCTGCGGGTT TAGCTGTGGC AGTNGNAAAG      300
CANCCAAAGG TCAACAGTGT TTTNGNTTCA TGGCCACCAG TCC                        343
```

(2) INFORMATION FOR SEQ ID NO:968:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

```
GGCANAGCCA TNATGCTTTC ACCAAGGCAA TCCAAGAAGC TCGGCAAATG AAGGAGCAAC      60
TCCGACGGNA ACAACANGTN CTTTANGGGT AAGGTGGCTT TTGTGAATAG TCTGGGTCTC      120
AATAACTGGC CGAACAGAAA AAAAAAAAAA AAAANCTT                        158
```

(2) INFORMATION FOR SEQ ID NO:969:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

```
TTTTTCTCTG AACTATTTGT TNATATCACT TTGCCCATTT TAAAAATTGG GTTTCCGCCC      60
CTCTTAATGA GCAGGAGTAG CCTTCTGTGT ATTGAGTTTA ACTTTGTGAT ATAAGTTGCA      120
GATTCTTTTT CTCAGGTTTT CATTCTATT TTTCTGTAG TTTGTACCTT TTCCATTTTT      180
ATGGATATCT AACTCAACC TTAAGTGCA GAACTTCACT GATACTTTTG TTAGGTAAAC      240
```


| | |
|--|-----|
| ACACATCTGT CCCAGGATA ATTTAACACA ACGACAGAGA AGGGAGGTAG NAAAANNAGT | 300 |
| TNGTAGAGAG CTCAGNAAGG GGCTGG | 326 |

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

| | |
|---|-----|
| GGCAGGAGCT AATATATAGA ATACACTTTT ATAATATATT NTAATATATA GAATACACTT | 60 |
| TTATAATATA TTNTAATATA TAGAATACAC TTTTATAATA TATTCTAATA TACATAATAT | 120 |
| ATTCTAATAC ATGTAGACAC ACCCAATTTA ATGCTTTGCA TGGGCATAGT TATGCAAAGC | 180 |
| CTAGTTCTTA AGTGCGGTGG TCTCAATGTG TCCCCCAGAA TTCATATGAT TGANGCTTAA | 240 |
| TCCCCAGTGG CAACAGTGTT GAGNAGCTGG GGCCTAATGG GAAGTGTTTA GTTTNTGAAG | 300 |
| GCCTCTGCCC TGCATGAANN AGGTTNAATG TTGTTGTGGA AAAGGGTGTG GA | 352 |

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

| | |
|---|-----|
| CTTATCTAAT TCCNCTGGCT AGANCCTCAA GTATAAGGTT AAATACAAGT GGCAAGANTG | 60 |
| AATATCCTCG TCCTGTTTCT GAGCTTAGAG GAAAAGCCCT ATCTTTCACC ATTAAATTTG | 120 |
| CATGGTGGTC GTCAGTTTAA CATAGCTGTT CTTTATCAGG TTGAAGGTGT TCCATTCTAT | 180 |
| TTTTNAGTTT ATTGAGTGGT TTTACTATAA AAAAGCATGT TGNAATTTTG TNAAAATATA | 240 |
| TATGCCTTTT TCCTATTGGG NATACTTAGT GGGATTTTGG TCCCTTTAAT TCCCGNTNTA | 300 |
| TANGGTTTTT TAACANTTAA TTTGGATTTT CAG | 333 |

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

| | |
|--|-----|
| GGCANAGTCG CATTGCCCC GCGGCAGCCC CACCCCGCT CCCTTCCCCA GGCACCGCGG | 60 |
| CGGGANGCCC TGCCCTGCCG CTGAACCCCC TGTGTCCTGC TCCGGCCCTC TCGCCAGGNA | 120 |
| CTCCTGGCCT AGCCTTGCAC CCCGACCCTT TCCCGGGGAA GCCGGGGGA CCTTACGCTG | 180 |
| GGGGCTTGGT GCCGCCCCGAA GTNATGACCC CGCGTGGGAA GAAGCAGGGT TAGGGGGTNG | 240 |
| GGAGTCCTTG GTAAGATCCC TGGACGTCAG NACAGTAGAG GCGGGTGGTA GANGGGTNGG | 300 |
| | 300 |

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

| | |
|---|-----|
| GGCAGAGCG GGAGCAAGAG TCCGCTGAGC TGCAGTGTCT GGTGAGAGT ACCCGTGGGA | 60 |
| CGGTCGNCNC GGGGAGGCAG CCGTCCCGGG TTAGGTGGCG TGGCCGACCG GACCCCCAAC | 120 |
| TGGCGCCTCT CCCCCTGAGG GGTCCCNAGC TAGGAGATGG GAGGCACAGC TNCGTGGGCC | 180 |
| TNGGCGGAAA GNAATGCGGG GTCCGCTTN | 209 |

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

| | |
|---|-----|
| GGCAGAGCGG GGACATAGTG AACACTTGTT CGGGGACATG NTAGACACTT ACAACTAAGG | 60 |
| CATAAGAACC CGTTTATGGA GTCGCTTATG CCCTGGGAAT GCNAGAAATA CCATGTCATT | 120 |
| ACGTACTGAG TTTGTTTNGT TCGCCTCGCA GGNACGGGGC GACATCCGTT CCCTCTGCCG | 180 |
| TCGCTTCGGC ATTTNACCTG CCACCGGTTA CAAGTGGCTC CAGCGCTGGG CTCAGGAAGG | 240 |
| TGCCGCCGGT CTTCAGGACC CCCCCNGCC ATTCCGCACC ATTCCCCGAA CCGTTCATCT | 300 |
| GAACGACATC ACGGCCCTGC TGCCTATGGN CCCATGAACC GTAAGNAACG TTGGGGAGCC | 360 |

CGNAAGTTTA AGCGTTGGTT CNAGGGGGGG CCCGTACCAT TGGCCTTTAA TNAGTCGATT 420

A 421

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GGCACGANAA GCGTACTGCA ATTAAGGCCT TCAATNAGAC TATCAAGATC TTTNAAGAGC 60
AGGGCCAGAC TCAAGAGAAA TGCAGCAAGG AATACCTGGA GCNCTTCCGG CGTGAGGGCA 120
ACGAGAAAGA GATGCAAAGG ATCCTNCTGA ACTCCGAGCG GCTCAAGTCC CGCNTTGCCG 180
AGATCCATGA GAGCCGCACG ANGCTGGAGC AGCAGCTGCG GGCCCAGGCC TCGGACAACA 240
GAGAGATCGA CAAGCGCATG ANCAGCCTCA AGCCGGACCT CATGCAGCTG CGCAAGATCC 300
GAGGACCAGT ACCTCGTGTG GGTTCACCCA GAAAGGCGCC CGGCAGAAGG AAATTCAANG 360
NTGGTTGGGG GTTTAAAAATG NGATNNGTGG TAT 393

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

GGCAGAGAAA CAGCTGTNTG AATTATGTCT GCACTAAGTC TCTGGCAGAG GAAGCCCAGA 60
GGCCGTGAAC AGCATATCTA AAAGCCCCGA CATGTCTTGA AAAGGTCAGG GANACGTCTG 120
TAAATAAGGA CTGACGTTTG GGAAGGAGGC CTGAAGGATT AAGTAGACCT TNCCCCAGTG 180
GGGNCGAAGG AATGGGGAGA GAAGTCCCTG GTAGAGGGGA ACCCCATTTA NCAGAGCTTC 240
CGGAACGTGG GNAAGGAAGC TTGAACTCTG CCGAAGGNAA CTGGNAGGAA AGACCTGTGT 300
TACTGCCAGG GTCCAAGAGC TTGGGAAGAG GGTAGGTTGG GGGCCAGATG GTGCCCCGGT 360
TTTGGTTGGN CGGTGAGGAG GAGNCTGGGG ATTTGGAACA CCTGCCTTTT TGGAGCTGTT 420
NGAAAGGATC CAATGAGTTC ATCCTTCTTN TTACCAATNC TGGNTTCCCA TT 472

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

| | |
|--|-----|
| GGCACGAGTG GCCACAATAG AGGCCATTAT GCAACCTTGA AAAGTTATTG TGATAATGAC | 60 |
| CACATAGCAA TGTGAAGAAA TAGGCATGAC ATGTATCTAA GTGAAAAAGA TGACATAAAA | 120 |
| NCTCTGCACC CAAGTAAAAC TATGCAAAAAG GTAAATATGC AAAAAGGAAA TAATGCAAAA | 180 |
| NGAAAAGGGT TGTATATGGTG ATAAAATTAT GGCCATGTTT TTATTCTTTA TTTCATAAAC | 240 |
| TCTGTAATAT GTTATTATTT TCATAATTAA AAATTATACT TTTAAGAAAAG GAATGCCAC | 300 |
| TNGGAATTGA GCTCATTTAG GCATTGAGTG AAATTACTGC TTTCAAAGNN ACAGCNTTAT | 360 |
| GAAGGATTNA CAAATGTGTT TAGAAGCCCN TTTTGTGTGTT TGTAACATT | 410 |

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

| | |
|--|-----|
| GGCACGAGNA TAAACAGCTC AATGAAATTA CTAAAAAGGA AAACACTGGC ATAAACGGTC | 60 |
| CCCAGATCAA GATATAGAAT GTNACTAGCA CTTGTAAGGC CCTCTTGTTT CCACCTTTTCT | 120 |
| AATTCTGTTC CATGGAGAAC CACTATCCTG AACTTCTGAA TACCATAAAT NAATGCTTAT | 180 |
| TTGGGGGTTT AATTTTGAAA GGGATTAGGA AATACATAGT GTTCTGGGTC TGGTTTTATC | 240 |
| CATGCCATTG AATTATGCTT GTGGTTCATT NCATTCTCAT TGCTGNCATA TTAATTCCTT | 300 |
| TTGAAATTNT TNTGAGCACA ATTTAATTTT AANTGTTGAT GGGACATTTT TCCCTGCA | 358 |

(2) INFORMATION FOR SEQ ID NO:979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AAACATGGTG CTGTTTACTG NGGACCCGAN CANCGTCCAG GAAGCATGGG GTCCGGTCGG 60
AGCGAAAGAT GGCGNGTTTG GTNAGGAGGC ACTGGCGAGG 100

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GGCACGAGCG GCACGAGGGA ATGGAGTNAA ATGGAATGGA ATAGACTCGA ATGTAATGGA 60
CCAAAATNAA ATGGACTCGA AGGGAATGAN CTCGAATGCA ATGGAAGCGA ACGGAAAGGA 120
ATGGAATAGA CTCGAATGGA ATGGACTGGA ATGGTATGTN AATGGNAATG GNAATGGAAA 180
CGAATGGTAA TGGAATTCAA TGGGAATCGA ATGGGAATCA AATGGNAATG GNAATGG 237

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

GGCAGAGGNC ATGGCTGGCT AGTTGTCTGG AGTGTGGATC AAGAGAGACA GGATTATATT 60
ACATGCTCTG GTATATTACA TTAAGCTGGG TCCTGATTCA GGGCCAATAT TTAAGTTCAC 120
TGAATGCTTG TTGCCTCGGA ATNTCTCTCT GGCTGAATGG CTGAATTTAT CTCCCTGAAA 180
GAAACATGGT GGTAAAGTCT CATGAAGCAG TCCATAGACT TATGAAACAA AATGCTGCAG 240
CACTTTTCTG TCTCAGGGAT AGAGACATGT AGGGAAAATG AGCACTGGGC TGAGAGTCAC 300
ATGTACTATA TTCTAGACCT GACACTGCCG TCAAGCAGGT GTTTTCACTC AGGGGCAATT 360
CTGTTGTATT TCCGAAAAA CTCNNTTCT NAATCTATAA ACTNNGGNGA AAATG 415

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

| | |
|---|-----|
| GGCACGAGCC CTGCACTCGG GTTGATTCCA ATCCATTCCA TTCCATTCCA TTCGATTCCA | 60 |
| TTCCAATACA ATTNITTCCA TTCCATTCTA TTCCGTACCA TGCCATTCCA TTCCACACAA | 120 |
| TTCCATTNCA TTCCATTCCA GTCCGTNCCG TTCCGTTCGG TTCCATTCCA TTCCATTNN | 180 |
| ATGCTATTCG AGGTTAATTC CATTCCATNC CATTGATTG | 220 |

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

| | |
|---|-----|
| GGCACGAGCT GGGTCGCCAC CCCTTCCCTC TCCACCTCCT CCAGCCCAAG CCCTAAGGCG | 60 |
| TAGNAAGGTG GCCCTGAGGC CCCGCTTGGC GTNGGANNCG GGGGTCTTTT TGCCTTAAGG | 120 |
| AACCCGCCGC CGCATTCCTA GGGTTTTTAA AGATCCTCTC CCCCCGCTCC TCCAGCTCCT | 180 |
| CGTTGAGCCG GAGGAAGGCC TC | 202 |

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

| | |
|---|-----|
| CTGCTTCCTA GAGGGCAGCA AGGTCTCCCG GGTNACCCTG CACAACGAGA GCTACATAGA | 60 |
| GGAGTTGGAC ATCCGCATCG GGGACTGGTT TTTGGTGCAC AAGGCGGGCG GGGTCATCCC | 120 |
| CAAGGTCCTC CGGGTTNCTC AAGGATTNC GCACGGGGGA GGAAAGGCC ATTCGCTGGC | 180 |
| CCGAAACCTG CCCCATTNC GNCACCGTT TCCTTCAAGG TAGGGGNAAG GTTNCACCGC | 240 |
| TGGCCCCCAA CCCCTTTTNT CCCC | 265 |

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

| | |
|---|-----|
| CTTGCCAGN AATGTGGTTT TAATTTGTAT TCCCCTGATA ACTAATGAAG TAGAACTCTT | 60 |
| TTTCATATAT TTACTATTCA TTTGGAGTGN TAAAAAATT TTATGANCAC TTGCATTTTA | 120 |
| AANTATTAAA CTTTCCTATG TTAAGAAGGG CTGTTGTAAA TTAGTTATGT NCTAAAACAT | 180 |
| TTGGGCATAN TCATTGCAGT CTATCTCTGT GATTTGCNTA AGTTGTGNAT TCTTTGGAAA | 240 |
| TATTTTTTTC CNT | 253 |

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

| | |
|--|-----|
| GGCAGAGNCA CCTGCGGTCT CCTGCATTAT CAGGAAGATC AAGGNAGCTG GTGGAATCAT | 60 |
| TCTAACAGCC AGCCACTGCC CTGGAGGACC AGGGGAGAGT TTGGAGTGAA GTTTAATGTT | 120 |
| GTCTCAGACA AAATCTACCA AATCAGCAAA ACGATTGAGG AATATGCTAT ATGTCCTGAT | 180 |
| CTCCAAATCG ACCTATCTNC GACTAGGGAA GACAAGAATT TGAACCTAGA GAACAAATTC | 240 |
| AAACCATTCA GAGTAGAGAT AGTGGGACCC ATGGGATTAT CTATCTTNAA CCTCCTTTTCG | 300 |
| GGACCATCTT TTGGACTTTN CATGCCCTTC AAGGAGTTTG GCTTGGNACT NGGGGGCCCC | 360 |
| AGGCCCAAAC TNGGAAAGGA TTTTCGGCGG TTTGGTAN | 398 |

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

| | |
|---|-----|
| GGCAGAGGTA ATTCTNCGTT AATTCGGCAC CANAGGATTC AACTGGAGA GAGACCCTAT | 60 |
| CACTGTAAGG AGTGTGGGCG AGCCTTTAAT GATAATGCAA ATCTGAATCA GGCATCAAAN | 120 |
| AATCCACAGT GGGGNACAGA CCCTATTACT GTACAGAAAC ACGTGAATGT GGGAAAAGCA | 180 |
| CCAGGACATC CCCACAGTGG AAAAATATCC AAGGAAAGGT TCCAAGGAAT CCCCTGTGCC | 240 |

| | |
|---|-----|
| AAGGGAAACC TTTGCATATG TGAAGGTAGT GTGGGGAAAT CCTTTCAGCT TACTTTTCCT | 300 |
| TACTNTTGCT TAGGNCACCA GTGTNTTCC AACTGGGGG NGGAAACCNT ATGGNGTGTA | 360 |
| ATTGAGTTTG GGCAAAGCTT TTGGNAAGGN CTTTCCCTTT TAGGCCANCA NCAGCGTTTT | 420 |
| TCNCACAGGG GGGAAAGGCN TTATTCTTGT AAAGTATTGT GGGCCAGNCT TTCAATTTTT | 480 |
| CCTTCCAAAC TTA | 493 |

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

| | |
|---|-----|
| GGCACGAGGG CTAAGTGAGA GGGGGCAGTG CTTCAGGCTT GCTTCAGGTC ATCCAATAGA | 60 |
| CAGCAAATCC TGCCACCTTG TCCATCAGAG AAGCCATTCG TCCTCCCACT AAGAGAAGTG | 120 |
| AATTAGGGTA CAGAGGAAGG AAAAACCAGA AGTAATACCC CCAAATGCA CCCCTCCTGG | 180 |
| GGGCTAAGGC AGGAATCCCC TCATCAAAAC AAGACTGAAT TAAGAAGTGC TTGACCTTAT | 240 |
| GAGTACTAAG CCCATGTCTC TGTCATTGAG TTCCTGTGCT ATCCTTTGGC ACTATGGATG | 300 |
| AGGACTTCGA AGGGAATGAT GATGTCCTTA TTCTTTCACA ACATCACTAT CCAAGCTTGA | 360 |
| AGGAAGGAAN TATGGGCACA CCCGAATTAA NTGCAATATT TTAGGAAAAC TGTAGTGGA | 420 |
| GTTTTNAAAT TGTGGTACNT GCCCAGTATT GGATGGGGGT AAAAAGGAAG GTTCCAAAA | 480 |
| GNGNTNAAAA ATT | 493 |

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

| | |
|---|-----|
| GGCACGAGCA CATCCTCACT AGTATGCCAT TATTTCTTCA TGTACTTTTT CAGTCCAACT | 60 |
| GTCCCATTTG GCAGTTCTGA TACCACCAGA GAAGGCTGAC GGAGGGAGTC CTATTAATGC | 120 |
| TGGTTAGGGG TGGAAGTCCA GATAATCCAG GCAATCTCCA CTGCCACTGT GTGGTGGGAG | 180 |
| CTTGTTATNA CCTACTGGAG TAGAAGGTTT TGGGGTCCCT AAACAGTCAG CCACCTCTNA | 240 |

| | |
|---|-----|
| CGTTACCCCA ATGTGGGTTT GAGTGCTTCG TTACTGCCTG ATGGTGGTGA AAGTCTAGTA | 300 |
| TCTCCAATTG ACCTTACTCG TGTGGGTGGG GATTAGGTCA CAGTTTTTTG GTGTGGGGGG | 360 |
| CAGAGGGGGT TGCTNNTTGA CAGCAGGGTA GTGGTTATTG TTTAAAAGTT TTCTGTTCTT | 420 |
| AAATAGGGTG ACCTTTTCCT GGTCTTTGG CTAGAGAGAG CAAGTTTTTG TTGGAGTTCT | 480 |
| TTCTGTCTGT CCNGTTGGTA T | 501 |

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

| | |
|--|-----|
| GGNGGAGATG GCCTTCTCCA CGGTGNCCTGC GGATGTCCCA CGNGTCTCCG NCACCCACTG | 60 |
| GACATCTGTG CTCGCAATTA TAGATGCCCT TTAGCTCCTC ATTTTGAGCA AGAGGAGCTC | 120 |
| GAGTTCTCCT TTGGCTCGTG NATGGAATCN ACAGCAGGTC AGGAGAGATT CAACAGCATT | 180 |
| ACCTCAGCTT ATTACAGAAG TGCCAAGGGG ATCATATTAG TATATGAATA TCACTAAGGA | 240 |
| NGAAGTTAGA AATCCTTNAT GAAGGTACC ANCAACAGCA NGTGN | 285 |

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

| | |
|---|-----|
| GGCAGAGCCA CAATGTAAGC ACCAAACTTC AGCACTTGGT CGTACATATC TATGGAGAAT | 60 |
| GNGACAAATT AGAAATCAAG AAATTTCTCT TCCTCAAAGC AGTACTTTTA AACACTGTTC | 120 |
| AGGACCTCTG GCCACGNAGA AGCCTCCTTT NACTATGCCT CCTGTTTGGC CACCCTATAG | 180 |
| ACTAAAGGGA GTATCGACCT GTATCCCATT CAAGACTCCA GAGGATCTTC AAAAGCACAA | 240 |
| GACAGCAACA GAGAGATGCA CTGTCTTTCA CAAGATACAG TGTGTAAGTC TTNCCAGATT | 300 |
| GNCCTTTCCC ATTTTATATC CNCTCNGNAT TTCTGTACTC ACGGTTTTCA CCNCCNTTAA | 360 |
| TTTCACATTT GGTCTTACA AAGGTTGGGG TATTTTCCA AG | 402 |

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

| | |
|---|-----|
| GGCACGAGGT CCTTTTATT CCAGTCCACT GCATTCTGGT CCATTCCATT TGATTCCATT | 60 |
| CCATTCTATT CCATTCCATA CAGTTGCATT GCTTGGATT CCATTCTATA TCTATAANTT | 120 |
| CAATTCGAGA CCATTGCTTT TGAGTGCATT CTATATGATT CCATTCCATT CAAGTCCATT | 180 |
| ACATTTGGTT CCATTCCATT CCATTCCATT CCCTTCCATT CCATTCCATT TGATATCAAT | 240 |
| CCATTCGATT CCATTCCATT CGAGCACATT CCATTCGAGT CCATTCCATT CGNATGCCAT | 300 |
| TCCATTTGAA TTCTATTCCA TTAGTCTCCA TTCAATTCCA TTAAANTTCC ATTCCATTCC | 360 |
| ATNCTATNCC AACTGN | 376 |

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

| | |
|---|-----|
| GGCAGAGNAA AAAGTGCTN CTTTGACCA GATTCATCA CTGTCACAAA GGAAAATNAA | 60 |
| GAATTAGACT GGAATTTACT GAAACCAGAT ATTTATGCAA CAATCATGGA CTTCTTTGCC | 120 |
| ATCTGGCTTA CCCCTGGTTA CTGAGGAAAC ACCTTCAGGA GAAGCAGGAT CTGAAGAAGA | 180 |
| TGATGAAGTT GTGGCAATGA TTAAGGAATT GTTAGATACT AGAATACGGC CAACTGTGCC | 240 |
| AGGAAGATGG AGGGGATGTA ATCATTACTN CTGAAAAATG GAATTCCAGA ACATGCTGCC | 300 |
| AGTTTTATAT TCCGGAGGTA GAAGGCGTAG AACAGGTTAT GGATGATGAA TCAGTTGAAA | 360 |
| AAGGANGCAA ACTCACCTTA AATNATCTNG GNTTTTTTTN GGCNTAACA TCCGANTGTT | 420 |
| GATATATATT CCAGTTTTTA TTATTAAANG CTGGGGACTN NAGGTTATNA AATTGCCTTC | 480 |
| CGGGATGTTT TTAANTG | 497 |

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

| | |
|---|-----|
| GGCANAGCCA GCACTTTGGG AGGCCGAGGG GTGGATCACG AGGTCAGGAG TTCAAGACCA | 60 |
| GCCTGGCCAA GATGGTGAAC CCCATCTCTA CTAAAACTA CAAAATTAG CTGGGCATGG | 120 |
| TGGCAGGCTC CTGTAATCCC AACTACTTGG GAGGCTGAGG CAGGAGAATC TCTTGAACCT | 180 |
| GGGTGGCAGA AGTTGCAGTG AGCTGAGATC GCGCCACTGC ACTCCAGCCT GGGCAACAGA | 240 |
| GTGAGGACTC CGTCTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAANN NTGGGGGGGG | 300 |
| CCCCNANCCC | 310 |

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

| | |
|---|-----|
| ATTTATTATT ATTGTTTATT TATNCTTGCA CTTGATGAAA TGTAATTAAN CGCTTTGTCT | 60 |
| TATGTGGTTT TTTAATTGTC ATTTTACTGT TTAATTTCTC CATAGAGTAT ATGTATTTTT | 120 |
| GNANCTCAGA GACTCTGCCT TTTCCCCTCA TAGTACACAG CATAATACTA AGCTGTTAGA | 180 |
| AGAGTTCAAT TGAATGTTAA TTCATCTGAG TAAACAAACT TGTATATGTA TTTCAAGTAC | 240 |
| CTCTACCAGT GGTAGTTGGA ATCTGTTCCA TCAGAAGAGN TTTCTTAAAT CTGNAATAGT | 300 |
| NAAAGTGTTT TATATTCTTT GCTCACAGAA TGAAGGGCAG GAGACCTTTN AAAATGGTAA | 360 |
| TGATGGTGGG ACCACATATT TTTAAAAGNG GTGGAGGTTG TTCCGGCNGT GGTATTGNTT | 420 |
| TAANCCATGG T | 431 |

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

| | |
|---|----|
| GCCCCACCCN GGNCCGCCCC CCCTAGANCT AGTGGTTCCC CCGGGCCTGC AGGNNTTCGG | 60 |
|---|----|

| | |
|---|-----|
| CAGAGCAGTC TTTGGCCTCC CAGTAAATTC CAATTTCAAA CAACTTTTAA CTCAAACTTC | 120 |
| ACTCTTAGAT TTTTAACAAG CTTTTCACAC ATACATCATT AATGCTTCCC CTAATCTTTC | 180 |
| ATGTTGTACT GGCTATTGGG CAGTTGTGTT AAAAAAAAAA AAAAAAAAAA AAAAAACAG | 240 |
| CACTCCCAAA GCGCTTGAAT TTATTTTNNT TTGGGGGAAT AAGAGACCTT TTNTAAATNG | 300 |
| TTTTTCGATA AAAGGTAATC CNTTTT | 326 |

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

| | |
|---|-----|
| GGCACANGAT TTTNTNAGTT TTTGGGTGTC TGTAATTAA AAAGGAAAAG TAGAAATAAG | 60 |
| TAAAACTNAG GTTGAAGGAA ATATACATAA ATAAGATAAA GCTGACCTGT AGATATAGGC | 120 |
| AGGTTATAAG AGCTTAGAGT TGTCTAAGTT GGGTGCAAAT TTNCCTCTGA NCTTCTGAT | 180 |
| GCCGAGACAA AAAAGGCAGT CCATATTTNT TACGTGATTG GGGTGGAACC CGAGAGGAGA | 240 |
| ACATGCTGTN TTCTTNTGGG ACAGGAAAGC TTGCNTGGCA CCAAGTCTGA ACCANNACT | 300 |
| TCATTGGTGA CATAGATTAT NTGCTGGAAC ATATTTTCAC ANCGGCCTGG CATAACCNCT | 360 |
| TGTTAGTGTT TGTACATTGG GAACGGTTCA TTTTCCCTTA AGCACCATGT GTTTTTGCCA | 420 |
| TGGAATGGT CCTCNCCCT TAAGGACANT TNCCTCGNAG TTATGC | 466 |

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

| | |
|--|-----|
| G TTCACAAGT NGGGGAGCCT GTAGCTTTGG GTCTCANTAG CTCCTGGGGT AGTATTTNCC | 60 |
| CTTNATTTCT GGCCCTGTAT ATCTAATTTN AATGACATCT GTNAAGGAGA CAGTGGAGGG | 120 |
| | 120 |

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

| | |
|---|-----|
| CCTACCCATT TAACTTATAT GCAGAGTACA TGATAAACGC TGGGCTAGAG GAAGCATATT | 60 |
| GTCCTCGATT CCAAGCATAT TGAATCAAG ATTGCTGGGA GAAATATCAA TAACCTCAGA | 120 |
| TATGCCAGAT GAACACCACC CTTATGGCCG AAAGTGNAAG AAGAACTAAA GAGCCTCTTG | 180 |
| ATGAAAGTGN AAAATGGAGA GTGCAAAAAN TTGGCTTAAA AGCTCCAACA TTCAGAAAAC | 240 |
| TAAGGATCCA TGGCATCTGN GTCCCATCCA CTTCCATGGG CAAATAGATG GGGGAAACAT | 300 |
| GGAAAACAGT GGGCTGACTT TATTTTCCTG TGCNTCCAAA TTCACTGCAG ATGGTGGACT | 360 |
| TACAGCCCTN AAATTTAAAA GACGTTTTAC TCCCTTGGA AGAAAGTTTT GACCCAACNT | 420 |
| GGNCCGGCTT TTAAAAACC GGGTTTTTTA CTTTGTTC ACGGGGTNCC NTTNGTTCAA | 480 |
| GGTTTGTTTT T | 491 |

(2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

| | |
|--|-----|
| GGCACGAGGN GAAGGACGGC AAGGCCTACT NTCGCAAGGA CTACTTCGAC ATGTTTCGCAC | 60 |
| CCAAGTTTGG CGGCTGCGCC CGGGTTCATC CTGGAGAACT ATATCTNNGC CCTCAACACG | 120 |
| CTGTGGNCAT CCTGAGTGCT TTGTGTGCCG GGAATGCTT CACGCCATTC GTGNAACGGC | 180 |
| AGCTTCTTCG AGCACGACGG GGCAGCCCTA CTNTGAAGGT GCACTACCAC GAGCGGCGCG | 240 |
| NCTCGNTGGT GNTTCTGNCG TGCCAGAGGC AGAT | 274 |

(2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

| | |
|--|-----|
| ATGTTTTTCAT CATGGACAGC CATGATGATA TATTATTATC TCANCTTTAA TCCTTGGTGT | 60 |
| GGTTGATTTG GGATCTGCCC CTGAANCATC TNTCGAGAAA TGCTCCAACA GAGCAGNAAT | 120 |
| CTTAACANTC ATTCACAGAA ACATTGTTAA GAAGTGCCTT GAAGCTGTTT TTTGAGGTGG | 180 |
| CAGAAGACAA GGAGAATTGC AAGAAATTCA ATGAGGCCTT ATCTAAAAAT CTAAAGCTTG | 240 |
| GGNCCAGTTG TGGGTATCTC ACCTTTGTAA TCTCAGGCAC TTTGGGGAGG GCCAAGGCCA | 300 |
| GGTGGGNTTT GNTNGGNAGC CCAGGGGTTT TTGAATACCC ANCTTGGGGT TG | 352 |

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

| | |
|---|-----|
| GGCACGAGGN AACTTTNAGT GCAATGTTCC TCTGGGCATG GAGTCTGGCC GGATTGCTAA | 60 |
| TAAACAGATC AGTGCCTNAT CTACCTACTC TAATGNGAAG GTGGACCCCT CAACAAAGCC | 120 |
| GGNTCCATGG TGATGACAAT GGCTGGACCC CCAACTTGGG ATTCCAACAA GGAGTATCTC | 180 |
| CAGGTGGNCC TGCGNTTTTT AAACCATGCT GACGGCCATC GCAACANAGG GGAGCGATTT | 240 |
| CCNGGGNAAA CACAGGAATG GCTACTAATG TGCAAATCCT ACAAGCTNGG NAAGTTCAGC | 300 |
| ACTTAATGGG TGAGGACTGG NATGGTGTTA CCGGTGATGG CCAAAAACCA CANGGTTTTT | 360 |
| TNCA | 364 |

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

| | |
|---|-----|
| CCTCTNAAAA TGTGCTTTGC TGCTAGAAAC CTAAGCATGC CGGATCTGGA AAACAGATTG | 60 |
| ATAGAGCTAC ATTCTCCTGA TAGCAGGAAC ACGTTGATCC TACGCTGCAA GNATACAGCC | 120 |
| ACAGCACACT CCTGGTTCGT AGCTATCCAC ACCAACATAA TGGCTCTCCT CCCACAGGTG | 180 |
| TTGGCTGAAC TCAACGCCAT GCTTGGGGCA ACCAGTACAG CAGGAGGCAG TTAAAGAGGT | 240 |
| GAAGCATATT GCCTGGCTGG CCAGAAACAG GCAAAACTAG NTGGTGGGAG GACAGCAATT | 300 |

| | |
|---|-----|
| GGNGACCTGT TCCTCATGGG NTGTGAACTG NGAAAGGGAT TTGCTGGNTC TNTGGACTGT | 360 |
| TATGCCCTTG GGACCAGGGT TGCCTGGGGN TTCACCCTGG CCACAGTTAC CCANTTTTTN | 420 |
| GCCACCAGGT TTGGTTTCCT TTTTGGTTC CGGATNTTGG TTCCCCTTCC CTTTGGGT | 478 |

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

| | |
|---|-----|
| GGCAGAGGTC TTNCTTNGG AGATGGGCAG AAGCTGAAGG ACTGGCATGA CAAGGAGGCT | 60 |
| ATCCGGTAGG AACGCTCAGC GCGTAGTAAA TGGAGAACAA GGAAGACCTT ACCCCATGAA | 120 |
| CCGATGCTGA GAGAGTGGAT CAGGCATACC GNGAAAATGG TTTTNAACAT CTACGTCATA | 180 |
| ATAAAATCTC CTTGAATCGC NNTCTCCCAG ATATCCGGCA CCCAAACTGC AACAGCAAGC | 240 |
| GCTACCTGGT NGACACTTNC CACACAAGC ATCATCATCC | 280 |

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

| | |
|---|-----|
| AGTATGAAAG TCTCAGCAAA TTTATTTTTA TTCAGTTAAA TATGTTTTAC TCAAAGTGAA | 60 |
| CTGAAATAAA TTTCATCAAA TTTGATATAT TATGAGTTTA TTTAGAAGAC AGACAAATGT | 120 |
| AATCCCCAAA GTTCTGAACC TTCTAACTTC AGTTCAGTTG CTCAGTTGAG TCTGACTCTT | 180 |
| TGTGACCCCA GGAACCGCAG CACGCCAGGC CTCCTTGTC ATCACCAACT CCCAGAGTCC | 240 |
| ACCCAAACCC ATGTCCATTG AGTCGGTGAT GCCATCCAAC CATCTCAGCC TCTGTTGTCC | 300 |
| CCTTCTCCNN CTGCCCTTNA ATCTTTCCCA GCATCAGGGT CTTTCAAAT GAGTCGGGTC | 360 |
| TTACATCAG GTGGNCAAGT ATTGGGNTTT CAGATTCAAC GTCAGTCCTT NCAATNGAAC | 420 |
| ACTCAGGACT GATCTCCTTA GGGTGGACTA GTTGGGTCTN CTTGCAGTCC AGGGNCTTTC | 480 |
| AGGGTCTTTT NACGG | 495 |

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

| | |
|---|-----|
| GGCACGAGCG GAGGAGAAAA GGTGGTGCTC NGACCTAATG ATGTTTCAGT ATTTACGACG | 60 |
| CTCACCATTA ATGGACGCCT NTTTGCTTGC CCGCGAGAGN AATTCGATTC ACTGACTCCC | 120 |
| NTACCAGAAC AGGAAGGCC AACTGTTGGA ACAGTGGGAA CTTTTGAACT GATGAGCTCC | 180 |
| AAAGATTTAG CATACCAGAN GACANTTTAT GATTGGGAAC TCTTCAACTG CGTGCATGAG | 240 |
| CTGGAGCTAA TCTATCACAC ATTTGGAAGG CATTAATTTT TAAAAAGACC ACAGCAAAC | 300 |
| TGGGATTTGT TCCTGAGGAG ATTTTAATTG AAATTCAGTT TTGGGTCGTG CACTGAGATC | 360 |
| TNCCTTTGTT TCTTCAGCTT CAGNAAGCGG TGGTTTCAGN TATTTAAAAA AAATTTGTTT | 420 |
| AAGNTAGCAG NCCACTGTTA AGGGGTNTAA AAAATCTGGA ATTCC | 465 |

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

| | |
|---|-----|
| CCAGGCGCGA ANATCCCTCC AAATTNANGT GGGGCGATTT TGGCGCTGAN TACGTCGTGG | 60 |
| AGTCCACTGG GGTNTTCAC CACCATGGGA GAAAGGTTGG GGGGTTCAAT TNGCANGGGG | 120 |
| GGGTGNCCAA AAGGGGGTNC ATCATGTTTG | 150 |

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

| | |
|---|-----|
| GCNTCGTNGC GAATATNTGG NACCCAAAAN TAGACCGATG CCATCACCGC AATATTAAAA | 60 |
| ACAGCGATCA ATAAAAAGGT GTACGCCAGC TAAATTCCTG ATTTAAATAC GTTCCCAGCG | 120 |

| | |
|---|-----|
| GAATGCCCAG CAAATTGGCG ACTNTGNATC CCGGAAACCA TCCCCGNCAC GGCGNCGGGT | 180 |
| GAACTTTTCC GGGTTTGAAT ATTTTNGAAT AACACGATCG NTTCCGACGG CCAATAATTG | 240 |
| CGCCCTGGGG AAAGCCGGNT ACCAGCCGNC CATGGGGGN | 279 |

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

| | |
|---|-----|
| AAATCTAACA TTCGAATCAA AGGTGCCATT AAGCAGCCAG TCAAACTTA CGCCAAGAGC | 60 |
| TGACGCAATT CCTGGTAAAA AGCGTGGTCG CTTAGTTTTA CCGTTTTCAA GCTGCTCTAT | 120 |
| AGACTGCTGG GTAGTCCCCA CCTTTTAAGC AAGTTCAGCC TGGTTAAGTC CAAGCTGAAT | 180 |
| TCTTTTGCTT TTAAACCCTG GAAGAAATAC TCATAAAGCC ACCTCTGTTA ATTTACCCCC | 240 |
| AATCTTCCAC AAGAAAAACT GTATTTGAAC AAACAAGTTA CATTGTATGG AAAATTACAA | 300 |
| GAAAGTTTGT TTGATGGGAG GCGGTTTTGC AAATCCTTT NCTGAAACGG CTTCAAGAAG | 360 |
| AGGGGGATTT GCGGTAAAA TGNACGGCAA ACCGGAANTG GGCAACCAAG GCCGGTGTTT | 420 |
| AAACNGCAAT TCATTTCAANN GGTGA | 446 |

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

| | |
|---|-----|
| CCTCGCTNAA ACTNTNACAG GTCGGCGGCG CACGTNTTTC TGCNACCCTT GCGGCGCGTA | 60 |
| TTCCCGCTGA AATTGGCTGT AAGTTGCAGC AGGTGTTTGG NNATGGCGGA AGGCCTGGT | 120 |
| GAAACTNACA CCCNGCTTGA ATGGATAGCG CCGNGAAAA TTAATCCATA CCCAGGGTTT | 180 |
| ACCCAATGTN TTCCGGTTGG NCGGAA | 206 |

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

| | |
|---|-----|
| AATAAAGATG CAGGANTTTA ATATTGCGGT GGGGTAAAAC CCGGATGANA TGGCTCATCC | 60 |
| GCTANGATTA AAGNATTTAA AATNCCTGNA TTAACGCGTG CNAGGCCGTC CCTGAATNAT | 120 |
| TGCCGCTTCA CCCGTNGCCA CCAGGCAGCA AGCCATCTGG TTTTNAAGCG AATTCGGGAA | 180 |
| TCGNTTCGCT GCCAGCANGG CAACG | 205 |

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

| | |
|---|-----|
| CAAAGACGCC GCCTCGAGAA CATCAGGTTT CTGAAAGGGA TGGGCTACTC CACGCACGCG | 60 |
| GCCCAGCAGA TTCTGCTCAG CAATCCTCAG ATGTGGTGGT TAAATGATTC CAATCCTGGA | 120 |
| AACCGACAAC CGTCAAGAAA GTCCTTCCCA GGAAAACATT GACCGATTGG TGTACATGGG | 180 |
| TTTTAATGCA CTCGTGGCCG AAGCTGCGCT GAGAGTNTTC AGAGGCAACG TCCAGCTGGC | 240 |
| CGCCCAGACC CTTGCTCACA ACGGAGGAAG CCTGCCTCCC GAGCTGCCGT GTTCGCCAGA | 300 |
| AGACTCTTTG TCCCCGCCAG NCACGTNCCC TTTTGACTTC GNNGAACCTT TTAGTGNCTN | 360 |
| | 360 |

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

| | |
|---|-----|
| CCTAAAAAAA ACAAACTA AAGAATTGGT TAGAACAGCA AAATTTTCTT AAGGTATTGA | 60 |
| TTTACTCTTA ATAAATTAC AAGAGATTTT AATTTTTTTT TAGCCCAAAG TTCAACTTTT | 120 |
| ATTGCATTTT GCTGTTTTCA GCTTTCTCTC CCCTTTTAAA AGGCCTGAAA TAATAACTCT | 180 |
| CCTTCANCTG CATTTTCAGC TCCTGTGAGT TTTTCTCCCC TCAGGTCTA ATTATTGTT | 240 |

| | |
|---|-----|
| GTGGCCTGAT GCTTAAAAAT GTTTTATCTT AAAGGTCTAA AGGGAAATGT TTTCTTGCTT | 300 |
| AACATAGTGT CCCGTGGCTC TTGGGNTTNN AAANTGNTN CTATGGA | 347 |

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

| | |
|---|-----|
| CAAGCCCCAT AGGCAGGAGG CCCCCGGGNA GCACATCCTG TCTGCTTGTG TCTGCTGCAG | 60 |
| AGTTCTGTCC TTGCATTGGT GCGCCTNAGG CCAGGCTGCA CTGCTGGGAA GCTGGGCCAT | 120 |
| GTCTCCCCAC CCCACCGCCC TCCTGGGCCT AGTGCTCTGC CTGGCCCAGA CCATCCACAC | 180 |
| GCAGAGGATC TGCCCAGACC CTCCATCTCG GCTGAGCCAG GNACCGTGAA TCCCCCTGGG | 240 |
| GAGCCATGTG AACTGTCGTG TGCCGGGGCC CGTTGGGGTT CAAACATTCC GCCTGGAGAG | 300 |
| GGAGATAGAT GCACATACAA TGATTATTGN AAGATGTGTC TCAAGTTAGT NCCNTNTGAG | 360 |
| TCANAGGGGC CAATTTCCGC | 380 |

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

| | |
|---|-----|
| CCGCCTTCGC TGGCATGACC AACCACCAGC TGAGCACCAC TGAGTGGTAA TGACGAGACT | 60 |
| NTCTACCAGG AGTTCAATGG CCTGANGAAG ATGAATCCCA AGCTGAAGAC CCTGTTAGCC | 120 |
| ATCGGAGGCT GGNAATTTCA GCACTCAGAA GTTCACAGAT ATGGTAGCCA CGGCCAACAA | 180 |
| CCGTCAGACC TTTGTNAACT CGGCCATCAG GTTTNTGCGG CAAATACAGC TTTGNACGGG | 240 |
| CCTTGACCTT GGACTGGGGA GTTACCCAGG GAAGCCAGGG GGAGCCCTGC CGTAGGACAA | 300 |
| GGAGCGNTTT CACAACCCTG GTTACNGAAN TTTGGCCAAT GNCTTTNCCA GCAGGAAGGC | 360 |
| CCAGACCTTT AGGGGAGGGA CGGCTTTTTT TTGAGTNCAG GGGTTTTCCA ATTGGGGNAG | 420 |
| ACCTTTNTNG GGATGTTGGT ACGGGGGTTG GNCAAAATTG GCCCGAACTG GGTTTTTTTN | 480 |
| AACTTTTTTG CT | 492 |

(2) INFORMATION FOR SEQ ID NO:1016:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CTTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TNAAAANNAA AAGG 54

(2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

CAGGGNCTNC CCGACCTCAA CCACTCCCAG GNTTATGCCG TNAAGACTGT NCTGCAAAGA 60
CCACTGAGCC TGATCCANGG NCCGNCAGCA CGGGGTAAGA CGGTGACGCG TTCCACCATC 120
GTCTACNCAC CTTGCCCCGGC AAGGCAACGG GCGGTTNCTG GTG 163

(2) INFORMATION FOR SEQ ID NO:1018:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

CCGTCCCCTT CGANAGCAAC GTGGGGNAGT ACCGGGCGGT GAACGGAGCT GGGGCGNCCT 60
TNATGCCNAG TACTGGAACA GCCAGAAGGA CCTCCTGGAA GCAAAGGCGG GCCGCGGTGG 120
AACACCTACT GCAGACACAA CTNACGGGGT TGGTGAAAAG CTTCANAGTG CAGCGNCGAA 180
GTTGAAGCCT GAAGGTGACT GTNTATCCTT CAAAGAACCC AGCCCCTGGC AGCACCACAA 240
CCTCCTGGTC TGCTCCTGTG AATGGTTTNC TATTCCAGGG CAGCATTNNA N 291

(2) INFORMATION FOR SEQ ID NO:1019:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

| | |
|---|-----|
| CGCAACATTT TGGGAAAATA CAGTTCCATT GTACCTGCCA CCNTNNAGCT GTAGCCAGAG | 60 |
| ACCTTTATCA AAATGGGCTT GTTTCACAG AACAGCAGAA CGGTTGGGGG TTTGCATGTA | 120 |
| CAGTTAACCA GCATAAGACT CGTACTGGGN AAAATCCAGC TGGGAATGTG ACACAGCTTA | 180 |
| ACTGATAGCT TAAGGCATCA GTATTGGGAC CAAAGGCTGG TCAGATTTGT ATCATTCTGA | 240 |
| GGACCAAATG ATGGGGAACA ATAAAATTGT TCCATGNACA GTTGTTCCTC ATTTTGCTGT | 300 |
| NCCAGATGAA GACTCTTAAG ANTGACAGAA GGTGATTTTT CCTGGGTGNN TCGAGGACTT | 360 |
| CCGGGGGTAA TGACCNTGAT GGAAATGCCA GGGGACCCGG TTAGGTTTTT TTTTGGGNGA | 420 |
| NTAACCGGGG GGTGCCNCG TGGGACAAAC AGCNGTTTNC CAGGGTTTGG GTTGGTC | 477 |

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

| | |
|--|----|
| CTTTTTTTTT TTTTTTTTTT TTTTTTANCT TTNCAANTTT TTNAAAAAAA | 50 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

| | |
|---|-----|
| AGAGGTGTCT GTGTTTGAAG TCAACATTCG ATTTATTGGA GGCCTACTTG CAGCATATTA | 60 |
| CCTATCAGGA GAGGAGATAT TCAAGATTAA AGCAGTGCAG TTGGCTGAGA AACTCCTTCC | 120 |
| TGCCTTTAAC ACACCTACTG GGATTCCCTG GGCAATGGTG AATTTGNAAA AGTGGAGTAG | 180 |
| GGCGAAACTG GGGCTGGGCA TCTGCAGGTA GCAGCATTCT GGCTGATTTT GGTACACTAC | 240 |
| ATATGGNGTT CATGCACCTG CAGCTACTTG TNNAGGGGAC CTGACTTNNC TACAAAAAGG | 300 |
| TTATGGCACA TTCGGAACT TACTTTCAGA AAATGGGTTC GTGCCAANGG GTCTTTTATT | 360 |

| | |
|---|-----|
| CCAANTANTT TGNACCCAG NACAGGGCGN TGGGGGTGAN TATTCANACA TNTGTTCCGT | 420 |
| GGNCCGGGAG ACAGTTTTTA TGGATACTTA CTGGAAGCCN GGTGTGATGT CCAGTTAAAA | 480 |
| CAGACCCTG | 489 |

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

| | |
|--|-----|
| GGGAGCCTCA GTGAAGGTGG CTGTCCGGGT AAGGCCCTTC AATTCTCGAG AGACCAGCAA | 60 |
| GGAATCCAAA TGCATCATTC AGATGCAAGG CAACTCGACC AGTGAGTACA TGTTGTTTTTC | 120 |
| TCTCAGCTGT GTATCTTACT TTCCTTTCTT CTTTCCCTGT CGTCTTGCTG TGTTTCAGAAT | 180 |
| AGATGAACAT CTGTATGTTA ACACTTTGAA CTTTGCTATT CTGAATGATC CATTGGAATG | 240 |
| TATTCCTCTC TGTGGTATTT GCTATAGTAT ATTTGAAATA TGGACTATTT ATTTTACCCT | 300 |
| GTACAATTGA GAAACCCGGA ATAACCTGAAC NATTTAGCAA GTGTTTATGC TTATTAAGTT | 360 |
| GAAATTTAAT GGTATAAAG GTTTAAACAG TGCTTTTTCG CCAGTCCNAA GGGGNATTAT | 420 |
| ACCCATGGNG GNGGCAGATT CCATGTTTTN CT | 452 |

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

| | |
|---|-----|
| TTCAAAGAAC TACTTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTTGT AAAGACATAT | 60 |
| GGCCATTTAT ACATGCAAAA TTCTGAGCTA TTAAAGATC TCTTCGTAGA GTTGAAACGT | 120 |
| TACTACGTGG TGGGNAATG TGAAACCTGG AAGNAAATGC TNAAATGAAC TTCTGGGATA | 180 |
| CGCCTACCTG GAGACGGGAT GTTCCCGCCT GGTGAAACTA CCCAGTGACC ACTTTGACAG | 240 |
| ATGGAGTTTA CTGGGAATGT GTGAGCCAAA GTNTGACGGT GNCAGCTGNA AGCCCTTNCG | 300 |
| GAGATGTACC CACGACAAAT TGAAAGCNCC AGGTTTACT | 339 |

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

| | |
|---|-----|
| TTCAAAGAAC TACTTGAAAA TGCAGAGAAA TCCCTGANTG ATATGTTTGT NAAGACATAT | 60 |
| GGCCATTTAT ACATGCAAAA TTCTGAGCTA TTTAAAGATC TCTTCGTAGA GTTGAAACGT | 120 |
| TACTACGTGG TGGGNAATG TGNAACCTGG NAAGAAATGC TAAATGAACT TCTGGGNTCG | 180 |
| CCTCCTGGNG CGGATGTTCC CGCCTGGTGA ACTNCCCAGT ACCACTTTGA CAGATGGAGT | 240 |
| ATCTGGNAAT GTGTGAGCAA AGTATACGGN GNCAGCTGGA AGCCCTTCGG GAGATGTGCC | 300 |
| CTGCGCAAAT TNGAAGCTTC CAGGTTTACT CGTGGCTTTT GTNAGCAGCC CGTTANTTTC | 360 |
| GTTCAAGGTT AGCGGTTNCG GGGAGATGTC GTGGAGCAAA GGTCTNCCGN GGGTAAAACC | 420 |
| CCACAGNCCC AGTGTACCCC TGGCC | 445 |

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

| | |
|--|-----|
| CACGGCAGGT CAGGAGCNAT TCCAAAGCCT GAGGACACCA TTTTACAGAG GTTCTNACTG | 60 |
| CTGCCTGCTT ACTTTTAGTG TCGATGATTC ACAAAGCTTC CAGAACTTAA GTAAGTGGTA | 120 |
| GNAAAGAATT CATATATTAT GCCAGATGTG AAAAGAGCCC TGAAGAAGCT TTCCTTTTGT | 180 |
| GAATTCTGGG TAACAAGGAT TGACATTAAG CGAAACGGCA GGTGTCTTAC AGNAAGGAAG | 240 |
| CCCAAGCTTG GTGNCAGGGG ACAACGGGCG GACTTATNCC TTATTTTGAA AACAAGTGCC | 300 |
| AAAAGATTGC CACAAATGTG GCAGCCAGCC TTTGAGGGAA GCGGTTTCGAA GAGTTNTTGT | 360 |
| TACCGAGGNT AGGTTCAAGT CNTTTGATTN CGNACAGACA CGTCATTTTT CACCGGAAGG | 420 |
| CCCAGCCTAG TTCANTTGCT GTTGNTGTGA GGTTGTTGNT GCNTTTTAAC CACTTACACT | 480 |
| TTTNCCCAAT TCACCT | 496 |

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

| | |
|---|-----|
| CCTGGNGGAC CATGAAAGCC TTTAAACCT CGTNATTAAT TGGACACAGT GCCAGAGTGT | 60 |
| ATGCACTTTA CTACAAAGAT GGACTTNTCT GTACAGGGTC AGATGACTTG TCTGCCAAAG | 120 |
| CTGTGGGAAT GTGAGCACAG GGNAGTGCCT TTATGGCATC CAGACCCACA CTTGTCCAGC | 180 |
| GGTGAAGTTT GATGNAACAG TAAGCTTGTG AACAGGCTCC TTTGAACAAC ACTGTGGGCT | 240 |
| TGCTGGGNAA TGGAGTTCCC GGAGCCAGGA CCCAGCACTT TTCGGGGGGG CACACGGGGG | 300 |
| GCGGTNTTTT AGCGTGGGAC TACAATGATT GAACTGGGAT ATCTTGGTGA GCGGGTTCTN | 360 |
| CAGACTTNAN TGTGGAAATT ATGGGNTTTA TTCTGTTNGG GGACATGCCC TGAACACANT | 420 |
| NACCGGGGCA CAGGGATTGG GTTCACCCAG GTAGTTTTTT CCAGAAGTTN CAAGTCAGTT | 480 |
| TTTNT | 485 |

(2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

| | |
|---|----|
| CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAAAAAAAAA AAAANNAANA NAAN | 94 |

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

| | |
|---|-----|
| CCCATTAAGG AAAGAGAGAA GAGGTGGCCA TTTACTTAAT TCAGNAGGTG GAGCCAATNG | 60 |
| GCTAGTAAAA CATACTTTTT TCATTTTCCC TTTCTNTAAT TTCCTGCGTT TCCTGTTTCT | 120 |
| CACATTCAGA ATCTGAATTT AGTTCTTTAC ACTCGTCCTC ATCTGCCTCA TCTGNAATCT | 180 |

GCCTCATCAT CTGNTTGAAA TGGCTCAAGA GTTGCTTTTA TTAGTGCCCA TATTGACCAA 240

ACCAAGACTG GGAATTTTNT GGCTCCATCT TGATATGCTT TTTTANAAAA NNCN 294

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

GTCAGGACCA GCTGGATGAC TTGGTGGTGG AGTGTAGAGA TATAGTTGGC AACCNCACTG 60

AGTTAGNATC AGAGGNTATT CAAATAGAAG CCTTGCTGAT GAAGAGCCTG TNATGCCCAT 120

TAATTCAGAA CTTCTGCCAC GGTGTGNAAT GATACCAGAT TAGACTCTGG GGGACCTGNA 180

TGGNAGTGTC TGGNTACAGG NCAAAACACCA GAAGGGACAT GTAACGAGAA ATGTTGCCAT 240

CGTTGTTACC CACTTNCAGT 260

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

CAACAAAAAA AGATATCCTC CGGCATATGG CCCANACGGC AAACCAAGAC CCCGCTTCAA 60

TAATGTTCAA CTGAATCTCA CAGATGAGGA GAGAGAAGAA ACGGANGAGG AAGTTTATTT 120

GTTTGAATAG CACAACCTCTT TAACCTGAGG GNAGTCATCT ACTTTTTTTT CCTCCTTGTA 180

CAAAAAAAGG AAGGTNANTA TAAANCCGG GTTTTTGTCA ACATGGTTTG CANATAAATG 240

ACTGGTGGA ATNG 255

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTGGANTNC

50

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

| | |
|---|-----|
| CGGACCTGCT GAAGGACCAG AGAGGGAGCC CTGCCTACAT CAGTCCCGAC GTGCTCAGCG | 60 |
| GCCGGCCGTA CCGTGGCAAG CCCAGTGACA TGTGGGCCCT GGGCGTGGTG CTCTTCACCA | 120 |
| TGCTGTATGG CCAGTTCCCC TTCTACGACA GCATCCCGCA GGAGACTCTT CCGCAAGATC | 180 |
| AAGGCTGCCG AGTATACCAT TCCTGAGGAT GGACGGGTTT CTGAGAACAC CGTGTGTCTT | 240 |
| CATNCCGGAA GCTGCTNGGT CCTTGANCCC CCAGCNGTGN CTTGGTCCG | 289 |

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

| | |
|--|----|
| CGGAGNCCA GAGGCCGAGT CGGTCACCCG NACGGATCAC TGGAAAAGTC GCACATCGGA | 60 |
| GGGGATNCTC NNTGAAGATT GT | 82 |

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

| | |
|---|-----|
| CCTGTGAATT ACCTAGAAGA GAAGGGTATT GAAACCTACC TCATCATTGC CTCCAAGCCA | 60 |
| GAGGTGAAGA AAACAGCCAC CCAGAATGGC CTCAATGGCT CGGCCCTGCC CAATGGAGCA | 120 |
| CCAGCTTCCT CAAAGTCCAG CTCCCCTGCC CTCATTGAGN ACCAAGGAGC CCAACGGGGA | 180 |
| GTNCCCACAG CAGTGGGTTC CACGTCGGAG AAAGCCCAG GAGCAGGATN CCCAGGNCGA | 240 |

CAACCCCTNA TTTCCCCAAC CCACGTCGGA GTTNCGGCTT

280

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

| | |
|---|-----|
| CGGCCTGGTT TCTGGTGGCC TCTATGNATA CCCTGTAGGG TGCNGACAGT ACTCGATNCC | 60 |
| TCCCTGTAAG CACGACGTCA ACGGTTCCCG GCCATGCCAC GGGGGGAGGG CGGATACCCC | 120 |
| CAAGTNTAGC AAGCTGTGAA GCCTGGCTAC AGCCCGACCA AACAGGNACA NGTACTACGG | 180 |
| ATATTCCTNA CNGTCT | 196 |

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

| | |
|---|-----|
| CTAAAAATAN TGGNTAAAAT TACCTTGCAA GCTATGTTGT ATAAGGTGNA TATAAAACAA | 60 |
| AGNAATTTNG NNGTTTAGAC TTGGGTCTAC TCCCAAGANG ACCTCATNAT ATATATACAA | 120 |
| AAATCCCCAA ATCCAAAAAC ANTTGNAAAC ACTTCTGGTC CCACACATTT TGGN | 174 |

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

| | |
|---|----|
| CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNCNCGG GN | 52 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

| | |
|--|-----|
| CATTTTGGGC AATAAACCTT ACAGCAAAAA GGACTACAGA TCCTAAGCCG GCCCCGCCCCG | 60 |
| CNTGCTCGGT ACAGTTTCCG TTCCCTCCTA GTCTCTGTTC GCTCGCTTAA GCTGTTTTTAA | 120 |
| AGACCAAGTG AAAGAGTGTG GTTTGCATCC AAGAGAAAAC ACCACACTGT GATGTCATCG | 180 |
| GGNAAATGAA TCTCCCAAGT CGCTGCCAGA NACCACCCAC TGNTTCGCCG GACAATGTCG | 240 |
| AAGTCCAGTT TGTNGCCGGG GGAAGGCNTG GTTTAGGGAA GGATGTTCAA ACGGTCCCAC | 300 |
| CCANGCNTGT NNAACTCTGG TTGATTCCTT NCAAGAGCCA CCCAGGTTTT TTCCCAGGNC | 360 |
| ACAGGCCAGT TTNCCAAAG TTCAAGGGNC CAAAGATTTT TCCAAGGTTT CCCCAGTNC | 420 |
| AAGGGCCAGG GNCAAGG | 437 |

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

| | |
|---|-----|
| CGGTAGGTAA GGAAGGGGCC TTAACCTNTG CTGGTGACCA GAAGCCTGCA TTTCTGCATT | 60 |
| CTGCTTAATT CCCTTTCCTT AGATTTGAAA GAAGCCAACA CTAAACCACA AATATACAAC | 120 |
| AAGGCCATTT TCTCAAACGA GAGTCAGCCT TTAACGAAAT GACCATGGTT GGACACAGAG | 180 |
| ATGCCATTCT GGCCACCAA CTTTGGGATC AGCTCCGTGG ATCTCTCCGT AATGGAAGAC | 240 |
| CACTCCCACT CCTTTGNATA TCAAGCCCTT CACTACTGTT GGACTTNCTT CCAGCATTTN | 300 |
| CTNATTCAC ATTACGGAGG ACATTCCATT TCACAAGGAA CAGATTCCAT GGTTTGNCNG | 360 |
| | 360 |

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

| | |
|---|-----|
| CGGCCATGGC TTTCTGGGCG GGGGGTTCGC CCAGCGTCGT GGACTATTTT CCTAGCGAGG | 60 |
| ACTTCTACCG CTGCGGCTAC TGCAAGAACG AGTCGGGCAG CCGCTCCAAT GGCATGTGGG | 120 |
| CACATTCCAT GACAGTACAG GATTATCAGG ATCTCATAGA CCGAGGATGG CGAAGAAGTG | 180 |
| GAAAAATATGT GTACAAACCT GTCATGAATC AAACATGTTG TCCTCAGTAC ACAATAAGGT | 240 |
| GCCGACCTTT ACAATTTTCTAG CCTNCAAAAT CTCACAAGAA GGTTTTGGAA ANAAATGTTG | 300 |
| AAATTTCTGG CTAAAGGGGA GGTTCCCAA GGAAGTTNTN AAGGGTGAGC CCATGGGTTT | 360 |
| CCACAATGGG TTGATGTTGT NGCCGGGTGG ACTTTGGCAT TGATTAAATA AACTNGGTTT | 420 |
| TACCGTGNGG NTCNTTAAAC CA | 442 |

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

| | |
|---|-----|
| AAGTTTGTNT TCAGGTAAAC AAACCTCGTN AGGNGNNGG GGGGTNTNT TCNGACTCAC | 60 |
| ACTTCCATCT CCGTGTGTAG GTGTCCATCA GCGGAGAATG GTCTCCGTGG CAGGCCAAGG | 120 |
| TGCCTCAAAT TGAAGTGGAG ACGCACAAGG TGGCAGCCCC TAATGTCGTC GTGCCAACCC | 180 |
| TGGGACACAG TCCGCCACGA AGCCCTCTTG TACACTTGGC TGGCCGAACA CAAGCCCCTG | 240 |
| GTCTTGTNTG GCCCTCCTGG GTCTGGCAAG ACCATGTACA ATTTTNNANN GNCTTCCGGC | 300 |
| CTT | 303 |

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

| | |
|---|-----|
| CNCGTNTGCA CGCGGGCTGC CCAGCTCTNT CCTGCCGCCC TGGCCGCTGT NCTCTCCTGC | 60 |
| NTCCAGCACA GCCGGGAGCA ACAAACACTC CAGGTTGCTG TGGCCACCGG AGCCGAGTNT | 120 |
| NTAANNGGCA CCCCAGGTTT TGCAGCGTCC TGCAGGGACA NTAATGCTCC TGGGCCCCGA | 180 |
| ATGCAATGTC TCNTAATCCC CTCTGTGGAT GGTGGTGGCC GGGGAGTGGC GATGGTGACT | 240 |

GCCNTGGCTN NCCGTTTGGT TGCCACCGGG GCTGTNGAGG AGACCCTGGN CCCATTTCGGT 300
T 301

(2) INFORMATION FOR SEQ ID NO:1043:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

ANAAGGTCCC CCCCTNNGGC CGTTTTGGGC CATGCTTTTT TCCCATTGAC TTAAAAANCAA 60
TCGGGAGGGG GNGGGGCCTG CCCCCTTTNA CCCTTTTCCC CCTTNCA 107

(2) INFORMATION FOR SEQ ID NO:1044:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

CAACTTTATT CATGGCAAAG AGAAAGAAAA GTAAAGACAG AATTTTCCCT TCATGATGGA 60
CCTCCTTATG CAAACGGTGA CCCTCATGTT GGACATGCTT TAAATAAGAT TTTGAAAAGA 120
CNNAGCCAAT CGATTCCATA TGAATGAATG GCTCCAAAAT ACATTTNGTG CCCC GGCTGG 180
GAATTGTNAA TGGGTTGCCC ATTGAAATAA AAGTATTATC CAGANCTTGG TAGAGAAGCT 240
NCAGAATCTT TGCAGCTATG GGAATTAGAA GGAAAGCTAG NTCCTTTGCT NAAGGCAGCC 300
CTTGNGGAAC CNGGATCCAG CATTTTTTTCG TTGGGGGGAT TAATGGGCNG TTTGGAATAA 360
TGGCT 365

(2) INFORMATION FOR SEQ ID NO:1045:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

ACCCTGATTC CGGAGGCACC AATGGCACTN AGGAGCGGAT GTCCGTGAAT CTGGGACAAG 60

| | |
|---|-----|
| GCTGTGGTCA CTGGGAAAGA TGGATGAGAA CCAGTTTGTG GCTGTGAACC ANCACCAATG | 120 |
| ACAGCCAAAG TNTTCAAGGT TTACGNGNGG GAAAGGCCGC ATTGCTGTGG GATCCGATGC | 180 |
| CGACCTGGTC ATCTGGGAAC CGNGACAGCN TTAAAACCAT CTNTGGCNGG GACACANAAC | 240 |
| AGCTCTTTTC G | 251 |

(2) INFORMATION FOR SEQ ID NO:1046:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

| | |
|---|----|
| CTTTTTTTTT TTTTTTTTTT TTTTTTTTTT AAAAAANNNN TTNTTTTCCC CAAAAA | 56 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1047:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

| | |
|---|-----|
| CGGGTCTCCC CGACCGAGGC TCGANTCCAG GTCGAAGGT NGCCGGAGNN ATGGTTGGAG | 60 |
| AATGTGGAAG GAGCTGGAGG ACACCCGANT ATTCTTAAAG CAATCCCCAT GGCCAGATGT | 120 |
| CATCAGCAGC TGAACAGCAT CTCCAGAAAC CAGCTGCAA GACAGAAGCA GAACAACTGG | 180 |
| TTTGGTGGAG AGATCTGATA AAAAAAGTT GGGAAACAGG TAAAATAATA ACTTGGGGTA | 240 |
| GAAGTTATGC TTGTTTTTCT CCAGGCCAAA ATCAACAGCT GATCTGGATA CCATCAAGAC | 300 |
| ACCTGAAATT TTATCATGAG CCAATGCTGA GGGAAGAGAN TCCGGGNGTT TCCNCAGGAC | 360 |
| GCCCCATTTN CAGCCCTGTT TGAGANT | 387 |

(2) INFORMATION FOR SEQ ID NO:1048:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

| | |
|---|-----|
| CCCCAAAGTC CTGGGATTAT AGGTGTAAAC CTCCATGCCC GGCCGGTTTT AACATTTTNA | 60 |
| AATGGTTAAA AAAATAGTAT TTTNTGAATA CATGANCATT ATATGTAATT NCCNTTTCAN | 120 |
| CATCTATAAA TAAAGTGTTT TTTTGAACA CAGCCATGCT AATTCATTTN CATATTGTNT | 180 |
| GTGGCCACTT TTCCTATTAA AATGGTGATT TCGAGTAGTT ATGACAGGGA CTGCATGGCC | 240 |
| CACAATGCCT AAAATATATA CTATTTGGCC CTTTACAGAA AAAGTTTAGG CTGGGTGCAT | 300 |
| GGGCTTACGC NGTAATCTCN GCNNTTGGGA GGTCGAGGCG GGTGGGTCCT CTGNGGTCCG | 360 |
| GGGTTCGGGG | 370 |

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

| | |
|--|-----|
| CCCACTGTG AGNTGCCCAA TTACCTGCCC TCGGTGNGCT CNNCCATCGN GAGGNAGGTG | 60 |
| CNCCAGCGCT ACGTGTGGCG TTTCTGCATC GGCCTGCACT CGGCGCCTCG NTTCTTGGTG | 120 |
| GCCTTCGCCT ACTGGAACCA CTACCTCAGC TGCACCTCCC CGTGTTCCTG CTATCGCCCCG | 180 |
| CTCTGCCGCC TCAACTTCGG CCTCAATGTC GTGGAGAACC TCGCGTTGCT AGTGCTCACT | 240 |
| TATGTTTCCT CCTCCGAGGA CTTTACCATT CCACGGNAAA GGCTTTCATT NGTGTTTATT | 300 |
| GNCTTCATCC CTTNNGGGCA CATGGTNCCT TCACCTGGCA TTCTCTGGGC GGTGGAACCA | 360 |
| AGAAGCACAC AGTTAAGTTC AGGNGGGNTC GCAA | 394 |

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

| | |
|--|-----|
| CCTGTAGGAG TGCAATTGGA ACCTAAGCGC TTGGTCAANA TCCTAGAGGT GCTTCGGGAA | 60 |
| CTCCCTGTCC CAAACTACAG GACCCTGGAG TTCCTCATGA GGCACCTGGT ACACATGGCC | 120 |
| TCATTCAAGTG CCCAGACCAA CATGCATGCN CGNAACCTGG CCATCGTGTG GGCTCCCAAC | 180 |
| CTGCTGAGGT CTAAGGACAT AGAGGCCTCA GGCTTCAATG GGACAGCGGC CTTCATGGAG | 240 |

| | |
|---|-----|
| GTGCGGGTAC AATCCATCGT CGTGGATTCA TCCTCACACA CGTGGACCAG CTCTTTGGGG | 300 |
| GTGCTGCCCT CTCTGGTGGT GAGGTGGAGA GTGGGTGGCG NTCGTTTCCA GGACCCGGGG | 360 |
| CNTCAGGCAG CCCCAGGAC NTATGCCCAG GCCATGNNTT GTTCACNGNN NGAGCTGATG | 420 |
| CAGTTGGCGT TGGACCCCCA CAATGGGGNC TACCTNATTT TCNTCGGGTT TGCCAGAGCA | 480 |
| CAAGAGGAAG GGGTTTTTTA AANGTTCAGN AAT | 513 |

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

| | |
|---|-----|
| CTTAAGCGCT AACGTCTTTN TNTNTCCCCG CGGTGGTGAT GACGGTAAAA ACTAAGGCTG | 60 |
| CTAAGGGCAC CCTNACTTAC TCCAGGATGA GGGGCATGGT GGCAATTCTA ATCGCTTTNA | 120 |
| TGAAAGCAGA GGAGGATGGG TCTGAAACGA ACTTTATTCA GAAGATTGCC AATNAACTCC | 180 |
| TAATGNCATG CAAACACCCT GAAAGTTCCA GTCCATCTTG AAAGATCTCC CAACCTCCAG | 240 |
| GNAGCCTGAA GCTTATGAAA TGCCAACCCT TCTTCCTCCA CCAAGTCCTT TCTTNAGGCA | 300 |
| AATCAACCTT GGGCCCGTGC GTCCCAATCC TGCATGGGTT AAACCCTNCT GAAGCTTTTA | 360 |
| AATTTTTTTG GAAAGTGNAT TCGGGAAAGG GGNCNTTTTT TTGGGNAAGG GTTTTTTCTT | 420 |
| | 420 |

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

| | |
|---|-----|
| CCCGAGAAAC ACTTATCAGT TGCCATGGG GAAACAAGCC ATGGGTACTA TAGGATACAA | 60 |
| CCAGCGAAAC AGAATTGATA CTCTCATGTA TCTACTAGCA TATCCACAAA AACCCATGGT | 120 |
| TAAGAACAAA AACCATTGAN TTGATAGATT TTGNAAACT GCCAGCTGGA CAGAATGCAA | 180 |
| CANTTGCTGT GNATGAGCTA TAGTGGCTAT GNTATTGAAG ATGCTCTTGT TTAAACAAG | 240 |
| GCCTCTTTAG ACAGAGGCTT TGGGCGTTGC CTTGTATATN AAAANTGCTA AATGTACGTT | 300 |

| | |
|--|-----|
| GAAACGATAC ACCANTCAGA CTTTTGATNA AGTGCTGGGG CCCTGTTGGA TGCTGCTACA | 360 |
| GGAAACNTAT TNGGGGACNG GAATNNTAGN TGCAGATGGT ATTTGTTTCNA CCAGGTGAGN | 420 |
| AGTTGGAAAA CANACAAGTG GTTGTTAATN AAGTNCCNGC CCACAGTGAC TCCGATTCCT | 480 |
| TGGAAGGNAG TTATG | 495 |

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

| | |
|--|-----|
| CGANTCAAAA AGGCTGACCT CCCTTTACTC ACCAGCACTT NCCTTGGCAG CCACATGTNC | 60 |
| TCCTGCTGCC CCGAAGGACG ACAACTGGAC ATAAAGAAGT CAAGCTACAA AAAGCTCTCT | 120 |
| AAGTNCTGC AGCAAATGCA GCAGGAGCAG ATTATACAGG TGAAGGAGCT GAGCAAAGGG | 180 |
| GTGGNGAGCA TTNTGGCTGT GGA CTGGAAA CACCCGAGGA TTACATCTTT NGTCATACCC | 240 |
| GAGCCCTCCC CGACCTCCCA GACTATCCAG GNAGGGTNGC AGGGGACAGC CCTNATTNAC | 300 |
| CCTTCCAG | 308 |

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

| | |
|---|-----|
| CCCCCGGCCT CATNAGTACC TNTCCCCAGC GGATCTGCCC AAAAGCTGGN ACTGGCGCAA | 60 |
| TGTGGATGGT GTCAACTATG CCAGCNTCAC CCGGAACCAG CACATCCCCC ANTACTGCGG | 120 |
| CTCCTNCTGG GCCCACGCCA GNACCAGCGC TATGGCGGNT CGNNTCAACA TCAAGAGGAA | 180 |
| GGGAGCNTGG CCCTCCACCC TCCTTTCCGT GCAGAACGTN ATCGACTGCG GTAACGCTGG | 240 |
| CTCCTNTGAA AGGGGGTAAT NACCTGTCCG TTTGGGACTA CGCCCACCAG NACGGAATCC | 300 |
| TTNAA | 305 |

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

| | |
|--|-----|
| ATGGTCCAGT AANTNNTGAG CTGTTCTGGN TGTTAACNAG ATGGAGCCGT TTTTGTCCCTG | 60 |
| CATTTGGAAT TGTATGAGTG TGGGACAGGG AAGGTCTGTT GNTTTNANNA CAAGTTTtag | 120 |
| TTAGGAGTTT TTGGGTCGTT ANGtagGT | 148 |

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

| | |
|---|-----|
| CAGGACTGCT GGGACCCCCT GCACCTCCTG GCCACGGAGA GATCCTGCTC CCAGGGACCA | 60 |
| GCGTCTGGNT GGGACACAGT TCACTCCTCT NTCCACTTCA TGTTCCTTTT CTTCAGCAGA | 120 |
| TGGCTCAAGT TCCTTGTTTT TNTCCTTGCT TTCTGACAGC NGTAGCTTCT GAAACCTGCC | 180 |
| ATTTTTGGTC TCCTGATGCC TGATTTCTTA ATTGTCCTGA CTGTGTCTTC TAGGAAGCAT | 240 |
| TAAGTCTGAA CTGACTTATT AGGGAACCTT AGAAAGTTAA ACACACAAAA CCCTTCTTTT | 300 |
| GACTCCTATC TTNAAGGACA TGGAGATACA GTTNACATAT ATTTATACAC AAGGNTATTT | 360 |
| CATATGGCAA AAACGGGGAG AAGGCACAAT TTTAAGAGCC CAATGGGGAC TGGGGTTGTG | 420 |
| TATGCATCTN TACAATGACA TGTTATGAAG TCATTCTGTT TTTAATAAAA CTTTTTAGTG | 480 |
| GNCATGGGGN AAATACAAA | 499 |

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

| | |
|---|-----|
| TACTTATCCC CCCACTATGG ATTCTGGGTN ANAAGGCTGA GGAAGGGAAA TAAGTACCGA | 60 |
| NCAGGCACCG ATNAGTACCC AATCCTNTCC TTNCGGGTCC CTCCTCGCNG GGTGGNAATN | 120 |

| | |
|---|-----|
| TNCGTGGATT ATAAGGCCCA TNANATTNNT TTNTACAATN TNACTAANTG TGGCTCCCAC | 180 |
| ATCTNCACTT TCCCCCGCNA TCCCTTCCCT GGGCGCCTCC TGCCCTATTT AAGTCCTTGC | 240 |
| TACAGCATTG GAACCAACAA CACTGCTCCT NTGGCCATCT GCTCCCTGGA TGGGGAGGAC | 300 |
| TTAAGAAAGC TNACCACCCT AACCACAGAG GCTTTGGAAT TGGGNCTGGC CCCCATGGGG | 360 |
| CTTGGAGGAC CGANCCACTT GAAAGGTATC CCCTGAAAAC TTAAGNTTGA GCCCAGTATT | 420 |
| CCAAGGATTC CTCTGTTNTN ATCCTTTGGT CTTTGCTACC AGGGNTGAAG | 470 |

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

| | |
|--|-----|
| CGGTCTACTT ATCCCCCAC TATGGATTCT GGGTNANAAG GCTGAGGAAG GGAAATAAGT | 60 |
| ACCGAGCAGG CACCGATNAG TACCCAATCC TNTCCTTGCN GGTCCCTCCT CGCNGGGTGG | 120 |
| AAATNTTCGT GGATTATAAG GCCCATAAAA TTTTTTTNTA CAATNTAACT NANTGTGGCT | 180 |
| CCCACATCTT CACTTTCCCC CGCNATCCCT TCCCTGGGCG CCTCCTGCCC TATTTAAGTC | 240 |
| CTTGCNACAG CATTGGAACC AACAACACTG CTCCTTTGGC CATCTGCTCC CTGGATGGGG | 300 |
| AGGACTAAAG AAAGCTTACC ACCCTAACCA CAGAGGCTTG GGAATTGGGC CTGGCCCCCA | 360 |
| TGGGGGTTTG GNGGACCGAG CCACTGGACA GGTATCCCCT GAAACTAAGC TGAGCCCAANT | 420 |
| ATCCAAGGAT TCCTCTGTTT TGATCCTTTG GGTCTTTTGT TACCAGGGTT GAAANTTTTA | 480 |
| AATGGAAACC ATTTTNTT | 498 |

(2) INFORMATION FOR SEQ ID NO:1059:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

| | |
|---|-----|
| TCANCCCCC AAANTGGATT CTGGGCAGTN TTTTTTTGGT ATGGGAAAAA AATATTGGGC | 60 |
| TCTNACCTCC CCAATAACTG CCGTACCCCT GCGGACCCCG CTCCANGATG AGGGATTTTT | 120 |
| TTGGACTATA ATGCTGGTAA GGTCTCCTTC TACAACGTGA ACAAGAAGGT GTCACACCTT | 180 |

GCACTTTCTC TGNATGGTAA CCTTTTGTNG GCCTNTCCCG GCCCTNACTT GNAGTNTGAN 240
NTAACTTCGG GAAGGGGAAA AGTGCCAGTT CCTCTGAATC CATCTGCCCC CATGANTGGG 300
NATAGATGGG TTTTGTGGN CCATGTTTGG GGNATTCATG GN 342

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

AGGGTGCCCA GTTACCCAG GNTGAGGTCG CTGCTTCTGN CAATCCTGAN TGCNCCACCT 60
GGTTGAGGNG CTGGGAGGTA CCCCTTTCCA AAGCCGTGTG GTCCAGGNAG GNGCCCGNCC 120
ACCTCATGAG CNTGTTTGGT GGAAGCCCT GATCCTNTAC AGGGCGGCAC CTCCCGGAGG 180
GAG 183

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

CGCTTCCTTC NTGNGGTGGT GGAGCCAGTT TTTGGCCAAC TCAGCCGACC GCAAGAGGNN 60
GCTTCTGGGG GCTGNGAGTC ACTTCCGCAG GTGGAGGACC TTTCTTGACC TTCGCCCANT 120
GGTCTGCNT TCAAC 135

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

CCTATNAAAT GCGACGCTGG AACGAGGCCT TGGTCACCAA CATGTTGCCT GAGCACGTGG 60
CACGCCATTT CCTGGGGTCC AAGAAGAGAG ATGAGGAGCT GTATAGCCAG ACGTATGATG 120

| | |
|---|-----|
| AGATTGGAGT CATGTTTGCT TCCCTGCCCC ACTTTCCTGA CTTCTACACA GAGGAGAGCA | 180 |
| TCAACAATGG TGGTGTGAG TGTNTGCTTT TCCTCAATGA AATCATCTCG GNATTTTGAA | 240 |
| CTCTNTCCTG GGACAATCCC AAGTTCCCGG GTGGATCACC AAGATCAAAA CCATTGGCAG | 300 |
| CACGTTATTT GGCGGCTTCA GGAAGTCACC CCCGATGTNC AACACCATGG GNTTTGNCAA | 360 |
| TTCNCAACAA GNAAGACAA | 379 |

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

| | |
|---|-----|
| CCTATNANAT GCGACGCTGG NAACGAGGCC TTGGTCACCA ACATGTTGCC TGAGCACGTG | 60 |
| GCACGCCATT TCCTGGGGTC CAAGAAGAGA GATGAGGAGC TGTATAGCCA GACGTATGAT | 120 |
| GAGATTGGAG TCATGTTTGC CTCCCTGCCC AACTTTGCCT GACTTCTACA CAGAGGAGAG | 180 |
| CATCAACAAT GGTGGTGTG AGTGTCTGCN TTTCTCAAT GAAATCATCT CGGNATTTTG | 240 |
| AACTCTCTCC TGGGACAATC CCAAGTNCCG GGTGGTTCAC CAAGATCAAA ACCATTGGCA | 300 |
| GCACGTATTA TGGCGGGTTC AGGAGTTCAC CCCCATGTN CAACACCAAT GGGTTTGN | 360 |
| AGCTCCCAAC AAGGNAGGNC AAGTTCCNAG AG | 392 |

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

| | |
|---|-----|
| CTTNTNCTCT TCCCTGGAGA CCTGAGAAAC CAATCTGAAC CGACAGNNAG CTGGCAGAGG | 60 |
| NAATACCTGT ACCGCTATGG TTACACTCGG GTGGGCAGAA ATGCGTGGTA GAGTCTAAAT | 120 |
| CTCTGGGGCC TGCNTNGCT GCTTCTCCAG AAGCAACTNT NCCCTGANCC G | 171 |

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

| | |
|---|-----|
| TAAACGGAGG AGCTGTTCCA AAGGCTGCCC NGAGGATGCC GCAANTCCCC CNTAGGCNTC | 60 |
| TGTTTTACCC CNTACCCGGA GCCTTCAAAG TGCTCCTGGA AGAACCCCGA GGCAGAAGCN | 120 |
| GCCCTTAANC TGGCGTTAAG ATCACGGAGN NGTGCCTTCC TGGGGCCGAT TAAANCTTAC | 180 |
| CGGTTCGGGC TGATGTTTCC GG | 202 |

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

| | |
|---|-----|
| CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA ANAANAANAN AANAANAAAA | 110 |

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

| | |
|--|-----|
| CCCCAGAACC TGGATTTTNT NAACCTTATG GCCTACGACT TCCATGGCTC TTGGGAGAAG | 60 |
| GTCACGGGAC ATAACAGCCC CCTCTACAAG AGGCAAGAAG AGAGTGGTGC AGCAGCCAGC | 120 |
| CTCAACGTGG ATGCTGCTGT GCAACATGGG CTGCAGAAGG GGACCCCTGC CAGCAAGCTG | 180 |
| ATCCTTGCCA TGCCTACCTA CGGACGCTCC TTCACACTGG CCTCCTCATC AGACACCAGA | 240 |
| GTGGGGGGCCC CAGCCACAGG GTCTGGCANT CCAGGCCCTT TCACCAAGGA AGGAGGGATG | 300 |
| CTGGCTTACT ATGAAATCTG CTCCTGGAAG GGGGCCACCA AACAGAGATT CCAGGATCAG | 360 |
| AAGGTGCCTT ACNTTTTCCG GGGACAACCA TGGGTGGGGT TTGATGNTGT GGAGAGTTTC | 420 |
| AAAACCAGGT TCAGTATTTG AAGCAGAAGG GATTGGNNGG GCCNNGTNTT GGGCATGGGA | 480 |
| TTAGATGATT TGCCGGTTTT CTGCAACCAG GCC | 513 |

(2) INFORMATION FOR SEQ ID NO:1068:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

| | |
|--|-----|
| TCACGGATCA TATGCTGACG GTGGAGTGGT CCACAGAGTT TNGATGGGNG AACCTCATA | 60 |
| TCAAGCCTCT TNAGAACCTG TTATTGCACC CNNGACTTCA TCAGCTTTGC ACTANGCANT | 120 |
| GGNATTATTT GAAGGATTGA AGGCATTTTCG AGGAGTTAGA GAATAAATTC GACTGNTTCA | 180 |
| GCCAANCCTC AACATGGA | 198 |

(2) INFORMATION FOR SEQ ID NO:1069:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

| | |
|---|-----|
| CCCGGAGGTG TACCCGACCC CCCAGGCTTG GAGGCAGCCA AAGAGGTGAT GGTGAAGGCC | 60 |
| ACTGGNCCTC TAGAGGACAC CCCAGCAATG GAACCCAACC CTTCAGCAGT GGAGGTAGAC | 120 |
| CCCATCAGAA AGCCTGAGGT CCCACAGGA GACGTAGAAG AGGAGAGACC TCCCAGGGAC | 180 |
| GTGCACTCAG AAAGGGCTGC TGGAGAGCCA GAGGTGGCAG CGGACTTATN TGNAAGTTCT | 240 |
| CCAAGGAGAA GTACATCCTG GACTTCATCG CCAGAGAAAC TCCACAAGGA ATTGGGAGGA | 300 |
| GGAGCTTCAA ACTCAGCAGC ACGGATTTTC CGCAGCCATG CCTGGTTACC ATGGTCCGNA | 360 |
| TTCCCCCGAG AGGTCTTCGG AGACCTTNGT TACAAACGGC AAACGGNGAC TTTCTCATN | 420 |
| CCGGGANTCA ATTCAACCAG TCTTGGGGGA TTATGTGGNT CAAGT | 465 |

(2) INFORMATION FOR SEQ ID NO:1070:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

GGNCTCCGTA GCCGCACAAA CCAGGGCTCN NCATGGAAGC CAGGATTCAN TCCCCGTGGG 60
GGTGGCTTT 69

(2) INFORMATION FOR SEQ ID NO:1071:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

GGCAGAGTNT AGGGCCTGTN CACAATGAGC TTGCATTCCA GCCTCCCATT TCCAATCATC 60
CTGCTCCTGA GTATTGGTGT TCCATTGCTT ACTTTGAAAT GGATGTNCAG GTAGGAGAGA 120
CATTTAAGGT TCCTTCAAGC TGCCCTATTG TTA CTGTTGA TGGATACGTG GACCCTTCTG 180
GAGGAGATCG CTTTTGTTTG GGTCAACTCT CCAATGTCCA CAGGACAGAA AGCCATTGAG 240
AGAGCAAGGT ATTGATTGTA TAGTCAGATA GTTACTTTTA AAAAATTGGN GCATAGTACA 300
TTGTCTTTTA ATTCAAGGTT NAAGTTTTTC CCCTGTTACA TNATATGTNG TTCCTTAAAT 360
TNTAATT 367

(2) INFORMATION FOR SEQ ID NO:1072:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 317 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

GGCAGGAGCA GCAGTGGAGA AATTTGTTTA TTCCTGTNCA GGCTACTGTN TGGNANCCTT 60
TGTCTTGGGA ATAGGCGACA ANCACAATGA CAATATTATA ATCACCGNGA CAGGAAACCT 120
ATTTAATATT GACTTCGGGC ACATTCTTGG GAAATTACAA AAGTTTCCTG GGCATTAATA 180
AAGNGAGAGT GCCCTTTGTG CTANCCCN TG ACTTCTCTT TGTGAATGGG NAACTTCTGG 240
GAAAGAAGGC AAGCCGACAC TTTCTGAAA TTTCAGGACA TNTGTGTTGA GGCTNATCTA 300
GNCCTTCGTC CTCNCAC 317

(2) INFORMATION FOR SEQ ID NO:1073:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

| | |
|--|-----|
| TCCTTCCTCG CGGCACCNNC CTCCCCCGCG GCCTTCCTCC GCCGCCGGGN NCTCCGGCAG | 60 |
| CTTTATCGCC AAATTCCCTG AAACNTTCGC TTTCTTTTAA ATCCCCTGCA TCGGAATCAC | 120 |
| CGGCNTGCCC CACCATGTNA AAACGCAGCC GTANACACCA GCTCCNAAAT CACCACCAAG | 180 |
| GAACTTAAAG GAGAAGAAAG GAAGTTTTGG AAGAGGCAGA AAATGGAAGA GACGCCCCCTG | 240 |
| CNTAACGGGA AATGCTAATN AGGGAAAATG GGGGGAGCCA GAGGCTGACA ATGANGGTTA | 300 |
| GNACGGAGGA AGAGGGAAGN | 320 |

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 296 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

| | |
|---|-----|
| GGCAGGAGGA CCAGGTGACG GCGGGCGCCA TGCAGCGACT GGGGGCNGGG GGCCTNACGN | 60 |
| TGGACAGNAT CCTGCAGACA GATGATGCCA CGNTGGGAAA GCTCATNTAC CCCGTGGGTT | 120 |
| TCTGGAGGAG CAAGGTGAAA TACATCAAGC AGACCAGNGC CATCCTGAAN NAACACTACG | 180 |
| GTGGGGACAT CCCAGCCTTT TTGGCCGANT TGGTGGCGCT TCCGGGTTTT TGGGCCCAAA | 240 |
| TTGGCACACC TGGGTTTATG GNTTTGGNCC TGGGGGANAA TTTTTTTCGG GNTTTT | 296 |

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

| | |
|---|-----|
| CAGATGATGC AGAGGNAGCN ANCTGAGCNC NTCCAGGAAG AAAGTTAAGG GAGAAAGGCG | 60 |
| GGCCCGGGAA ACAGGCTGAG GCTGAGGTGG CCTCCTTGAA ACCGTAGGAT TCCACCTGGT | 120 |
| TGAAGAAGAG CTGGACCGTG CTCAGGAGCG CTTTGGCCAN TGNCCTGNAA AACTTGGANG | 180 |
| AAGTTGAAAA AGCTGNTG | 198 |

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

| | |
|--|-----|
| GGCACGAGCG TCGCGNCGCC TTCTGAGTGG TCGGGTCGAG GCTTCTCGGN CTAGCAGTGC | 60 |
| CCTCGCTGCG CGATCTCAGG CGGGTTCTCC TCGGCTCCGC GCAGCCGNGN CGCGNTGGGG | 120 |
| GACCCGGCGC ANGGTCACCT GCTGCCGAGG GACCCCGNGG CCCGCCCGG TGCTCGTGAT | 180 |
| GGNGCTGATC TNCGCCAAAC TGTGGAGCCT CNNCTGTAAC CAAGAACACA AAGTAATTAT | 240 |
| AGTGGGACTG GATAATGCAG GGAAAACCAC CATTCTTTAC CAATTCTTAA TGGAATGAAG | 300 |
| TGGTTCATAC TTNTTCCAAC CATTAGGAAG CAATGTTGAA GAAATTAGTT TGTGAAGAAC | 360 |
| ACTTCATTTT TCTTTATGTG GGGATTATTG GGTGTTGTTCA GGAGTTCTCT GCGGATCATT | 420 |
| NNTGGGGAAN CACATTATTT ACNTCAAATT ACAAGAGNTT CATTC | 465 |

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

| | |
|---|-----|
| GGCACGAGCG ATAATGCACA GTCCTGGTCT GTGGACCCTG CCACATTCCA CGGACTGGGN | 60 |
| CGCCTACACA CGCTGCACCT GGACCGCTGC GGCCTGCAGG AGCTNNGCCC GGGGCTGTTC | 120 |
| CGNGGCCTNG CTGCCCTGAA GNACCTNTAC CTGNAGGACA ACGTGCTGCA GNAACTGCCT | 180 |
| GGATGNCANC TTNCGTGACC TGGGCAACCT TACANACCTC TTNCTGTACG GCAACCGCAT | 240 |
| CTCCAGCGTG NCCGAGCGNG GNTTCCGTGG GCTGCACAGN TCGACCGTTT CCTACTNCAC | 300 |
| CAGAACCGCG TGGGCCCATG GTGNAACCGG ATGNTTTTCC GTGANCTTGG CCGTCTCATG | 360 |
| ACANTTTTAN TCTGNTTTC CAACAATCTA TTCAGCGGTT NCCANTTTA GGGCCCTNNG | 420 |
| CCCCCTNNG NTTGCCTGGA AGTAACCTGA GGGTCAAAGG GCAAACCCTT GGGTGTTTTG | 480 |
| AATTTCCGGG GAAGGTCAAT TTTGGGGG | 508 |

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

| | |
|---|----|
| GGCANAGGNA GTAAACAGAT AACAGGTGGT GGTACCTGGT TGGGGGAGGG GGGCGTGCAC | 60 |
| TGCCATGTCT TTTTTTTTTT TTTTTTTTTT TTCCCNANT | 99 |

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

| | |
|---|-----|
| GGCAGAGCCT TGGTACTAAG TCATCCTCAG GTTTNATAAC TAATGGTGCC TTCTTTNATC | 60 |
| CATCAAAGTT ATGACTGANT GTGGCACCGG GGACAGTTAG TTGCTGTCCT AGAGTTAATT | 120 |
| TCCTAGCTTC TTGTGTTACA NATNGGTGGC AGCTAATGCC TTAAAGGCAA AGGGGCCATC | 180 |
| TTAACACCAC GGGGTCTAGT TGTTGGGNAT AAATATGGCC ACTGGGGTGA CGGCCATGAT | 240 |
| NCCTATAAGT TGGGGTCAGA GCCCCCTATG GGCCATTGTT TTTTNGGGTN CAGGAACATT | 300 |
| NTGGGGAAGG CNTTAGTTAA TGT | 323 |

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

| | |
|---|-----|
| GGCACGAGGG ACAAATATAC AGCTGTTGTA AAGATGATTG ATTCTGGAGA CAAGCTGAAA | 60 |
| CTTGACCAGA CTCATTTAGA GACAGTAGTT CCAGCACCAG GAAAAAGAAT TCTAGTTTTA | 120 |
| AATGGAGGCT ACAGAGGAAA TGAAAGGTAC CCTAGGAATC CATCANTGNA GNAAGACTTT | 180 |
| TTNCAGCTAC TATCGTGCAT TGGNAACTGG GCCCTTTGAA AAGGGACGCA GAGTTGGAAG | 240 |
| GGAATTCAAT GATGGAAGGA CATTTCTAAA CTTGNCCTGA GTTTTGGAAG ATTTGTTAAA | 300 |

CANTGACATT GAAAATCTTG AAAGCATNCA AATTGGGTGT TCCGNCCAAG GGCATTNATG 360
AAGGACTCNG ACTGTGGTTT AGGGGT 386

(2) INFORMATION FOR SEQ ID NO:1081:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

GACCGAGGNC NNCCTGAACC CCCAAGGACA ACCGAGAGTN GATGACCCAA ATCATGTTTG 60
AGACCTTCAA C 71

(2) INFORMATION FOR SEQ ID NO:1082:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GGCAGGAGGT GAAACTCATC ATGGCAAATA TGCTTATNTG NATATATCCT TTGCCATACA 60
TGNCCTGCAA ACTGTAATGA AATGTTATTT ATAAGACTCG TAAGGCATGT NTNATTAGAC 120
TGGGACACAC AAAAGCCCNT GAATTATCTA GGCAAGCAAT CCTCTAGGGT CCAGATGTAG 180
TTTGGTAATG TGGGTGTTCA GTGATCACTG NTAATTGCAT TGANTGGATT TTNAATTTGC 240
TATGCCTGTG TTGAANTAGT NATTAG 266

(2) INFORMATION FOR SEQ ID NO:1083:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GGCAGGAGGT TAAACANCCG ANNCTNNGCN GCAGGTGCC CNCNTTGGGG CTGCTGGCTG 60
CTGCNTTTC GGCAGGAGGT GGTGGCCGCG GTCCCACGAG AGGGGGTATT TTNCGTCAGC 120
CAAGATGGGT TCCAAAAGGA GAAATTTGAG CTGTAGTGAA AGGCATCAGA AATTAGTAGA 180

| | |
|---|-----|
| TGAAACTAC TGCAAAAAT TACATGTCCC AAGCTCTAAA AAANCGTCCA ACAGTCCAAT | 240 |
| TNNGGGTNTA NAATTG | 256 |

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

| | |
|---|-----|
| TAAGTAACAC GNGGTGAGGG TTGCAGATGC AGTTNCCTGT TTTAATCGTA TAGACAGGGC | 60 |
| AGCTCTACTG CGGAGATGGT CAATGTCCCT AAAAGCCAAA GAACCTTGTN TTAAGAGGTG | 120 |
| TGGTAAGCAT CACCCTTACA AAANTAACAC AGTATGAGAA AGGGCAAGGT TTCCCTGTTA | 180 |
| TGCCCAGGGA AAGAGGTGCT ATGAATTGGA AAGCAGAGTG GCTGTGGTGG GCAGACAAAG | 240 |
| TCAGTTTTC AAAAGAAGGC TGGTGC GGTT TGGNCTGTNT CCCCACCCAG NTTTGCCTCT | 300 |
| TGATTTTCCC ACATGTTNNT GG | 322 |

(2) INFORMATION FOR SEQ ID NO:1085:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

| | |
|---|-----|
| CTACATCCAG TCCCTNCCAC AAACCCCAGG AAGGATTTC CTCAGCTGTT CCCACGGGCC | 60 |
| ANCCCCCAGG GTNAGTNTNA AAGCCCGCTC CCCAGGGGCC TCTNAGCGTA TCCCAAAGGG | 120 |
| CGGGCTCTCC CAGCCCCTGG TGTNAGGCTC TTGGCTCTNC CCCTGCAGCT GCGGACCTGC | 180 |
| TGGAGAAGAT GCTGGAGCTA GACGTGGACA AGCGCCTNAN GGCCGCGCAG GCCCTCACCC | 240 |
| ATCCCTTCTT TNAACCCTTC CGGGACCCTG AGGAAGAGAC GGAGGCCAG CAGCCGTTTT | 300 |
| AATGATTCCCT TAGNACACGG AGAACTTNA CAGTGGGATG AATGGGAAGC NTTAAGANCT | 360 |
| GGGGGCCTCG GGGTTCCTCG CCTTCGNCTG CAGGCT | 396 |

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

| | |
|---|-----|
| GGAGCTCTCA GCATACCGTG CAACAGTTCT GGGAAATGCC AGTNCAAAGT GGGTGTNATT | 60 |
| GGCTCTATAT GTNACCGATG CCAAGATGGA TATTATGGCT TTAGTAAGAA TGGCTGCTTG | 120 |
| CCCTGCCAAT GCAATAATCG GTCTGCCAGT TGCATGCNC TCACAGGTGC TTGTTTAAAC | 180 |
| TGCCAGGAAA ATAGCAAAGG TGATCACTGT GAAAGAATGT AAAAGAAAGG NTTTTATCAG | 240 |
| AGTCCTGATG CCACTAAAGA ATGTCTTCGC TGCCCTTGTT CCAGCAGTGG ACATCTACAG | 300 |
| GCAGCTGCTC CTATTAAAAT TCGAGTGGAA TTGGGNGCCT GGAATGTGGA ACCAGTGGTN | 360 |
| AAAGANGGGT TACATAGGGC CCGAAGTGGC ATTAAATNTG GNAAATGGGT TATTTACAAT | 420 |
| TTTNGACCAG CATCTGTTGG AAAGTGCCCA T | 451 |

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

| | |
|---|-----|
| GGCANAGGAA GACCTACATC GCCAGCCAGN GNTGTTCTGG AGGCCACGGG TCAATGACTT | 60 |
| CTGGCAGATG GCGTGGCAGG NGAACAGCCG TGTNCATCGT CATGACCACC CGAGAAGGTG | 120 |
| TAGAAAGGGC CGNAACAAAT GCNTCCCATT ACTGGGCCCG TAGGTGGGCA TGNCAGCGTG | 180 |
| NCTTGATGGG CCCTACTACT GTNAACCAAN TTTCGGGGGA GCATGTACAC AACCGATTNA | 240 |
| CAAACTNCC GTACCTTACA GGTCTGCCCC GTTTTGGACA ATTCNCCG | 288 |

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

| | |
|--|-----|
| CGTCGAGATC ACTTTAAAGA AGCCATGCCC TTTGCGCGNG TTNTGTAAGT AACAAATAACA | 60 |
| TTCGGAAGTN TGAAATGTTT GCCCAGACCC TTNAGCAGAG TCGGGGCTTT GGCNAGCTTN | 120 |

| | |
|---|-----|
| AAATTCCCTT NNAGGGAAAC CAGGGTGGAA GCTGGCCCCA GTNAAGGGCA GTGGAAGGCG | 180 |
| GGCACAGGTG GCCAGTNTAT ACACAGNAAG ACAATGAATG GTGAACCTGT NTGGTTNAAG | 240 |
| TGGTGGTGGC CAGCGTGCCA GTGAAGCTGG ACCTGNCCTG GT | 282 |

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

| | |
|---|-----|
| ATCAAGACGG GCAACAGGGT ATCTTGGGAA GTACTTTNCT GACATCATCA AGGAGGTTAT | 60 |
| GTCAGACCTG GGAGGANAGC ANNTACCAGA NTGCAAGAGC TTGCGGCTCT GCCATTTACT | 120 |
| GGGCGCTCGA NGGGTGGATT GGGGACAAAG CT | 152 |

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

| | |
|---|-----|
| GGCANAGACT GGACTGGTTC AAGCGGCCCCG ACGGCTTCCT GCTGGTGCTG GAGCGGCCCCG | 60 |
| AGCCGCGCAG GACCTCTNCA ACTTTATNAC GGAGCGCGGC GCCCTGGAAC GANCCGCTGG | 120 |
| GCGNCCGTTT NCTT | 134 |

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

| | |
|---|-----|
| GAAAATACGA GGTTAGAAAC TTAACCATTG AAGAGGAGTA AGGCTACTTA AAGCGTTAAA | 60 |
| AACTAATTGG GTAAGGTATG GTTGACCCAG CTACTTCATT TGCCTTACGA TGTATATTCA | 120 |
| TTAANCTAAG TCACTCACCT TCTCTGTGNA TGTGTATGGT TTGGTACAGT AAACATGAGA | 180 |

| | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| TATGATTAA | GGTGATT | CAG | GGATAGAT | CA | AGTGTCTGCC | TAAGTAAATC | TGTGTTTTCA | 240 |
| TTTTTTTTTC | TAGTACCATA | ACAGCTTGGG | GGAAAGACCA | TGAAAAAGAT | GCTTTTGNA | | | 300 |
| CATATTGTGA | ACACAGTTTT | CCATCATGCC | CTGTTNCTGT | GGGTCCANCG | NTAGCTATGG | | | 360 |
| ACCATTTTTN | AATGCGTGTG | GAGNAAATTN | NGGGGGTGAA | GGTTNCAAGA | CATTTNATTA | | | 420 |
| GTTTCCGGGA | AGTACNCCNG | GCNCCNNTAT | TATTCAGACC | NGTTTTCGGG | AACCCNCTNG | | | 480 |
| NCACNTGTTA | AAGGTTTGGG | GGTTT | | | | | | 505 |

(2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCAGAGGGC | ACTGGGGAAA | ACAGAGGAGG | AGGCACTGAA | GCACTTCCAA | GTAAAGTTTA | 60 |
| ACGANNCCCT | CCGTGAAGAC | CTGGCAAAC | CAAAGTAAAC | TGGCTGGCCC | ACAACGTGTC | 120 |
| CAAAGACAAC | AGGCAGTAGT | GGCTCCTCCC | AGCTCTGGGC | CCAAAAGGAG | GCGGCTNCGG | 180 |
| GTCGTGGGGA | CCAAGCACAT | TGGTNCTAAA | GGGGCTGAAG | AGCCTGAACT | GCACCTTAAC | 240 |
| GGGCAAAGAA | ACCGACATGG | CTGCCTTTTG | TTTACACTGG | TTATTTGATT | TCATGANCTT | 300 |
| TGAAATAGTT | TANGGTGGCT | AAACAGCCAT | AAACGGAAAC | GGCTNCTTTT | ATGCANCGGN | 360 |
| GGT | | | | | | 363 |

(2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCAGAGGNA | GCAGCTCACC | CCCTGGGGGN | CCCCNAAGC | CCGGGGGCCA | GCTGGACAGC | 60 |
| ATGCTGGGGA | AGCCTGCAGT | NTGACCTGAA | TCAAGCTGGG | GGTCGCCACA | NTCGCCAAAG | 120 |
| GAAGTCTGCG | GGGCCTGCAA | GAAGCCCATC | GCCGGGCAGG | TTGTGAACCG | CCATGGGGAA | 180 |
| GACGTGGCAC | CCCGAGCACT | TCGTCTGCAC | CCACTGCCAG | GAGGAGATCG | GATCCCGGAA | 240 |
| CTTCTTCGAG | CGGGATGGAC | AGCCCTACTG | TGAAAAAGGA | CTACCACAAC | CTTTTTTTCC | 300 |

CGGGCTTGTT ATTATTGNAA AGGGCCCCCA TCCTGGGTNA AATGGGTGAA CAGCCTTTTA 360
ACCGGACGTG GGAACCTGAA AAATTTTTTTT TGTNGNAANA TTTTGGG 407

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

ACTTTNTTGG CCCCAAACCT AGGNCCTGGG GGATCCCCTG ANCCCACTGG AGAGTNTNCA 60
GGGCTGGCCC CTGTCCCCAA AATCCCAGGC TCCCATTITT TCCCAGGTGT CCTGCTTTTT 120
AATCTCATCT TCATGTTGAG GCCGTTTTAT TTGACCCTCA AAGAGGAAGA CCAGCTTCTA 180
GGGCTGTCCC CGCCCCAGGA CCAANAGTCC TGCAGGGCTA AAGTNTCCCA CTGTGCCATG 240
TTAACACACT GCACAATTAA CTCCAGGGGG TGCCGCTCAT NNTTGAAAAT TNACAGTCAA 300
TGCTTGAAGT CACGACATTT TTTCCAGAAG ATGGGCNTTA AGGNTCTCGA AGAAGGGGGC 360
ATTTCTTAAT CCCTTACAAA NTNGTTTTGG GGTNTNGGT GGAGGTCGNT CTGGTNTCAG 420
NAGCCCTAAT TTTCTCCCC GGACCTGTCA AGAATT 456

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TAAATAAATA AATAAATAAT AAAATGAATG AGGAGCCAGG TGCAGTGGCT CGTGCCCTGT 60
GAATCTCAAC ACTTTGGGAA GGCCAAGGGT GGAGAATCAC TTGAAGCCAG GAGTTCTAAA 120
CCAGATTGGG CCAACAAGTG AAGAACCTCA TCTTTACAAA AAGTTAAATT AGCCAGGCGC 180
GNTAGAGTGT ATCTGCCAGT NCCAAGTAC TTGGGAAGGC TAAGGCAGGA GGATTCACCT 240
GAGCCCCAGG AGGCTGAGGC TATAGTGAAG CTNTTGACCG TGNCCATTGN ATTNCCAGCC 300
TGGGGNAACA 310

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

| | |
|---|-----|
| CAGGTTATAA GTTGAGAAAA CCACTAAGGG AAACGCCTGA TGACGCCCAT TCTGAATCAC | 60 |
| TATTTTCCCC GTATTAACGT GTCGGGAAGC TGCTGCGNTC AATATTGATA CGCTTNGTGC | 120 |
| ATTGCNCTGA AAACACAATT GCACCATTCG GTTTGAAAAC CTCGACGTTT TGCTGCCGAG | 180 |
| GGAAATACAG CTTGATAATC AATCGCCGGA AGAGAACTG GTGATAGCCC GTCGTGGCGG | 240 |
| TTACTGTTTT GAAGCAGAAT GCGTGTTTN AGCGGGTGTT ACGCGAGCTT GGGTTTAACG | 300 |
| TTTCGCAGTT GTTAGGGCGC GTAATGTTTA TTCAAATTCC GNCCAGNTTA NCNGCNGGGA | 360 |
| ACCCATCGTT TGCTGTTTGG TGGGACTGGA GGAGGAAAAA TGGGTTGCTG A | 411 |

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

| | |
|---|-----|
| GGCANAGGGT ATTTACCTAC TGTAACAGC TAATAAGATG TGTGTATGGA AGACTGAAGA | 60 |
| CAGTCTGAGA GATGCATCTC AACAAGGCCT AAGTCTCCCT TCCTCTGGGA ACTGTCCGGT | 120 |
| AGTGNCTAGT TCACTGGGGT CCTTGCTCTG AGGCTGGTGG GAACTGGAT TTCAGGGACA | 180 |
| CAGGCTGACC ACACAGGGNG CTGTACCGNA CCCCTTCCAA CTGGGAACTC CCCTCGGTTT | 240 |
| CTCACACTGT GGNCACTTAG TGGGTTTGGG NAGGCTCTAG GCAAGGGGGA TGGGTAGTAG | 300 |
| GGTGGTTGAG GATNGGTGGT TGANTATGGA CAAAGGTACG NGTTATGGGT TTTCACCCCA | 360 |
| GAAATCCCAC NANA | 374 |

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

| | |
|---|-----|
| GGCANAGTGA TTAACAGATG CAGGCCTATT CAAATTTNCT ATTTNATGTC AGTCTTGGA | 60 |
| AATTGTAATT TTNAAGATAT TTGTCCATTT NATCTAATTT TCCTAATTC TTGGCATGAA | 120 |
| GTTGTTTCGTA TTTNAATCCT TTTNACGCCT CTAGGATCTG TAGTGAATGT CTTGCCTCA | 180 |
| TGTTGCTCAA AGAACCAACT CTTTTGGCTT TGTGAAGTN ATCTGNTTGT TTTNATGGAT | 240 |
| TCTGATTCCN TAAGAATTC CNTGCTTGCA TTTAGT | 276 |

(2) INFORMATION FOR SEQ ID NO:1099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

| | |
|---|-----|
| GGNANAGTGC ACGTTGGCGC TACCGGACGG AATGCTGTAT CCCCCAAAAA GCCCGTCGTG | 60 |
| GCAGCGCAAG AGCTGGACGG CCTCTAAAGC TTCCNGNACG ACTTCTCCAA NAACCAANGC | 120 |
| CGGGGNTTCA | 130 |

(2) INFORMATION FOR SEQ ID NO:1100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

| | |
|--|-----|
| TGTATAAATC CTTATTTTAT TAACAGNATA CTATCATAAA TAGTATTATA ATGCTGNNAT | 60 |
| TTCAGGTAAG NAAATAGCTA AACTNCAGTA CACTCTACAG TAGCAACTCA GGACAGCTGG | 120 |
| TTACAAGCTG GTTGTNNTAG GACATTGGTT ACACGGATTC TTAGACACTT TAATGGCTGC | 180 |
| GATAACTGTN ACTCTCCATG ATCCATGTTT CTTTTATGCG CATATNATTT GACGCACACT | 240 |
| CATTCAGAGT CCTCCGAGAG GGGCACCCAT ACACGGCAGA NGTGTTTCATC TCCAACATGA | 300 |
| AAGTGACCAG CTCTCATCCT CGTCTCCCCA ACACCATAAC GTCCTCATCC CGCCTCCAAC | 360 |
| CCACACCAGG NCGAAGCCCT TCANAGGGTG TTTTCATCCA GGAACCACT CTCGAACCTG | 420 |
| AAGGTTTNAC TTTAGCGTTT AGCNAACCCA GGGCGGGTGT GTGTGTTTCC CGTTTTGTTT | 480 |
| TTCTG | 485 |

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

| | |
|--|-----|
| GGCAGGAGGG NCCCCTGTGC AGAGACTGCT TATNTNCTGG GGAACATAA GACGGAGCCT | 60 |
| TGCAAGAAGC CCCC GCGGCT GTNCCGNCAA GGCTATGCCT GTCCCTACTA CCACAACAGC | 120 |
| AAGGNCCGGC GCGGAGCCN CGGAAGCACA AATACAGGTC CTTAGGCCCC AGGAGGCCAG | 180 |
| CCACGGGAGG GAGGAGTGGC AGGGAAGGGG TCAGGCAGAG GCTGCTCCCA CTGGCTCTCC | 240 |
| GGGAGGTGNG GNGGTTGGTT CTGGGGATTA CAGGATCGCA AAGCCCAAGG GCCCAAGGGG | 300 |
| AGGGCATTAG TTNAGGATTA GTTGGACAAT TAAGGAGNCC CAGTTTTAAA CTTNCTTNCA | 360 |
| ATTAATTTNG GGG | 373 |

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

| | |
|---|-----|
| GGGNTACACG CAGGCGCCAA CCAAAGTGGC CAGGTCTTCG GCCTGGGCCC GGNAGATATA | 60 |
| TAACCCCAAG TACTGCCCCA ANGGAACAGT GGCCGATGGG GTTCCCTCGG GNNACNGGGA | 120 |
| ACTGNCCGGG NCCCGGGGGA AGGTCCCTGA ANTATCCCCC TTNATNACCA GGAGGAGGCC | 180 |
| GGCTNACTGA GNGCTCCCAG CACGTTTTCT CCCCAAATGC GTNTTCCCCA TCTGGGATTT | 240 |
| TGGGGNTTTT CATGTGTTTT AAANTTTTTT TTTTTTTTTT T | 281 |

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

| | |
|---|----|
| GGCAGAGGGA CCTCTGGCAA GTNTNTTCCT TTCTTGGGGC CTCACCTGTT TCATNCGCAA | 60 |
|---|----|

| | |
|---|-----|
| ATGGGGATGT NCCACCTGAA CCCCACCCAC ATCTNCAGGT GGTGAGAGCA GATGGAATGG | 120 |
| CACTTTGCAA ATCCCCACCA GCTGGTAAAG GTGAATAGCC TCACTCTTCT GCTTAAAGCC | 180 |
| GTCAGTGNGC TGCTNCATCA CACTAGANTA AAATGGAAAC TCCTCACCAT AGGGATCCAG | 240 |
| NCTTTGCNCC AACTTTTTGA ACAGCATCTT CCCTGGGATT TTTCCANCNC AAAATTGG | 298 |

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

| | |
|---|-----|
| TGGNTTAANC GANTTANAGC TGCTAGCCAG GAACATGGAC TGANGTATCC AGCGCTCATT | 60 |
| GGGAATTTAG TTAAGTCCCA GGTGGAGCTC AACAGGAAAG TCCTAGCGGG ATCTGGGCCA | 120 |
| TCTTNCGGAG CCAAAGANTT TNAAATCTTT TGGGCTTGCC TTTGGCCCAG TAGGGAGGGC | 180 |
| NGTCACGGAG GGNTTTTCCT TG | 202 |

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

| | |
|---|-----|
| GGCANAGTTT CTCCACAAA ATATAATTNT NAATTAANGT CTCAAATACA ACTATTTAAT | 60 |
| CAACCACTGA TTAICTATAT NGTATACATA TATAAGGGAT ATGACAGAGT AGAATTTNAA | 120 |
| TAAANGTAAA TAACTAATTA TAAAATAGGG GTCTTATTTG AATAAACAAT TTTGAATGCT | 180 |
| ATCACTGCTT ACCTGANCAC TNCTGCTCAT TTTGGGCCCT CTGGGATCCA AAAATTCCAA | 240 |
| AGNCCTTGGG CNTTGGGGAA CCCNCCCAG GGTGAGAAG TCTTA | 285 |

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

| | |
|---|-----|
| GGCACAGGGA AATGTGTGCA GCAAGGTTGT CCTCAAGGGG CTCTTGTTCCA CGTGNCCTC | 60 |
| TACCCATGGT CCCACAGCG GGACCAGCTC CACACACAGG GAAAGANTGG NAAAGGAACA | 120 |
| CCCAAAGCCA ACCTGGCCCT GGAACCTCC CCTTCCTGGT TTTGAACGGC TCCTGNAAAT | 180 |
| TGGNTCANTN CACACCGAAA GGACTTTTTT GGAAGGNAGC GCACCAANTT TTTTNTTCTG | 240 |
| GGAAAGATGG TGGTAAGGCA GAGCTTGAGT TCCATTGCTT ATGGGAGGGG AGAGATTAGN | 300 |
| CCCTTGACA GAGCCTTCCT TCGGGGGTTN CCAGGGGNAN TNG | 343 |

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

| | |
|--|-----|
| GGACAGTAAG ATCTTAATCA TCCANAGCTT CTTTAACCCC AACATCGTGA GAATTCCATG | 60 |
| AGGTNTACGA AACAAACATG GAAATNTACC TGAATCCTGG AGTACGTGCC AGGGAAGGAG | 120 |
| ACCTTTTTTGA ACGCCATCAT AGAAAGTTTG AAAGTTCCCG GAGCCCGATG CTGCCCTCAT | 180 |
| GAATCATGGG ACTTATGCAA AGCCCTCGTC CACATGCACG ACAAGAGCAT TGTCACCGG | 240 |
| GACCTCAAGC GCGGAAAACN TTTTGTAAG TTTTGATTTT TTGATGATAT GGGAGAGGGT | 300 |
| NTTTTTAGAA TATGGGGTTA AATTTGNTN | 329 |

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

| | |
|--|-----|
| ACTGGGTTGA TACAAAGGAT TGGTCTCAA GCTCTGAAAT TTTTCTNCT GCTTCTCTA | 60 |
| GTCTGTNGTA TTTNAAAATT CCTATAGTAA ATTTTNNAAT TCCAGAAGT | 109 |

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-----|
| GAATAATTTT | CNCATCGNAG | ACCCACACCG | GGCAGCCAAA | TTAANC | GGGC | AAACGCAGCA | 60 |
| NATTTNNGGC | GGTNAGATCG | GTATCGGTGC | TGAACAGTGA | ATGTGGCATA | ACAAACTCCA | | 120 |
| GATAAGTNCT | TTTTNATGAT | TACGCCACAT | CATAAAAAGA | NTAAAAAATA | TCGATTTATG | | 180 |
| TCGAGTCTAT | GCAAAATTGN | TATGGATTAC | CGGTTTGCGA | GAGAGCGCTA | ATGGCCGCCG | | 240 |
| TTAACTTACG | TCATATTGAA | ATTTTTCATG | NGGTTAATGN | CCGCCGGAAG | CNTTGACTGN | | 300 |
| GGNGG | | | | | | | 305 |

(2) INFORMATION FOR SEQ ID NO:1110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| NCCTCTTGGC | ATGCCTGTCC | TAACTTNTNG | TAACATCAGG | CCTGCCCCGA | ATCACCTGTN | 60 |
| CGAGCCACNC | CAGTGCACAG | CAGGAACTGG | TAAAGTGCCT | GGNCTGCTTC | TNCCTTTNCT | 120 |
| CCCTTTCCAT | CT | | | | | 132 |

(2) INFORMATION FOR SEQ ID NO:1111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CACGGNATTA | ANAAACGGTG | ACGCGGGTAG | CACCACTTCA | AAGGCCTCGC | NACGGTTAAT | 60 |
| TGCNACCACT | ACACGTTGCT | GATTCANCA | GCGGACAAAT | ACCACCACGT | TATCTTCCGC | 120 |
| ATACAGCACC | TNANAGCCGC | CATGACGTAG | CGCCTGATTT | TTTTNACGCA | GCGCAATCAT | 180 |
| TCGCTGGTAC | AGCNNGAATA | ACGCCGTATC | CTGCTTTTCC | ACCTGCNAGG | GGAACGGTTT | 240 |
| ACGGCAAAAC | GGATCGTTTT | TGCCATCCAG | TCCTACTTCA | TCACCGTAAT | AAATGGGACG | 300 |
| GTACACCAGG | GCCAGGTGGA | ACAGGNAGGT | NCACCGNNCA | NGGCAGGC | | 348 |

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

| | |
|---|-----|
| ATTTNNGATT GTNCAANACA GAGAATCTCA TCCCGNACAA GATGTAGGAG GAAGAATTAT | 60 |
| CCAGGTCAAT GGA CTGGTG AATTCGATC CACCTGAACT NTGCCACAGT GAGTCCCGAG | 120 |
| TTCCTTAGGC TTNNTGGTNT AGNGG | 145 |

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

| | |
|---|-----|
| GGCCATTNAA ATTNCCCATC CTGCATGAAA TTCCCCTTGG TGTAATNAC CTGCACAATA | 60 |
| TGACTCCTCC TTTACTTCAT CATGACTTGA AGACTCAGAA TATCTTATTG GACGATGAAA | 120 |
| TTTNATGTTA AGATTGCAGA TTTTGGTTTA TCAAAGTGGC GCATGAATGT CCCTCTCACA | 180 |
| GTCACGAGTA GTCAAATCTG NCACCAGAAG GAGGGACAAT TATCTATATG CCACCTGAAA | 240 |
| ACTTATGNAA CCTGGGACAA AANTCAAGGG GCCCAGTATC AGGCACGGTT ATATATGAGG | 300 |
| CTNTGNCAGT TTTTTCACAT CGGNAAGT | 328 |

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

| | |
|---|-----|
| AGGTGACACA GGAGTGGCCT TNCCCTTCGA ATCTTTCCTG GGCAACTACT CCTGTGCTGC | 60 |
| CCAGGGCACC CAGGGTGGNC AGCAAGAAGT AAGCAGGGGA AAGGGCCAGG GAATGGGGTG | 120 |
| AAGTAAGGGC AGGGCCAGGN CAGGGAAGGG AAGGTGGAGA GGGTGGGCTT TTGGGGTCTN | 180 |

| | |
|---|-----|
| TTTCCCTTTC CTTCTCTTAA GCCCCTGNTN CAGCCCTGGG GATGGGGTCA AGACTGGGGA | 240 |
| ATCAAAGCAA GGCCCTGTGG GGCAGTTNTG GGGAGGGGGC TGAGTNTTCG ANAAGAACAG | 300 |
| TTCCAGTTAG GGGTNAACGG CCTTCCTTGA GCAATNGTTC TT | 342 |

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

| | |
|---|-----|
| GGCANAGGTT TACTTATCAG TCAGACCCAT TCCGGTGGGC CTCGAAAGGT ATGTNCATGT | 60 |
| TTGGAGTTTG CTTGGTTTTN TTCTCACCTG CTTTTNACCC TTTAAGAATT TNATATGGTA | 120 |
| TACATTGTAG TAGAAATATT AGATAATGNC AGGCAAGCAA GCATCAGAAT GACCTAAAAT | 180 |
| TCCAGTACTT TGAGTACAAG GCTTTAAACA TTTTAGTATA TACATCTTTC TGGTATATGT | 240 |
| ATGTGTGTAT ATATATATAT ATATGTGCCN CACACACACA TATATCTTNT TATAAAANTT | 300 |
| TATAATCTNT ANTTT | 315 |

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

| | |
|--|-----|
| AGGCACAACG TTTTNANCAG CTTTATCGCC GCTATCAGCA ATGGNCGATG AGCGCCGNAA | 60 |
| CAACACTATC TTCCAAC TTC CGCCCCGGCA CAGGCTGCCC AGGCCGTTGC GAACTTTATA | 120 |
| AGGACACGAT AATGAACGAT TTTNAATAAT TATGAAAGTG TGGTTTGTA ATTGGNAGCC | 180 |
| AGCATCTNTT TGGCCCCGAA ACCCTGNNTN AGGTTACCCC AACATGCCGA GCACGTGGTT | 240 |
| AATGCGCTGA ATTA | 254 |

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

| | |
|---|-----|
| CNAGGGGCCC TNAGGNTCCC TCCTGGCCCC CACGGAACCC GTGCTNCTNT TAACTCCTAG | 60 |
| GAGATGGTTT AGAAACGTTT CCCCCACTTT GACGGCATTG NAGGCACCAG GNGCAGCTCA | 120 |
| AAGTAATGTT CATCGGAGGC CCCCAACACC AGGAAGGACT TTTCACCTCG AAGAGGGGTT | 180 |
| GAAGGAGGTT GGGTTTNATT TGGTCTNCCT TGGNTTTAGG NCCTTNGGG | 229 |

(2) INFORMATION FOR SEQ ID NO:1118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

| | |
|--|-----|
| GGCAGGAGGG AGACCCGGGG GAGAACCAGG CGTCCAGGAC GCGCGTTGNA CCACCCTCAA | 60 |
| CACGGATATC AGCATCCTGT CCTTGCAGGT GAAGACCTGC TNCCGGGGTN CCCGGGCCCCG | 120 |
| GNGNCGGACA CTCCCGGGGT TTTCTNGTCC TGTGCACTAG GTAGATCCGT AGCCCAT | 177 |

(2) INFORMATION FOR SEQ ID NO:1119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

| | |
|---|-----|
| TGGGCCCATN TCCTCCTCCN TCTCCTCCCT GCNATCTTTC CTCTCCTCAA ATNTCCCTGC | 60 |
| AGTNTGAACC CCGGCCTTGA AGGCTGGGAA GCAGGGAGGC CAAGAGAAGG AAGCTGTGAC | 120 |
| TCCGCCTAGC TCCTGGTTGT TAAGCACCCA TGTTGGCCA GGTGNNAC AAACCTCTGGC | 180 |
| GCTCTAAAGG CTGATAAAGC CCCACAGCCT GCACGTTTGG NGCCTGGGCC TCCAGCCCTG | 240 |
| ATAAAGCTGG ACCTGTNAGC ACCATGGCCA CACCTGCTGT AGGNATGAAG CGGCCACCCG | 300 |
| TNTCCCTGG GCCATTCCA NTNAAGGGTT CCTGTTTCCC TGTGACAG NCAAGCCCTG | 360 |
| GGCCACCATG NCTTAGGCCA ACCCTTCCTG GNTGAAGGAA CAAATGGNNG TTGGCCATGG | 420 |
| GCAAG | 425 |

(2) INFORMATION FOR SEQ ID NO:1120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

| | |
|---|-----|
| GGCACGANAA GAACCCCGNG NAAAGTCTCA GGATGGNAGT TCAGATTTGG TAAGGCATCC | 60 |
| CCTAGTTNCA GCTTCCTGGC GGCCTGCTCC ACACAATNGC CTNTGGGCCC ATGGCCTTNA | 120 |
| TCC | 123 |

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

| | |
|---|-----|
| TTTAANCAGC TCAGGGGGTT TNATTTCCAA GTAGAAGGCC GGAATGGTG GCATTCCTCC | 60 |
| CANAAGTGCA CANTGAATA TAACTTNTT TGTGGTAGAT AGGANTGAAC AATTATCCGG | 120 |
| TTATCTNGTT TCCCTTGCCC AGAAATGGTT CTNTCCAGT GGAAATTGTG CCCCCTCTG | 180 |
| CCAGGACTGG AACTTGGTC ACAAANTGG TAGCAGAGGA TGCTGACAGT GGTCTAATG | 240 |
| CCTGGTTTTT CCTACCACAT NTCCCGGGCG TTTGAACTCT GGTNTCTTTT AGAATTTTCA | 300 |
| GCCAATATTA GGTNAGCTTC CNTAANTG | 328 |

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

| | |
|---|-----|
| CACCATTGAT GGATACTTNG GTTGATTCCA TGTCTTTCCT ACTCTGAATA GTGCTGTGGC | 60 |
| AAAACCTTTC ATGGCCTCCG GAATCTCCTT CCTTGGTCCT GCCACAGTNC CAGCAGTTTC | 120 |
| CATATTGTTT ATTATTTGGA ATTACAGCAC CAAAGTNCCT GTTAAATGT AACTNCTACT | 180 |
| TTGGGAAGAG ACCTGATTCC TCATGACAGG CATTAAATAC CTTAGTTTAG GCTAGTTTAT | 240 |

| | |
|---|-----|
| CTGCTTGGCC CTCNAGCACG GGGAGCCCTT GGGAATAGAA GGAAAGCAGA TAATGTTTCC | 300 |
| CTGGGGTCAG TATTGGGTTG TTACCTGGGG AAGGAANTGG GAAANCTTGG GGGGTTTCGA | 360 |
| GGGGGGNCCC NGGTACCCTT TNGCCT | 386 |

(2) INFORMATION FOR SEQ ID NO:1123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

| | |
|---|-----|
| CCCAGACGGC GGCAGTCCGG CTTNCCCTTG GAAGTCNAGG CTCGGTTGTC TTTTGAAGC | 60 |
| CATGGAGAGT AACTTTAATC TGNGCTACTA CGTGGGGCAC AAGGGCAAGT CCGGCCAGAG | 120 |
| TTCCTGGAGT TTAAGTTTCG ACCGGAGGGA AGTTAAGATA TGCCAACAAC AGCAATTACA | 180 |
| AGAATGNTGT NATGATCAGA AANGAGGCTT ATGTACATAA ANGCGTGATG GAGGAACTGA | 240 |
| AGAGATTAAT TGACGACATN AAATT | 265 |

(2) INFORMATION FOR SEQ ID NO:1124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

| | |
|---|-----|
| GGCAAGAACA AGCGCCTTAC GAANGGGGAC AAAAAGGGAG CCATGAAGNA AGTGGNAAAT | 60 |
| CCATTTTCTA AGAANGATTG GTATGCTGTN AAAGCACCTG CCTATGTTCA ATATAAGTGA | 120 |
| ATATTGGAAA AGAACGCTCC TCACCANGGN CCCACAGGCN NCCAAAATTT GCCATCTGAA | 180 |
| TGGTTNTTCA CGGGTCGTGT C | 201 |

(2) INFORMATION FOR SEQ ID NO:1125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

| | |
|---|-----|
| GGAAGAAAAC CAGAAGGGCA CACTTNAANC TAATTTGGGG TATCACTAAC CTGAAGANAA | 60 |
| AGAGAAAGGG GGAGAAAACC TAGCAAACCA CCATGTCCTA TGGGAAAGTT TGCANNATGC | 120 |
| ATCGAANATT NTNTGGTGGG GCTCCNCCTC CTNTGCCATC GGGGNTTAAT ATTTNCCTTT | 180 |
| ACTTTNCCCA ATGGGGAAAC AAAGTTTGCT TCNAAAAACC ANCTCAGCGG TTTGGTGTGG | 240 |
| TTTTTTNCTG GAATCGTGGG AGGTGGCCTG | 270 |

(2) INFORMATION FOR SEQ ID NO:1126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

| | |
|--|-----|
| GNCGCAATTT ACCTTTGCCA AATAATTACC TTTTATCTAC AATTTTNCCT GTTTTTTGGT | 60 |
| TCTTTTCAGAT CTCACTTGTA TAATGNCTTC TTTGNTAATT TTGTTATATT TTCCTTTCTA | 120 |
| TTGTCATAAG TTGGGATGAC TTAANTTANC TNCAGTCTTT GATTGTTATA GGTACTATGG | 180 |
| TATNGCAGAC CATAAANATC CT | 202 |

(2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

| | |
|---|-----|
| GAAANTTTTA GATANTACAT AATTATTGCT GTCCANAAAA TCTTAAAATA TATGNATTCC | 60 |
| ATGAGACAAG AGATGAAGTA TGAGGTNAAG AATACTATGT CTAAGCTGNA AAGGTACCTC | 120 |
| ATTAAGTTAT AGACAGNANT AAAATGAGGA GGGAGTATGA AACATATGGA NGT | 173 |

(2) INFORMATION FOR SEQ ID NO:1128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

| | |
|---|-----|
| GGCAGAGCAG CAGTTCCTGA AGAAGGCGNT GCAGGGGCTG CCANGGGACT TNCTGGGNGC | 60 |
| TGCGCTCGTN GCGGTGTGGG AGCAGCTCAT GTTACATCAA GGAGGGACCT CATCCTMNCC | 120 |
| GCACTACCAC ACCTTCTGAC GANCTTCATG CATCGCCAGG GNGAGGNTGT CAAG | 174 |

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

| | |
|--|-----|
| GGCANAGCTT TCCTCAGAGA CCACATCACT ATTCCATATT TAAGCAGGCC AGCATCGTGG | 60 |
| AAAGCNCTTT TCGGGCATCT GGGGCTCCAG AACCGCAGTA TCAACCTTCT TTCTNATGAC | 120 |
| TATGGAGATA TTGTTGCTCA GGAGCTTCTC TACAGGTCAG TGGAGCTTCA AACTTCAGCT | 180 |
| TATGAATGCT AGGAGAGTAC ATTGTTTCTG GACTGTTTGT ATCCTTTTNN CTCTCGTTTT | 240 |
| TCAGCGGTGC ACTGGTTTAA GGTGTTGCTCC AGCTTACATG TGTGNTNTCC TCGTCTNCCT | 300 |
| TTT | 303 |

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

| | |
|---|-----|
| NGNGCACGCT GCCCCGNTNC CCCACTTTNA ATGCAGGCTG GCATACCACT GTGAACTCAG | 60 |
| GATCTAAATT TAAAACTTCA ATTCATTTAA ATTTCAAAC AAAAGCANTG TAAATATTTT | 120 |
| NCCCTATCCC ATTACCCTGN TTTGANTCAT TACACATTGT ATACATATAT CCANT | 175 |

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

| | |
|---|-----|
| CAGCTCAATG TGTAAGCATT TTGGTGCCTG TCCACTAAGT TTCAGGGAGC CTCATTCTTC | 60 |
| CTTCACTCAG GGCAGCATTT GCTCTGAGAG AGGCGGCAGA TTCACAAGAG TAAGTAGACA | 120 |
| GTCTATTGAG GTTTAGGTTT AAAGTCTTCC TCCAGATACT CCAGATTGAA TGTACTAATT | 180 |
| AAAATAGCAA CTACAGTGGT GGAGCATTNA GAATGCTAAT GAATGTTTTA ACCCTTTGGA | 240 |
| AACCTGATGC ATTCCCATAG GTTCATATGG TCCATTCTCC AAAAACTGG GCATTGGTTA | 300 |
| GAATGGAGTA GACAGTAGAT GCTTAGCTTG AGGTGGGAGT GAAGCTGGGT TCCTCACCNT | 360 |
| TTTTNNNN | 368 |

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

| | |
|---|-----|
| GTCCTCTCCA AACTGAACCC AGAGAATCTG GAACTCGAAC AAACCTGGGA GNCAAACATC | 60 |
| CGTAAGCAGT CAGTCGCCAA TGCCTTCATC ATCTGTGGCA CCTTGNACAC CGTCAGCAGC | 120 |
| TACACCTCAG CAGATGCTAC CGTCAACTTT GCTTATGAAC ACAGGCACAG GTATCAGCAA | 180 |
| GACCCTGACC ATCCCATTC AAGAACGCTA TAAGTACAGC AGCATGATTG ACTACAACCC | 240 |
| CCTGGAGAAG AAGCTCTTTG CCTGGGGACA ACTTGAACAT GGTCACTTAT GACATCAAGT | 300 |
| TTTCCAAGAT GTGAAAAGNC TCCAAGTGTA CAGGCATGGG CAGAAGGGGG TTGNTCAGGG | 360 |
| TNTTGGGGGG AGCAGGTNNA GGG | 383 |

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

| | |
|---|-----|
| CAAAATGGGA TTTNTTCAAG GNCTGGGTTT AGAAAANTCA GCACAAGGCA TCACTGAGCA | 60 |
| TATCATACCT ACTCCTAAAG CAGACTCTAC AGGACTTGGT TATTCTNTTT AGAAGCGGTC | 120 |
| ACTATCAAGC CTCCAGAACC CATCCCTTTG ACCTGGAGGA ACTTTAAAAA CCTGTTCTAG | 180 |
| GTAGGTGGAG TGGCTGCTCC CAAAAAATAA AGCTNGGGNG GCNCTGCATA ATTTTGAGTT | 240 |

CTTGGAACAG TTTAAATTT NGGGA

265

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

| | |
|---|-----|
| GGCAGAGCTC GCGTNGNCTG TGGCCGCAGC TTGAGTATGC TCAGGCTTCA GAAGAGGCTT | 60 |
| GCCNTGAGTG TCCTCTGCTG TGGCAAGAAG AATATCTGGT TAGACCCCAA TGATGACCAA | 120 |
| TGAAATCACC AATGCCAACT CCCGTCAGCA GATCCGGNAA GCTGATCAAA GATGGGCTGA | 180 |
| TCATCCGCAA GCCTGTGAAT GGTCCATTCC CCCGCTTGAT GCCGGAAAAA CACCTTGGCC | 240 |
| TGCCGGAAG GGCNAANTNA TGGGGCATAG GTAAAGCGGA AGGGTACAGC CAATGCCCCA | 300 |
| TTGCCCAGAG AAAGGTTTAC GTGGGNTGAG GAGGAATGAG GATTTTNGCA CCGGNTGCTT | 360 |
| TCAGAAAGTTA CCNTGNATTT TAAGAAG | 387 |

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

| | |
|---|-----|
| GGCAGAGCGG CANGAGTGNG CGCTCCTGCT GGGGGTCACG GGAGTCGGGA AGANTGNCTG | 60 |
| GTGAACGGCT GCAGGAGGTG AGCTCACGGG ATGGGAAAGG CGACCTTNTG ACCNGCCTAG | 120 |
| TNCACGTCCC ACGTTTGTA TGGACGCCTC TGNACCCAC CCAGCTCTCT NCATCCTGTG | 180 |
| TGCA | 184 |

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

| | |
|---|-----|
| AATNTTTGGC AAAGCAGTGG AACATATGTT TGAGACAGAG GATGGTTCTA AAGATGAGTG | 60 |
| GAGTGGAATG GTCTTAGCAC GTGCACCTNT CATGAACACA TGGTTTTACA TTACCTATGA | 120 |
| AGAAAGMNCC TGTCTTGTGN CATGTGCCAA CTCTTAGATG ATTACAAAGA AGGCGACCTT | 180 |
| CGCATTATGC CTGATTCCAA TGGAGTCACC TCCAGCAGAA AGGGAACCAG GGAGAAGTTG | 240 |
| TGGACAGCCT GGTAGGCAAA CAAGTGGGAA TATGGCGAAA GAAAGATGGG NTCGNAAAAG | 300 |
| GGACTNGGCA TNGTTCATTT CATCCAAGGT AGGAAGGNCC AAG | 343 |

(2) INFORMATION FOR SEQ ID NO:1137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

| | |
|---|-----|
| GGCAGGAGCA ACAGCCTCGG NNNTACTCTG TCTGTGGCGT ANATNTCTTN ATTCCTTTAC | 60 |
| TCTCCTAATA AACTTNCTTT CCCTGTACTC CAAAGACTCG CCCTGAATTC TTTCTAGCAT | 120 |
| GAANTCCAAG AACCTCTTT TGGGGTCTGG ATTGGAAGTT NTTTCCTGTA GCATCTTTCT | 180 |
| GGTGNCCACT GAAGGGACTG NAGTGCAGAA AACCCCCACC CAAAGGCTTA NCTTTTGGTA | 240 |
| AGTGGTGGGG GCCAGTAACA TTTTCTAGT GNACCCTGAG GGGACGGTTA CTGAAGAAAC | 300 |
| CCCCCGGACC CAAAGGGAAA TAGGAGTTGC AGCACTGGTT AGGGCCAANT TTGGGTAAGT | 360 |
| GGTGGGGGTT ACCAGGTAA AGGATGGATT GGGTTTAGAG GCCCAANTAG GGGAGTCAGA | 420 |
| GTCTTTCCTA AGACAGATGG GTCAAGGCCG TTTGTGTTAA GGCAGGACAC TGACCTACTT | 480 |
| TGGTTAAAGN CCACTTAGGN GG | 502 |

(2) INFORMATION FOR SEQ ID NO:1138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

| | |
|--|-----|
| GATCAAGTAA TGAAACTACA GAATCTNTTT GTAGATGATT CAGGTCGATA TTTGGCTATT | 60 |
| CAATTCCATC TGGAAATNTGC ATATGTGTTT TNATATTATN ATGAGTACAG AAAAGCAAAA | 120 |
| NATCAGTTGG ATATTGCTAA GGACATCAGC CAATTACAAA TTGATTGAC AGGTGCTTTG | 180 |

| | |
|--|-----|
| GGAAAAAGAA CACGGTTCCA GGAAAAATTAT GTGGCACAAC TGATTCTAGA TGTAAGAAGG | 240 |
| GAAGGGGATG TCCTTTCAAA TTGTGAATTC ACTCCAGCAC CCACTCCTCA GGAACATTTA | 300 |
| ACCAAGAATC TTGAGCTTCA ATGATGACAC CATTCTGAAT GACATAAAGT TTAGCAGATT | 360 |
| GTGAACAGTT CCAGATGCCG GATNTGTGTG CTGAAGAGAT CGCTATTATT CTTGGATCTG | 420 |
| CACTAATTTT TCAAAGGATA ACCCAGTGCA CACATTA ACT GNAGTGGGGG TTTCTGGGCA | 480 |
| TTTACATCA | 489 |

(2) INFORMATION FOR SEQ ID NO:1139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

| | |
|--|-----|
| GGCAGGAGCT CGTNCGTATA ATAATTTAAT TTGGGTTTGT TGGTATAGAA ACTGTATNTN | 60 |
| CACAATAATG ATAAAGCCAC TCAGGCTCAT CTAGTCATTT CCTGGATTTA TGTGTGTAGG | 120 |
| AGTACATAAA AATANGGGCA CTGATTCGTT TTGTACTTGT CTAAAATTGT TATTNTTCAG | 180 |
| TTGTTCAAAG GTACACAAAA TGCTTTTTTNC TTTATAAGGT AANAAATACT TGGNGGTTAT | 240 |
| AAGANNTAAC TCTTAAGTAG CTTACTTTGA GTGGCTTTGA TATGTATTTN CTCATAATGG | 300 |
| AATTCATGAG CTTNCCTTCT TTCGCTTGGC CAAGATTTTT TTTTCCCTT GAATTCCTT | 360 |
| CTCCGGTGTT ATCTAGGATG TTTGCATTAC AAGCAGGCCG CTTTACCCCC TTTGTCCGTT | 420 |
| GTCACAGGTG AAAAGCCATA CAAGGGTACC CGGGGAGGCT GCGACTGGNG GTCCGGCGGT | 480 |
| CCGGATGAGC TGACCCGCCA TAC | 503 |

(2) INFORMATION FOR SEQ ID NO:1140:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

| | |
|--|----|
| AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAA AANNAAANNA GGGNGG | 86 |

(2) INFORMATION FOR SEQ ID NO:1141:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

| | |
|---|-----|
| GGCAGAGGCA CAAAAACACA CACCAGAATG TTCATAGCAG CCTTATTTAT AATAGCCAAA | 60 |
| ATCTGGAAAC AACACAAATA CCCATCAACT GGTGAGCAGA TAAACAAAAG AAACAACATA | 120 |
| AATACCCATC AGCTNNTGAG TAGATAAAGA AAACAGGGTG TTATCCATAC CATGGGAATA | 180 |
| TTGTTCAGCA ATAAAAGGGG AAGAAATACT GNTGNTTGCT ACATCACGGA ATGANCTTCG | 240 |
| GAAACATAT GGCTGGAAGC CAAAATGGAA AAACAACATA TTGTATGATT TTCCATTATA | 300 |
| TGGAATGGCC TTTATATGGA ANGGGAAGGG CAACTTTTG GAAACATAAG CCNTGGGTTG | 360 |
| NCCCAGGGTT NGGGGTTTGA ACNNGGTTTG ACTGCAAAT | 399 |

(2) INFORMATION FOR SEQ ID NO:1142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

| | |
|--|-----|
| GGCAGAGNCT CACTGGCCGA CAGTTGCCTG CTGGGGAATT TGCTGGCGGA CTTCGTTTCGC | 60 |
| GGNCAATCCT GNACGGACAA TATTCTGCTG AAATCGTTAG CGGGATCCGT NTGCTTCGCC | 120 |
| GCGTTGATAC CCTGACCGAC TCCCTGNCCC GAAGTGC GGA TCGCGCGCAN TAATTTCCGT | 180 |
| GGTGATTTCC GCCGCGTNTC GATGATCACG CTCGACGTGG TTGTGGGATC ACTTCCTGTC | 240 |
| GCGCCATTGG GGCANAATTC ATCCACAGCA ACCGCNGNAA GATTTTTTTTG CCGCCTGTTA | 300 |
| GCAGGTAATT AACGCCGTNT TTGCCCGATT TTGTCGGAGG CGTTTTCCAG AATCTGAAAT | 360 |
| GNCCTGGTTT NTGGNCNGAG CGTTGGATGG GAACGTTACT NCGGAATTCC TTTTATCGC | 420 |
| | 420 |

(2) INFORMATION FOR SEQ ID NO:1143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

| | |
|---|-----|
| AACNANTNAC GCAGGNACCA CNAAAATCAT GTTCCACGTG TCCAGAATGC TGCCTTACAC | 60 |
| CCCTAATAAC CAGCAGCAGC TCCTCCGGAA GCGCCACATT GGCAACGAAC ATTNTGAACC | 120 |
| ATCGTNTTNC AGGAAGCCTG GNCAGCAAGC CCTTNTGCCC CACCACCATC CGCTCGCACT | 180 |
| TCCAGCACGT NTTCTAGTG GTGCGGGCAC ACACACCCTG CACGCCACAN ACCACCTTAC | 240 |
| AGGGTGGCCG TGAAGCCGCA CCCAGGGACA CCCCTGNTTT CGGGGCCAGT TCTGCCTGCT | 300 |
| TGGGGANGGC CCCTTTCGNA GCCAACGGNG ATTTTCGGGN CTT | 343 |

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

| | |
|---|-----|
| AAGCCACANA ATTATCATTT TTTNTTTTTT TGTTAGGGTG GGTCTTCTTT TTTNNTTTC | 60 |
| CTCTCTCTTT TTTTAACAAA TGCCTTCTTA TAGAAAACT TTCTAAGAGG CAACAATTTA | 120 |
| GNAATGGGAT ATTTTGAACG AATCGGCATG AGTGTAACAG NTGNATAACC TGATCTGTTT | 180 |
| GTTTTNAAAG NATTATTAAC CAAGTGGAAG AATTCCAGNA ATGANTAGTA ATTTACACTA | 240 |
| AACATGCTAT ATAAAANGNT TNAAAGTCNT GATGCTGTGG AAGCAATCTN GTGCTATATT | 300 |
| TCTACCTCCT CATTGTCTTA ATTATTGGGT AGTGGGG | 337 |

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

| | |
|---|-----|
| GGCAGAGGGA AAATCATTTT CTTTATCTTC TCCACTAAAT CTAACAGCTT CATTAGTTCC | 60 |
| TTCTTTAAGA CAGAAGTAAC ACATTGTAAA GAAAATGTAC AATAGATTGC NCTCCAAAAT | 120 |
| AGCATCTATG TTGTAAAGTN TTGCAGATGG CCTTGGAAC ATCTGGTGNA ACAGGAATTT | 180 |
| GTGTAGCCTA TGTNCATTGT GCATGTGCAG TGAAGGTCAA CTGACAGAAG GAGAGCCAGA | 240 |

AAATAAAAAA TAANNAANCT GNGAGGAAAG ATTGAGTTAT TTGATGGACT GATTGNCTCG 300
ACACCTCTGC TTCAGAGAAA TGCCATTTTG CCAAACGGAT GGNTCCNCTG GTTATCANTG 360
NAAGGTTAGG GCATTTGTTC TGTGGGNCCN GNTACAGAGG TTGAATGTTC TTGGGTAGCC 420
CTGGTTTCAN NTGGGTTAGA ACCTCCGGTT TGCTTTTAAG CTGGGGTG 468

(2) INFORMATION FOR SEQ ID NO:1146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GGCANAGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAANN AAAAAAAAAA 60
AAAAAAAAA AAAAAAAAAA AAAAANN 87

(2) INFORMATION FOR SEQ ID NO:1147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TTTCCTGTTT CTGAAGCNCA TTTTTTGTTA TATTTTATAA TATATCAAAA TATAGATGGT 60
ATAAAATAAG TCCCTTCTCA TGTCTCTCCT TTAAATTCG ATTAGCTATT TATAGATCTT 120
TATTTTCCCA TATATATGTN ATAGTAAGTT TGAGAATTAT TCAAAAAGTC CTTCTAGGAA 180
TTTNGAATTT GAATTGATTG AATTTGTAGT TACATTTTGG AAGAATTAAC AGTTTCATAA 240
TGCTAAGTCA TCCCAGTCAT GGAAGAGGAA GATCTTTTAA ATNATTTAAT TGAGCTTTCC 300
CCCAACCTCA TGTTAATAGT TTTGGGGCAT NCTTTGTTAG ATAAATAGGC AAATACTTNG 360
TTTTTGTTGG GGGNGTTCNA C 381

(2) INFORMATION FOR SEQ ID NO:1148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

| | |
|---|-----|
| GGCAGNGTNA CGAAATACAG NTCCTCCCCA GATGACGCCA TTTTCCAAAG CTTNGCCCCG | 60 |
| GATATACTCT TCTTTCAACC CGGCCATGGT CTGACCCCAN TNGNCCACCA T | 111 |

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

| | |
|---|-----|
| GGCAGAGAAT GCCCTTCAAG ACATGGACAA ATTTAGCTTG AAAGACAGTG GCCGTGGTGA | 60 |
| CAGTAAGGCA GGAGACAGTG ATTATAATTT GGGGCGAGAT TCTCCAATAG ATAGGCTGCT | 120 |
| NNGTGAAGGA TTCAGCGACC TGTTTCTCAC AGATGGAAGA ATTCCAGCAG TGCAGCTATG | 180 |
| AGAACTCTGG CACGGAGGAG TGCANGGTCC TGGGACACTC TGACCAGTGC TGGATGCCAC | 240 |
| CACTGCCCTC ACCGTCTTCT GATTATAGGA GTAACATGTT CATTCCAGGG GAAGAATTCC | 300 |
| CAACGNAACC CCAGCAGCAG CATCCACATN CAGAGTCTTG AGGATGACGN TCAGCTGCCA | 360 |
| GATTCCGGTG AAAAGAAGAA GAGTTTTTTC CACNTTGGN AAAGGATTCC CCAAAGNTT | 420 |
| GNGGACATTG GGGTTACCNG CACATCATTT T | 451 |

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

| | |
|---|-----|
| GGCANAGGNN AATGTGATAT TGGAAGAAAA ATAGTCACAT ATATCAATGG AATATACTAG | 60 |
| AGAATCCACA GATAAAACCA TAGAAATATG CTCAACTGAT TTTGACATAG ATGAAAAGTA | 120 |
| TTTGTTATTT TACATTTGAT TGATCTTGCC TCACAAGATG GATTTTAATT TNCTTGTGGG | 180 |
| CACATACNT TATCTTTAGT CTATCTTTCA CAATGCCTGT TAATGGGATC TTAGGCATAT | 240 |
| AANTATACAT TGAACCTAAA ATACTGTTGG NNTTGATTAT AAAAGTTTTT CAGGGGGGAT | 300 |
| AAGTTATNAT TATNGGTTGA GAAGGAGGAT G | 331 |

(2) INFORMATION FOR SEQ ID NO:1151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

| | |
|--|----|
| GGCANAGCCC CCCCTTTTTT TTTTTTTTTT TTTTTTTTTT NNGGGGGGT TTTTTTTTTT | 60 |
| N | 61 |

(2) INFORMATION FOR SEQ ID NO:1152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

| | |
|---|-----|
| GGCAGAGTTT NAGAACCACA ATGTTAACAA TATAGCCAAT ANGACAGTC TGCACAGCTG | 60 |
| GGTTGGACTG ATAGCTGTCA TATGCTATTT GTNACAGCTT CTTNAGGTT TTNNAGTCTT | 120 |
| TCTGCTTCCA TGGGCTCCGC TTTCTCTCCG AGCATTCTC ATGCCCATAC ATGTTTATNC | 180 |
| TGGGAATTGT CATCTTTGGG AACAGTGATT GCAAACAGCA CTTATGGGGT TGACAGAGAA | 240 |
| CTGATTTTTT TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCANAAG GTGTTTTTCG | 300 |
| TAAATAAGGT TTGGCCTTCT GATCNNGGTG TTCCGGGGGC CCTCATTTTT TGGGGTTAGT | 360 |
| NCACCNG | 367 |

(2) INFORMATION FOR SEQ ID NO:1153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

| | |
|---|-----|
| ATTCATACC TACTAGGCTG ACTCACAGAC ACAGTACAAG TGGTGAAGAT GTAANGAAAT | 60 |
| TGGAACCATC ACACATTGCT CCTAGGATTG TAAAATGGTG GAGTCACTTT GGAAGAAATC | 120 |
| TCCCAACGGC TTCCACAGN GTCTGANCTA AATTACNTT CCCACCAGCA GTGTATAAGT | 180 |
| NTCCCTTTC TNTGCAACCT CACCAGTATC TGTAATTTT GACTTTGCAG TNATAGCCNT | 240 |

TCTGACCATT GTGA

254

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

| | |
|--|-----|
| GGNAGAGGGG CAAAGACTTG GGAACCTTAA AAGCTGAAGA TTCTTAAGAA GCTACAATGT | 60 |
| ATATAATTTN TNGTTTTATT TNATTGACTG GTTCTCATAG CATACATATG TATGAAAAAC | 120 |
| TGAGTACTTA TCTCTTTNTA ATATTTCTAT ACCTCCATTA CCCGTGCCCCG ATTTGAAGAA | 180 |
| CTGAANTGCN GNCCTGTTCC GTGGNACCCT GG | 212 |

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

| | |
|---|-----|
| GGCANAGGNA GATTCCATGC ATTGGGTCCA ATTTACTACA GAGNTTCAAA TGGAGCGATT | 60 |
| TTAGTTTATG ACATAACAGA TGAAGATTCT TTTCAGAAGG TAAAAAACGG GTCAAAGAAT | 120 |
| TACGGAAAAT GTTGGGNAAA TGAAAATCTG TTTATGTATA GTTGGTAATA AAATAGACTT | 180 |
| GGNAAAAGGA GAGACATGTT TCCATTCAAG AAGCAGAGTC GTATGCAGAA TCTGTGGGGG | 240 |
| GCAAAACATT ATNCATACTT CATCCTGTGA ANGTNCAACA ATNAAAAACC AATTTATGGG | 300 |
| GCTGCTTTTN GTGCACACTA GCCTAG | 326 |

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

| | |
|--|----|
| GGCANAGNTG CANATACTAG TGGAACTGG GAAGAACTGG TGAGGGACTT GCANTTNGCC | 60 |
|--|----|

| | |
|---|-----|
| CGTAAGAAGG CTCGAGAGTC CTATGTGGAG ACAGAACTGA TATTCGCACT GGCTAAAACA | 120 |
| AACCGCCTTG CAGAGTTAGG AAGAATTATC AATGGACCAA ATAATGCTCA TATCCAACAA | 180 |
| GTTNGTGACC GTTGTATGA TGAAAAAATG TATGATGCTG CTNANTTGTT GTACAATAAT | 240 |
| GTTTCCAATT TTGGACGTTT GGCATCTACC CTGGTTACAC CTGGGTGNAA TATTCAGGTC | 300 |
| AGCTGTTGGA TGGNGGCTAG GGAAAGCTTA ACAGTNANTC GNACCTGGGA AAGAGGTCTG | 360 |
| | 360 |

(2) INFORMATION FOR SEQ ID NO:1157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

| | |
|--|-----|
| ATAAGAAGGG TGGCGAGANG AAAAAGGGCC GTNCTGCCAT CAACGAANGG TNAACCCGAG | 60 |
| AATACACCAT CAACATTCAC AAGCGCCATC CATGGAGTGG GCCTTCAAGA AGCGTGCACC | 120 |
| TCGGGNCACT NCAAGAGAT TCGGNAAATT TNCCCATGNA AGGAGATGGG GNACTCCAGA | 180 |
| TGTGCCGCAT TGACACCAGG NTTCAACAAA GCTGTCTGGG CCAAAGGAAT ANGGTATGTG | 240 |
| CCCATAACCGA ATCCGTGTGN GGCTGTNCCA GAAAACGTAA TGNAGGATGG AAGATTCACC | 300 |
| AATTAAGCTA TATACTTTGG GTTANCCATG TAACTNTTTA ACCATTTTNA AAATTTTACA | 360 |
| GGACANTCAA TGTTGGGTGA NGAATTAATT CGTTGATTGT CAGTT | 405 |

(2) INFORMATION FOR SEQ ID NO:1158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

| | |
|---|-----|
| TGNATAGCCA GAAAACTGNG ANAACAAGGG ANCAGTGTGT AAGGNACTTG TGCACATCAC | 60 |
| TGACTGGTAC CCCACTCTCA TTTCAGTGGC TGAAAGACAG ATTGGTGNGG ACATTCAACT | 120 |
| AGATGGCTAT GATATCTGGG AGACCATAAG TNAAGGGTNT TCGGTCACCC CGNGTAGATA | 180 |
| TTTTNCATAN CATTGACCCC GTATACACC | 209 |

(2) INFORMATION FOR SEQ ID NO:1159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

| | |
|---|-----|
| ACTGTNTTTA TGGACTAGGA ACTTANTAAA GATGAAAGAG TTTCTNCCCT TGAAGTCCTC | 60 |
| CCNGATAGAG TTGCGACATC TCNAATCAGC GATGCACACT TGGGCAGACA CANTNATTGG | 120 |
| GCAAAGCAGT GGAACAT | 137 |

(2) INFORMATION FOR SEQ ID NO:1160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

| | |
|---|-----|
| GGCAGAGTGG CTATAAACTT TGTNACTGAA GAAGACAAGA GGATTCTCCG TGAACATTAA | 60 |
| GACTTTCTAC AATACTACAG TGGAGGAGAT GCCCATGAAA TGTGGCTGAA CCTTATTTGA | 120 |
| ATTCCTGGGA ATGAGAAGTT TTGGATGCAG TGCTCGCTGT TGCTGGAATA GGCGGATCAC | 180 |
| AACGTGCATT GTGCCTTCTT TGTTTGGGGA ATATTTGAAT CTTGTCTCAA TGCTCATGAA | 240 |
| CGGATCAGAA ATACAGNTTT TGANTAGCAA AGNANCCTTA GCCGNAGNCT CCTTGTGAAG | 300 |
| GGAAAGTCCA TTGGGCTTTA TNCCTCTTTA AGAGTTTAGA CTGTTTGGGG TGGGTTTTAA | 360 |
| AAGATGGGGG TCTGTGAAAA TCCTTTCNTT NNTNAGGAAA TTT | 403 |

(2) INFORMATION FOR SEQ ID NO:1161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

| | |
|---|-----|
| GGCANAGTGA TCACTCATCT AGATATCTCA NACTCTGAAA TAATATAATT NACTAATTG | 60 |
| GGAATTTATA AGTTAAATTT ATAAGGTTTT TAACAAATAT ATTTGTAATG GAATTATTG | 120 |
| AACTTTNCCA AATGAAATTG CATAAAGNAT GTGAAGGNTT GCAACAGTTT ATATTAAAAT | 180 |

| | |
|---|-----|
| TTTTNCTGG TTTGCAATAC TTGGGTGGCC TGATGAAAAG AAATTCTTCA ACTTTAGTCT | 240 |
| CTTTCCTGGC ATTGTGTTCA TACCACTCCA TATTTTAAAA GTTGGACCNG TACTTTTGGG | 300 |
| TTTCACTTCT TTAAATGGNT GNAAAAGGAN GCCCNCCAGG TAATTTTT | 348 |

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

| | |
|---|-----|
| TGTTAGTGGT GGGNAGGTGT CCTGTNAGCC CCCTCCAAGG AATTCACCAC CCAGCGAGGC | 60 |
| CACTAAAACC TCCAGAGTAA GTCAATCAGC CATACTAAGG NAAAGTCCTA AGGGGGACAG | 120 |
| ACAAGGTGAG NAAGAGGAAT CCTGTGGGCT GGAGGCTGCA GGNAATTAAG CCAAGTAGGA | 180 |
| AGGAGAGGAA TCCCAGCGGG AGGNAATGGG GGGAGCAGGG GCTTGGAAG ATGAGGACAG | 240 |
| GCTTTAGTGN ATGGTTTTTG NGGGAGACAG CTCTTNAGGT GGGAGAGCCA GGAGGTTAGG | 300 |
| GGGTTNAGAC AAAAGTTAGG AAGAGGGTTT TCAAACCNC AGGGCCCCCA CAAGGGGGGA | 360 |
| GGTTCCATGA GCCCCNTGAA GTTGTNTTTN CACATTNTTT CCCGTTACAG TTTTTTTTTT | 420 |
| GCGCAANACT TTTTGGTTTT CNTCAATTTT TTCAA | 455 |

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

| | |
|---|-----|
| GGCAGAGGNA TGAACAGTAC CAAACAGCAG TTTTCTCTC ATGGTCTGG AGCCTGGAAG | 60 |
| TCTGAAATCA GGGTGTCAAG AGGGCCATGC TCCTCTGAA GGCTGTAGAA CATTCTCTCT | 120 |
| TGCTTTTNCC TAGCTTCTGG TGGTTGCTAG CAATCCTTGG GCATTCCGTG GCTTGTGAAA | 180 |
| TGTNTCTCTC CAGTTCTTGC CTGTATCTTC ACATTGCCTT CTTACTATG TTTACAACAT | 240 |
| CATCGGTGGG ACTTGATGGA AGAAGGAAAG GGGGCTGTAT ACAGCTTTTG AATCCAGTAG | 300 |
| GGTCTTACCA GAGAGACTCC TTCAAGGCTG GGAGGCTCAG CAAGTGCCCA TGGTTACAGC | 360 |
| CCTGGTTTGA CAACCAGGTT GGTTTTAAAG GACCATGCAG NATTTNGGNG CAATTTCCNC | 420 |

TGTCCCTTGG CNAAGGCCAG GGGTTGGTGA AAAAAGTCTT CATTTTCGGG TTA

473

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

| | |
|---|-----|
| TCGAAATCTA ATTGGGGGCG CTGACATCAT TGTGATCAAA TACAACGTTA ATGACAAGTT | 60 |
| TTCATTCCAT GAAGTAAAGG ATAATTATAT TCCAGTGATA AAAAGAGCAT TAAATTCAGT | 120 |
| TCCAGTAAAT TATTGCTGCT GTTGGTACCA GACAAAATGA AGAGTTACCT TGTACATGCC | 180 |
| CACTAATGTA CCTCAGAACA GAGGGAGCTG TGTTTAGTTA CAACTGTAAG GGGNTCCAAC | 240 |
| TTNCAAANNA ACTAGGNGGC AACCTATCTT NGGAACCTCC ACAGGCCTTG GATGGACTTG | 300 |
| TTACATAGGN AAAGTTTTTT TGGGAGGGAG TGTTTGGGGT TTTTTTATGG ATTTCAAGNC | 360 |
| TTTAAANTCA GAAGGACAAG TGGAAAAAAA TGGAAN | 396 |

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

| | |
|---|-----|
| GGCAGGAGGG AAAAACAGAA ATCAGCGATA CATAGGATGT AAATATACAA CAGAGNAAAA | 60 |
| TCAACAAAGC TGAGATTTGG TTCTTAGAAA AGATAAATAA AATTAAGAAC CCTCTATGAA | 120 |
| ATGAGGACTG ATCAAGAGAA AGAAAGAAAA CACAAGTGAA CANTATCANG AATGAGGAAG | 180 |
| AGGNTATTAC ATTGTNTATC AAAAAGTTAC TGAGGNTTAT TCAAAGCAC AAAANCAAGA | 240 |
| CATTAGCATT TTGTNATGGT GAATTTGACA TAGTTTGGGT TAAAATGNGG ATGNTTGTTG | 300 |
| NGAGGCAAGC TTACCAAAC T G | 321 |

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

| | |
|---|-----|
| GGCANAGNCA GGATTTGATT CCACGCCATC TGGTGCTGGA GGCTATGCTC ATAACCACTG | 60 |
| CTGCATTCTG ACCTCTGTAA CATGCTCATG TCATTACCTT GCTCAAAAGC CACACGTGGG | 120 |
| TCCCCACTGC TGCAGGGACG GCATACTACT GTNTCTTATT CATCTTTGTA TCTTCAAGCC | 180 |
| TAATGCATCA CTGAACTGAA ATAGCAAATC GGCGGAACTG GAAATGAAAT TNCAATGTGC | 240 |
| AAGNAATGTN TCTGTGCAAG GGATGTTCCG TGCCTGGCCA ACGTTTGCTG GGTGGACANA | 300 |
| AAAGATTGAA CCCACCANTG GGAAGCCAGC TGGGCTTTCA CTGGTTCAGG TGNTTGATNC | 360 |
| CGGAAAGCAT CCAGGCCAAT TAAGCGNCCG GTTATGGCCC TGTATTGGG TTGNCACAGG | 420 |
| GTTACATTG CTGGAAGTTT GCTGAGCTGA AGGGAAAGGT TGATCGNCGT TTTGGTAAAA | 480 |
| GGTGGN | 486 |

(2) INFORMATION FOR SEQ ID NO:1167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

| | |
|---|-----|
| GGCAGAAAGG NGAATGGCTT AAGGCCGNA GTTTNAAACC AGCCTGGGNA ACATGGTGAG | 60 |
| ACCCTGTCTC TACAGAAAGA CGGAAGAATT GGCTGAAAGT GGTGGCACAT GTCTGTGGTT | 120 |
| CCAGCTACTG GGGAGGCTGA GAACCGGAGG ATACACTTGG GACCTAGNAA GTTCAAGGCT | 180 |
| GACAGTGAAG CTAATGAATA CCTTACCACT GGCCTNCCA GCCTGGGAAG ACAGAAGNCA | 240 |
| AGCCCCTTTT TNCTCTTACA AAATTAAAT TAAAAATCCC CCACAGTNCT TTGANGGAC | 300 |
| TAATGACTNA TGCTTTAATT AAATTAGGGT GGTTTTAGG TNAAATTTTT AATTTTNGGT | 360 |
| TTGGGA | 366 |

(2) INFORMATION FOR SEQ ID NO:1168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

| | |
|--|-----|
| TTCANAGTCA AGNAATGTGT CTGTTNAAGG AATGTTTCGTC GTGGCAACGT TNGCTGGTGA | 60 |
| CAGAAANAAT GAACCCACCA ATGGAAAGCA GCTGGCTTCA CTGCTCAGGT GNATTATCCT | 120 |
| GAACCATCCA GGCCAAANAA GCGCCGGNTA ATGNCCCTGT ATTGGATTGC CACACGGCTT | 180 |
| CACATTGCAT GCAAGTTTGC TGAGCTGAAG GAAAAGNTNG ATCG | 224 |

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

| | |
|--|-----|
| GGCAGAGGNC ACATNATGAT TNATTCTTCC TTTTTTTAAG ACAAAGTTTT CCCCTTTTAA | 60 |
| CCCAGGAGGC AGAGGTTNCA GTGAAGTCGA GATTGCCCCA CTGNCACTCC AGCCTGGGTG | 120 |
| ACAGGGCGAG TCCCACGTTT NAAAAAGAAA AAAAAATAAA CAGCAGAAAC AACAGCCAAC | 180 |
| ACCGACATCT CTATTGGTTC AGCTTACACA ATTTTGA ACT GAAAATTTAA AAGTTGNGCA | 240 |
| AACTTTCCAC TTGATGGCTG CCAAACCAG TTCAGCTGCA GNCAAGACCN GGGTTTCAAT | 300 |
| GGGAATTTGT TAAACAAGTG GGGTTCCTTT AGGGTTGCTT GCAAATTTAA TTTNTTGGTT | 360 |
| TTTGCCCCTT GAAAGGGATT NNCCAAAAAC CGGCAATGGG CTTTTGGNTC CCAACCCNTT | 420 |
| GGGT | 424 |

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

| | |
|--|-----|
| GGCAGAGCTT GACTTTAGAT AACCGGTTGA CTATGTCCTT AGGTNATGAT CTTTTTNCAA | 60 |
| TGAAATTTNT CAGGTGTCCT TTNAGCTTCT NGTATTTGGA TGCCTAGGTC TCTAGCAAGG | 120 |
| CTGGGGAAGT TTTCTCAAT TATTCCCTCG AAGATGTTTT CAAGCATTTN TCCTGCCTCA | 180 |
| NCCTCCTGAG TAGCTGGGAA TTACAGGCAC ACGCCACAAT GNCCCGGCTN AATTTTNNGT | 240 |
| ATTTTTAAGT AGGAGACGGG GTTTCGCCAT GCNAGGCTGG TCTCGGA ACT TCCTGGACCT | 300 |
| CCATGATCCT GCCTGNNNTT NAGGCCTNCC CAAANGGNTT GGGATTTACA GGGNTTNAGG | 360 |

| | |
|---|-----|
| CCACCAAGGN CCGGGCCAAN TGTGGTCCCN TTTNAAGGGG GAAGGTTACC CTATGTGGAA | 420 |
| CTGTTGNTNG GGTAACAATT TCTTGGTTAT GGCAGGCGGG GGAAAACCTG CAGGGTTNTA | 480 |
| GGGGAAAGTT NTNGGGAT | 498 |

(2) INFORMATION FOR SEQ ID NO:1171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

| | |
|--|-----|
| NTGTNCGCCT GNNGGTCATC TTCTTCTTTC ATGTGTCAAC TGCTCNTCTG AGCAAAAAGT | 60 |
| GCTTGGTGTA TCTTGGTCTG GGGANTTATT TGGAAGACAT TATTTGTGGA ACATAATGGC | 120 |
| ATANCATTTA CATACGTTCA CCTACTGACT TTGAGTATGA ATGTGTAGGT TGTGTATATG | 180 |
| TGTGAATATA TATACACCAC GGTGTCATTC TANGTGTGTTG GAATAACTGT TCANACAGTA | 240 |
| GTTACCTNTT CCCTNGGAAT TACNATCTG | 269 |

(2) INFORMATION FOR SEQ ID NO:1172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

| | |
|---|-----|
| AATTCGGGCA NNANCNATTA CACTTTGATA TTGCACATGA NATGACACGG GGTCTTTTGT | 60 |
| GGACCCTAGC AATGACCAAG GGCCCTGCAC GCACCCAAGC ATGTNCCCTC CCGAGTAGCT | 120 |
| GGGATTACAG GCATGCGCCC ACGATGCCCA GCTAATTTNN TTTTGTTTTG TTTTTTGTG | 180 |
| GTTTTTGTTT GTTTGTNTGT CTCAAAAAA AGTTTTTGGA ATNACCTTTT TCACCCAAAA | 240 |
| TGGGACACAA GTNAAGGAGA ATGCATTCCT CTGTNGTTTT TGTTTGTTGG TTTTTTTTTT | 300 |
| TTTTTTGGGG NCCCAAGNTN CCC | 323 |

(2) INFORMATION FOR SEQ ID NO:1173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

| | |
|---|-----|
| GGCACGAGGT TGGAAGTCAG GTAACAGGTA AGCTTCTTTG ACTGAANTAA CAGAAAATCC | 60 |
| AACTCAAATT GGCATGAAAA CGATAACAAA AAGGCAGGGA GGGCTCTCAG GTTGATTAA | 120 |
| TGGTTCGAAG ATCAATGAAA GATCCAGGCT TTTACTGTCT CTCTGTCTG CCATCCTGGG | 180 |
| TATTTGGCTT CTCCAAAGGC TGGCTNTNTC CTCTTGGTCA AGATGNCTGC CCAGAGGAAA | 240 |
| CCTNAGCAAT GGTTTTGGT TTGTNACCTA GTGGGG | 276 |

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

| | |
|---|-----|
| GGCACAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA NAAAAAAAAA AAAAANAAAA AAAAAANNN AAAAAA | 106 |

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

| | |
|--|-----|
| CCTCTCTCC AGCNATGCCC TCCACACACA CAGGCACGTG GACAGACACC GAGTGCAGCC | 60 |
| CTCNTACCTG GGGCCTGCNT CTGCAAGCAC AGTCCCCTCC TGTATGGACC CTGGCCTACC | 120 |
| NACCAAACAC TACATGGNAG CCACTGTCCT TTTTCGAGCAC CCAAACGAGG ATCTGCCTGT | 180 |
| TCCCGAGCTT CCACGTGTTT CCCAGGNCCA TTNATGGGGG CCCCCGGGGC CGCTGGGGGT | 240 |
| TAGGGACCGA GGCAATGCAT ACCACAGAAG CCCGTGCCGG GGCTTTTCCN TGGGGCCACA | 300 |
| TCCGTGNTTN NAATNGCTTC CTGGTTAATT CACACAGNTT CAGGGATGCG GNCCNTGGGG | 360 |
| GGGAAGGNAA ACAGNCCAAC CTTNGCCATT GGGTTTTANT NCAAGACGGG GGTTAGCGCN | 420 |
| TAAAAGCCTT CCAGTGCCTT TGCTTNCCCC TTNCTTCNTA AGCTTAGGCA GGCTTTTTTTT | 480 |
| TCCGGTNAG | 489 |

(2) INFORMATION FOR SEQ ID NO:1176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

| | |
|---|-----|
| GGCACAGAAG AAGCCTCTGC NACCCTCCAG GACCTGGTCT TTAATGAGTG TGGGATCACG | 60 |
| GATGATCAGC TCCTTGCCCT CCTGCCTTCC CTGAAGCCAC TGCTCCCAGC TNAACAACCT | 120 |
| TAAGCTTCTA CGGGAAATTC CATCTCCATA TCTGCCTTGC NAAGATGCTC CTGCAGCACC | 180 |
| TCATCGGGTT GAGGCAATCT GAACCCACGT GCCTGTGATC CTGTCCCCCT GGNAGNGTTA | 240 |
| TGAGGGAANT CCATGGGTAC CCTCCANCTG GGAANGGGTT GCCTGATCTG CATG | 294 |

(2) INFORMATION FOR SEQ ID NO:1177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 409 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

| | |
|--|-----|
| GGCAGAGCTC AAGCNNTCCA CCCGTCTCAN CCTTTCAAAC TGCTGGGATT ATAGGTGTGA | 60 |
| GCCACTGCAC CCTCAACAAG TGTTTTTAAG GACTTCTTAT ATGCTTTTAA GGGAGAAATT | 120 |
| ATATTCAACC AAACAGACAT GGATGTNTGG CGCTTTCTGC AAAACAGGGA GGTAGGTGAT | 180 |
| GATTATGTAG TTGCAAATGA AATATAATTG GCAGCTGTGN ATTAACACTT TTGNAGGGAA | 240 |
| AGATTCTTGG TGCTCTAGTA GCTTCTAAAT AAGGAGATTT GATGTAATTT GGGGAAGTNCA | 300 |
| GAGGAAGCAA GACCTGAGAT CTGATGCGGA GAGGAAAGGA TGCTCTGCGC CAGAGGGAAT | 360 |
| TGCNTTATGC AAAGGGACCN NGGGTAAGAG GGAAGGNTGG NAAATTATG | 409 |

(2) INFORMATION FOR SEQ ID NO:1178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

| | |
|---|-----|
| GGCAGAGTNA ATTTAGCAGT AATTATCCAT GATGATATCA TATTTCANCA GAGCCCCATG | 60 |
| ANCATAAAAA AGGTTAGCAC TGTCTCAAAT TTTAGCTCGG CAGGGAAAGA TTAAAAGCCT | 120 |
| TTTAACAAGT AAAACAATNA ATTTGAAAGT CAGAGGTGAC TGANTAACAG AGCAAGCAAT | 180 |
| GGTAAACTGC AGGTTNAAAT TTGAGTAATG GAATAGGTCC TTCTTAAAGG GGGAAAAATC | 240 |
| CATCTTGGA TAGGATTACC TCTTAAAT ATNATTTNAT TTTTNTGGGG TTTATTAATN | 300 |
| TTTGCTGGG GATTTAAGTA TTATGGTTTT AAAAAACCGG GGCTTTTGGA ACCCCTTG TG | 360 |
| GTAAATTNGG GTCTTTTTNT TACCGGCCCT TGGNAAAACC CAAANCCAAA CCTGGGCAA | 420 |
| TTTTAAATTG GGGTTCCAN CCCTTCCGG GAAGGCTTTT TAAANTTTGG GAAATTTTNC | 480 |
| CCCTGGAC | 488 |

(2) INFORMATION FOR SEQ ID NO:1179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

| | |
|--|----|
| GGCACAGGTT TTTTTTTTTT TTTTTTAA AAAAAAACC CTTTTTCCC TTTTTTNAA | 60 |
| AAAAAANCGG GTAAAN | 76 |

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

| | |
|---|-----|
| GGCANAGAGA GGGTGCTGTA CATTGACATT NATATTCACC ATGGTGACGG CGTGGAAGAG | 60 |
| GCCTTCTACA CCACGGACCG GGTGATGACT GTTTCCTTAT CATAAGTATG GNGAGTACTT | 120 |
| CCCAGGGAAT GGGATCCTAC GGAATATCG GGGCTGGCAA AGGCAAGTTA TTATGCTGTT | 180 |
| AACTACCCGC TNCCGAGACG GGGATTAATG ACGAGTCCTA TGAAGGCCAT TTTCAAGCCG | 240 |
| GTCATGTCCA AAGTAAATGG GAGATGTTCC AGCCTAGTGC GGTGGTCTTT ACAGTGTGGC | 300 |
| TTCANACTTC CCTATTCTGG GGGATTCGGT TTAGGTTTGN TTTCAATCTN AACTATTCAA | 360 |
| AGGGACCACG GCCCAATTG GTGGGNAATT TNTTCAAGAG CNTTT | 405 |

(2) INFORMATION FOR SEQ ID NO:1181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

```
ATACCACTGC ACCCTCAGTG ACAGAGTGAG ACCCTGTCTC TGCAAATAAA AATAAAAAAC      60
TTGAAGTGGA TGAAAAGATC TAATATGAAA GGTGAAAATA TAAAGCTAAT GNATGTGTAA      120
GTATGAGCAA TAGATTGTTGGG GACTTTAAGC TGGGGAAGGA CTTCTTAAAT ATGATTCACA      180
AAGCACTTAA CCATAGGGGG AGAATGGATA GATTTGTCTA CATCAAAATN GAGGATTTCT      240
GTTNCNCGGA NGCTCCCCAC AGNTTAAGTT ACCAGAC                                277
```

(2) INFORMATION FOR SEQ ID NO:1182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

```
GGCACGAGGN AAGCACAGAC TTCGGATGTA CAAAACAAAG ACTTTTCATC AACTCTTTTA      60
GATATGCTAG AAGAGCTAAA GGAAACCATG GACAGAGAAC AAAAAAATTA GGAAAGCAAT      120
GTCTCATCCA ATACAGAATA TCAATAAAGA GGTGTGAAAT TTGTTGGAAA AGGAACCCAA      180
TTNGAAATTT TTGGAGGTG AAAAGNTTTT TTAACNNAAA ACNTGAAAAT TTCCCTTAGG      240
GGGGTTTTCC                                250
```

(2) INFORMATION FOR SEQ ID NO:1183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

```
GGCAGAGTCG AGTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT      60
TTTTTTTTTT TTTTTTTTNN CNNNAAAAAA                                90
```

(2) INFORMATION FOR SEQ ID NO:1184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

| | |
|---|-----|
| GGCANAGCCT CAGTGAAAAT ATTTCTGCAG CTATCCAAGC TAATGGTGAA ATGGTTACAA | 60 |
| AGCAACCATT GATTAGAAGT ATGCGAACTG TAAAAAGGGA AACTTTAAAG TTAATATCTG | 120 |
| GTTGGGTGAG CCGATCCAAT GATCCACAGA TGGTCGCTGA AAATTTTGTT CCCCCTCTGT | 180 |
| TGGATGCAGT TCTCATTGGT TTATCAGAGA AATGTNCCAG CTNGCTAGTG GAACCCAGAA | 240 |
| GTGCTTAGTA CTATGGCCCT AAATTNGTCA ACAAGTTTAG GGGGGGNCAT ATTTNCC | 297 |

(2) INFORMATION FOR SEQ ID NO:1185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

| | |
|---|-----|
| AACCCTACAA ATGTAAAGAA TGTGGAAAAG CTTTTCACCG ATACTCAATC CTTAGTACAC | 60 |
| ATAAGAAAAT TCATACTGGG GAGAAACCCC ACAAATGTGG AGGAATGCGG AAAAGCCTTT | 120 |
| AACTGGTCCT CAACTCTTAT TACACATAAG ATAATTCACA GTGGAGGAAA AACCCTACAA | 180 |
| ATATGAAGGA TGTGGCAAAG CTTTGAACC AGTCCTCACA CCTTATGNGN ACATANGAAA | 240 |
| ATTCATAGTA AGAGNAACCT TTACAAATGT GNAAC | 275 |

(2) INFORMATION FOR SEQ ID NO:1186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

| | |
|---|-----|
| GGCAGAGTCT CAATGTTGGA CCTAAGATAT TGAAGACAGG CTGGAGTCCA GAGCCTTCAT | 60 |
| TCAATCTCAG ATTTATGAAA ATAATTACTG GATTGGATTA TCATATGATG AAAGGGAAAG | 120 |

| | |
|---|-----|
| TAAGTGAAAA TGGGATTGAT AATGGCACAT CTCCTGGGAT TAATTCTACA ATAATGCGTT | 180 |
| TTTCTTCTGG GAGAGGAGAA TGTGCCATTT TTGACCTCAA CAAGAATGGC AACTATTGAT | 240 |
| TGCATTCAAA CGTACAATTG TATCTGTGGG GAAGAGGAAT AGGACTCTAT TTTCTCTGG | 300 |
| ATTNCGGTGT GCGCCCAAGA AGGAAAAGGG TGGAAAATGG GNATGTTTTT CCCTTTTTTT | 360 |
| TGTTTTCCCC CNTAATAAAT TTNCCGGATT TATTAAATC CATTTGGCTTT TTAAACCGTG | 420 |
| GGGGGCCTTA GGTNAATTC CTTTCCAAAA GGTTTAAAGG TTGGAACCCG GGGNAGGGNA | 480 |
| AAAAGGGAAA ATTTATTTTT TTGGG | 505 |

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

| | |
|---|-----|
| GGCAGAGGGA ACAATATCCT CCATGAAAA CTGCCGCACT GTGTGAAGAG GAATTTAATG | 60 |
| CATATTCATC TTCCTCCCTT TAATACGCNG CAAACCAACA TGTTTCTTTA CAGCTTCTCC | 120 |
| TGGGGAAAGA GAAGTAACCA CTGAGCTTCC AGGTTGTGAA GATATAAAAC AGCTGTTGTT | 180 |
| CATTTTGGT TGGAGCTATT TTACATCAT GTTCATGGCC CCAGATAACA AGATCAATGA | 240 |
| AGTCATCCAA AAATTGTTCT GGGAATGAAG TTAGTACTTC CATGTTTACT CCTGTTCTG | 300 |
| ATGGAATCAC AATTAAGTTA AACCANGAGT TCNTCATCTT CCNTTGGTCT TCAACATGTN | 360 |
| AACTTTTTTA TTGACAAACN TTCG | 384 |

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

| | |
|---|-----|
| GGCAGAGAAG GAGAAGTCTT TACCTGGGGT CATAATGCTT ATAGCCAGCT GGGCAATGGG | 60 |
| ACAACTNATC ATGGTTTAGT GCCCTGTCAT ATCTCTACTA ATCTGTCAAA CAAACAAGTC | 120 |
| ATTGAAGTTG CCTGTGGGTC TTACCATTCT TTGGTGCTAA CATCTGATGG AGAGGTATTT | 180 |
| GNNTGGGGTT ATAATAACTC TGGGCAGGTA GGATCTGGAT CAACAGTTAA ATCAGCCAAT | 240 |

| | |
|---|-----|
| CCCTTGGAAG GTCCACTGGC TGCCTACAAA ATAAAGTAAG TTGTGAACCA TTGGCATGTG | 300 |
| GGCAGATGTG CTGCATGGGC ATTAGTAGAC ACGGGGGGAG GTCTATGTTN TGGGGTTTAC | 360 |
| AACGGAAACG GGCAGCTTGG ACTCGGGCAA CATGGCAACC AGCCAACNCT TGCAGATTGG | 420 |
| CAGTTTGCAA GGGCTTCNTG TNCCANGGGT ACGTCCATTT CCAATTTTGT GCGTGTATTT | 480 |
| TTAAGCTTNG T | 491 |

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

| | |
|--|-----|
| GGCANAGGTT CCATATAGAT ATTGCAGATA GAAGTCAAGT TGAACCAGCA GACTACAAAG | 60 |
| CTGATGAAGA CCCAGCATT A TTCCAGTCAG TCAAGACCAA GAGAGGCCCT TTGGGAACCC | 120 |
| AACTNNNAAG GTACTGNATG CTGACCTTTC TGAACAGGCA GAGTCTTGGG CAACAGAACA | 180 |
| CTTGACAGGT CCTGAGTCTT GAAAGAGCTG GTGACGTTTA AAGTGNAAAA ATAGAAATGG | 240 |
| GCACAAAAAT AGTTTTATTT GCGATTAAGG ACTTACAGCC AGTTGCAGTT GGCCAGCAAN | 300 |
| TCTGTGCTGC ATTAACAAAC AGAACAGNGC CAGACTGTTC ATTTTCAGNA TAATGCAGTT | 360 |
| CCATTAANCT TTAAAGGGAC AAGTGTTTGA GTCNTTGGGG TTNNNATGTT CTCTTTTGAG | 420 |
| ACCTGAAGCG TATAAAATNC CTTTAAATGA GGTTTTAGTT TAAATTNGTC TTATTAAAC | 480 |
| TGANCAGTTC | 490 |

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

| | |
|---|-----|
| TGGATAACAA ATCCCTACCT ATAGCCATGT GGAAGCAGCT TGTCACGTGA TTTTAACTGT | 60 |
| GTAACAATTA TTGAAGGCGA AAATAGNAGT TGGGTCATCT TTGAACACCT ACCTTTTATC | 120 |
| AATGAATATT TTTAGACTGT NCTTCAGTAT CTGAGTCAGA GTTTATTGTA ATTTGTTATT | 180 |
| TACACCAAGG TGGCATCTTA GTCTACCTTC AGTGAGACTT GCGTTTCAGG GGAGGGGCGT | 240 |

| | |
|---|-----|
| ATGTNCATCC TCGGTCTCCG TTATGTAAAC GGTCTGATCT GTNAAAATAG TGGTAGCACA | 300 |
| TGCCACGTGG GATAGTTGGT GGAGATGATA GATGGAGTTT AAGCACAGGG CCCAGCCTGT | 360 |
| TCAGCAGTAG CTACTATTAN TGTTGCCCAT TTCCCCTGCA ACTGAGGTGA GAGGTTTNC | 420 |
| NCGAGTTTTA AAGCTGACTG GGCCCACAGT TAAACGGTAA CAGACCAGTT TTTTCAGGGT | 480 |
| GTCAGCCC | 488 |

(2) INFORMATION FOR SEQ ID NO:1191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

| | |
|---|-----|
| GGCACGAGGA ACTGCTTGAG AGCTTTTCTT AATTGGGAAA AGAATGCCCC GGTAGATGTT | 60 |
| GGCTTCATGG TTTCTAAGCT GCTTTTGACC ATACAGTTAT GTCCAAAAAC AGAATTTCAA | 120 |
| CCTAGTGAAA AATTTGGTGA AGACCTAAGT GATAACACTT GGAATACAT ATTTNCCATT | 180 |
| GATCTGCTCT GCTGCCATCA GAAATGGATC TGGACGCATG ATAACATCAT AAGTAAGGAG | 240 |
| CTGTGGCCTG TGATGGATAA ATGGATAAAA TACAGAAAAG GACATGCAAA CATTGCGTAT | 300 |
| ACTCCTGATA TTATTATAGC CTCCAATTAC TGAGGCTGAT TGGTCGTTTA GGCCAATTGG | 360 |
| GTTTGAAAGA AGGGTTTTCC ATCTGCTGTG AAAAAATATT AAGTTCGGTT ATTGGTATGT | 420 |
| TTATTACAGC ATGCTCACGG TGAAGGTTAT TACCCNTGGG GGTATACCAG TTTAGCAGCC | 480 |
| CGTGTATGCT CCTTTGTGAC | 500 |

(2) INFORMATION FOR SEQ ID NO:1192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

| | |
|---|-----|
| GGCACGAGGT TTTTCAGAGAC ATAGAGGATA GCAAACAAGC TCAATTTTTTA GCCTTGGCAG | 60 |
| TAGTATACTT TATCTCTGTT CTTATGGTCT GCAAGTACAG AGACATTTTG GTAACCCCAA | 120 |
| AATGAAAGGC ATAGCCAGTC ATGTACAGAA ACTGGCAGTG GAAAATGAAG AATGTATCAC | 180 |
| TCTCTGAAAT CACACCAGCA GCATTCAGCA CTTTGAAC TA CGGCATCAGT GGGAAGGAAT | 240 |

| | |
|--|-----|
| CTGNAAGGCA CATCATCTGC TTCGAAGGAG GGAAGTCAAGC ATTGGGGGAA GAAACAGCCA | 300 |
| CTGGTTTAGG AAGCCATGTG GGAAGTAACT CNTCACACAG NACCTTCCTG GTGTTTCACTN | 360 |
| GCAGGNCCCA GTTGCAATCA GCGAGGTGCT ATTTTANTCT TTC | 403 |

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

| | |
|---|-----|
| GGCAGGAGNA AGAAGCTTGC CTTATGCATG CTAATGTTAC ACTGCCAAAG CCATCACATG | 60 |
| ACCCAGCTGG GTGCTAGAGG TACAAGCACT TGGNTATTAG GGGTGGCATT TGGGTACCAT | 120 |
| CCAGTATAAC AGAGTGGTTT ACCACCTTAT ACACATTGTA TATGATTTCT TGCAGTCAGT | 180 |
| TTTGTGGAAG GGAGTGCATT TTATTCCATT TTGTTTTGTC TACAGTGGAA TTTTGTGTT | 240 |
| ATAACTATCT TCCTCCTTTT AAAAGTTGGC AACCATAATA TTATACTTCA TATTTTGAGA | 300 |
| TAATGTTTAG ATTTTACCCA AAAAGTTGGC AAAAATAGTN NGGANTTNCC CTTATGGCCT | 360 |
| TNCACCCGGG TTTCTACTAA TGGTTAAAC | 389 |

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

| | |
|--|-----|
| GGCAGAGGNA ATTTCAATTGG GNACAGCAAC CATGGCAGCC AATCTCCCAG GAATGTGGAG | 60 |
| GAGAGGATGN TTGCAGTCAT TTAAAGGTGG AAAGGCTTTT GTGNCN | 106 |

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

| | |
|---|-----|
| GGCAGAGCCC AAGCACAGTG ACTCACGCCT GTNAATGCCA AACTTTGGG AAGGCTGAGG | 60 |
| TGGGAAGATT GCTTGANTCC AGGATTTTAA GGCCACCCGT GGCAACATTA AGACCCCATC | 120 |
| TCTACCAAAA AAAAAAAAAA AAAAAAANG GNNCCCCN | 158 |

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

| | |
|---|-----|
| GGCACGAGCG TTANCGNCGC NTNCGGTGAG TCAGTCCGCC CAGTGCACCA ACTGCGTGCA | 60 |
| GGACGACACG GCCAAGGCCA AGATCACCAT CGTGGCAGGC GTGCTGTTCC TTCTCGCCGC | 120 |
| CCTGCAGCCT TGCNTCGGAG GCCAGCCCAC CCCCAGAAGC CAGGTAAGCC CCCGCGCTGG | 180 |
| NACTGGGGCA GCTTCCCCAG CAGCCACGGC TTTGCGGGCC GGGCANTCGA CTTTGGGGCC | 240 |
| CANGGGCCAA ACTGCATGGA CTGTGAAACT TAACCTTTTT GGAGCAAGGG GGCTTGGGTT | 300 |
| ACCGNCNATA ATTTNACCAA CCCGTTGGAG NCCCATTTGG GCCGTTGNCC CCAATGTTTG | 360 |
| GGTTTGGGNA AGGGACCGGN AATCCTTGA AGGGGCATTT GATATTTTTT CAATTAAAAG | 420 |
| CTTTTGGTTT TTGNATTGGN AAAAAAAAAA AAAN | 454 |

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

| | |
|---|-----|
| ATGAGCCCC NCGCCCGGCT ACCTGAACCT CTTTGTGACAA GTNCTGATAT GAAGGCCCCA | 60 |
| TATCAGCTGG GGCCACGGCA GCAGCCCATG CAGGNGGGGC AGNCTGGGNG TGGCTGGCCA | 120 |
| GGGNAGGGCC TGGGTGGGNG CTTCAAAGCT GGTGGGNATG CGGGTGGGTG TGGGGCCACA | 180 |
| AGAAGGAAGA GGGGTATCCA GGGTGCCCC AGTTCCTACG TGNAGGAATG GTGTCTCCCA | 240 |
| AGAGCCATGG TGGCCTCCGT GGGGACAGTG AGANTAGAGG CTTGTNAGGN GGCCCTTTCA | 300 |
| CTTGGCNTNG AACTCACTG GGT | 323 |

(2) INFORMATION FOR SEQ ID NO:1198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

| | |
|---|-----|
| GGCACGAGGT TTTCTCATAT ACATGATGGT GTATGTAATG GTTAAGGTAT ACAAGGTGGT | 60 |
| TTGCCCATGA AAGTCTATTT AATCTCTAAC AGACATGAAG AGTGTTATTA ATAGAACCTT | 120 |
| TCCCCAAAAT GTTGTAGGGG AAAATGTCCC AGTTCCATGT GGAATTGTCA GAACAAGCCT | 180 |
| CAGCCTCTTC GAGGATTTCA AAGTGGCTTT CGTCTTTTAA GTTGATGTCC TATCTCTCTC | 240 |
| TCTGTGCTCC TTTTTTTTN AACTTTGTGT GCTTGAACA NGGACCCCTT GCCACTTTNA | 300 |
| AAGCTGAGTN ATTNAT | 316 |

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

| | |
|--|-----|
| GGCACGAGCT CGGCCTNTNT TNCAAGTTTC TCCAAGGGGC TGGCGGCGGC CAAGACTTGC | 60 |
| GGGGTNTAGG GGTGCTGCGG GCGGTGGAAG ATCTCGTCGN GGGCACCCAT TTCCACCACC | 120 |
| CTGCCCTCGC TCATCACCGC CACCCGGTGG GCGGATGCGT TCCACCGCCG CCAGTCGTGG | 180 |
| GGAGATGAAC AGGCAGGCAA AGCCTNACTG CGCCTGCAGN TTCGGATACA GCTTCAAGAA | 240 |
| ATCTGGCTTC TGGGATGGTC ATGTCCAACG CCGAGATCGG CTTTCATCGGC AATCACCAGT | 300 |
| TCGCGGGTGT CCGCACCAGN GCCCGGCCAA TGGNCACGN TTNGACGCTG GTCACCGGAC | 360 |
| AANTGGTGCG GGGAAGGGGT TCGACAAATT TTTCCGCCAG CCGATTGTTC CANCAGGGTT | 420 |
| TTTGGCCAAC CGTTCAAGAC GTTTNGGGGN TTTCATGCCC GGGGAAATTG GCGNAGGNTT | 480 |
| TTCGGGGAGA TT | 492 |

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

| | |
|---|-----|
| GGCACGAGCT TGTATTTGTC TACTGACAGC CCCTTGGTAC TATTTAGGTT GGGGGAGGGG | 60 |
| ACCTAAAATA AATAGACTTT AACATTTCCC TTGGGTGCTA ATCATAGTTG GAAGTTGAAT | 120 |
| TTAAGGTGAT TATTTGGGTG ACAATTAAAA ACCTAAGGAA AACCAGAAAT CTTGGTAGTG | 180 |
| GAAGAAATGT GTAAGGTCAC CCCAATCGGT AGATTTTAAT GAACGTTGTG GAATGTTGGG | 240 |
| AGAGGGGATG TTAAGTTGAA TGCAGAATTT CACTAAGTAC TTAGTGTAAG TTTTAAGGAT | 300 |
| GTTNGCTNNT TTTNATCNAA GGAATTCCAT GTAATGGCCC CAAAGGGCAG TTTTACNGG | 360 |
| TTTTAAAAAA TTNGGAATTA ATTTTACCA TGACCATTCT TGGAAATTCC CAGGNAGTTT | 420 |
| TTNTGTGTAG GGACCCTTTT TNAAAAATTN CCTCCCGNTT TTTTAAGGGG GAAATTAA | 478 |

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

| | |
|---|-----|
| CCAAGACAGA CTGCAGGTTA CGGCCTGACA TCAGAGCCAT GGAAAATGGA GAGATAGATC | 60 |
| AAGCTAGTGA AAGAAAAAAA ACGACTTGAG GAAAAACAAA GAGCAGCCCG CAAAAACAGG | 120 |
| TCCAAGTCAG AAGAGGACTG GNAGGACGAG GTGGTTCCAT CAAGGTCCTA ATCCCTACAA | 180 |
| TGGAGCACAG GACTGGATTT ACTCTGGGCA GCTACTGGGA CAGAAATTAC TTCCAATTTG | 240 |
| CCTGACATTT ATTTAAATG CATAAAGTC AGGGTGTTTG GCTAATCTAC AATAAGTCTT | 300 |
| TAAANCCCAT GTTTTTAAAA TTTTTTTTCC CCTGGGTTTC TNACTTANCT TTTTAAAAAA | 360 |
| AAATGGGNAA AACCTCCTG GGGTTAACNG G | 391 |

(2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

| | |
|--|----|
| GGCACGAGGA AATTCATTG GGAACAGCAA CCATGGCAGC CAATCTCCCA GGAATGTGGA | 60 |
|--|----|

| | |
|---|-----|
| GGAGAGAATG AATGGCAGTC ATTTTAAAGA TGAAAAGGCT TTGGTGACCA GTCAAAATTC | 120 |
| AGACTTACTG GATGATGAAG AAGTTGAAGA TGAGGTGTTG TTAGATGAGG AGGATGAAGA | 180 |
| CAATGATATT ACTGGAAAAA CAGGAAAGGA ACCAGTGACA AGTAATTTAC ATGAAGGAAA | 240 |
| CCCTGAGGGA TGACTIONATGA AGGAAACCAG TGCCCTGGAG ATGAGTTTGC AAGACATTCC | 300 |
| CCAGTTGAGG TTTTAAAGGA GGGNAGGATT TTTAAAGTNG GACTTTTCTT GCTCTTAGGT | 360 |
| TCCATNTTAA GGGCANTTTC ACCAGTTTGG CCNTCCAAAT TGAGGGGAAT TTGGGAGGTT | 420 |
| TATTCCATTN TTCTTNAAAG G | 441 |

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

| | |
|--|-----|
| GGCACGAGGT GGAATAGAGA AACTTAATGA GTGTTTAAAC CAAGCTTTTC AAGAGACCGT | 60 |
| TTCCCAGGCA CATACTGCG GGGCGTCTCA ACATCCTGTC ACCATTGTNC TTGAACTCAC | 120 |
| TTCTTCAACA CCACTCATGT GGACTIONATG GAAATAGGTG ACATAAGCCA GACTCTTCCT | 180 |
| CATAATGCCT GTCCACAGTT TTTTGCTAAT ACATAATAAC TGATTAAGAA AGACAATGTT | 240 |
| TCCAGTAAGG ACAGTGGTGA CATATTTAAG TAGATGAGTA ATGAACCTTG GCTTGTAAGT | 300 |
| GTCCTTTCTG CAGAATAGGG AGGGAAGAGT TAAAGCTGGT ATCCCCTCGG GCTCTTAGGC | 360 |
| ACCTGTTAAA CCCAGGCC AGGGGATCCT TCCGTCCTGT CCCTGTGAGT GCTTCAGCCC | 420 |
| AGGGACACAC AGAAGGGGCA TGTTTCATGG GTCCGAAGGA CCCGTTTAGT TTCATGTGGA | 480 |
| TTTCCAGACC TGATTCGA | 498 |

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

| | |
|---|-----|
| AGAATATTGG TAATATATTG CAGAAAGTTG TGTGCAGAAA ATTGACAATN ATTTGGCCTT | 60 |
| TAGTAAAAAC TTTTACTCTT TCAAAAGTTA CTATTTTAAA GCATGGTATT ATTTTGCATT | 120 |

| | |
|---|-----|
| ACAAAATGGT TTTATTTTCT TAGTGGTGAG ATAGAGGAGA AATTTGTACC TGCTCTTCTG | 180 |
| AATCTGAAAA GTTGTTTTCA ACTTTTACAT TACTTCCTTG TTTCTTTCTA TTGGTTGAGT | 240 |
| GTAANTGAAA AGTTTCCCAT TNACCATGCT GGCTTTGNAA ATTGAGACCN NATGTTGAAA | 300 |
| ATTT | 304 |

(2) INFORMATION FOR SEQ ID NO:1205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

| | |
|--|-----|
| GGNANAGGCG CGGCAAAGGG CCTCGTNAGT NGTGTTCAAG TTGCCCCCTGG GGATCTNCTG | 60 |
| TGTCTTCAGC GCCCAGCCCT GCGTGTTCTT GGTGAAGCAG TTTACATCA GTCTCTCCAG | 120 |
| ATAGCACTAC GAATGTATTC CGCTTCTGAA ACAGGATCCC ATGCCAGTTT GGAACACTTT | 180 |
| CCCAATCTTA GTTCAGAAGT GGCTTGATG ACCTGTTTCAG GGGTCACATG AAGGTCTCGC | 240 |
| CATTTCTTGG GTCCTCTTCA GAGGCCNGAA AGTTCTAAAG TTCTGAGTCC CCGGCCAGGG | 300 |
| TCCTTTAANA CCTTGGNCAC AGAGGCTGTT TGGGCAATGT AGAGGCTGNC TCTGTGTGTG | 360 |
| GTTTAAGTAA ACTGGAATGN GGACATGACG NGTTG | 395 |

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

| | |
|---|-----|
| GGCAGGAGNG AAAAGTCGGT GCGCTGGTCC TGCCTCATTA ATCCAGGGGT TGCAGTGCTT | 60 |
| TGAAGCCCAG TCGTTGTTGG TTTTNTGAT GNAAATACCT GTNAAGATGA GTGGNCGGGG | 120 |
| N | 121 |

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

| | |
|--|-----|
| GGCACGAGGT TGTGTGGTGT TTTTGGACAG ACGTTATTTT CTTTTTTGTA GAGTAGCCTG | 60 |
| TTTGTAAGTT TAAAGTGTTC ATTTTCTCTCC TTTGCAGCAT CATGGCCAGC CCAAGAACCA | 120 |
| GGAAGGTTCT TAAAGAAGTC AGGGTGCAGG ATGAGAACAA CGTTTGTTTT GAGTGTGGCG | 180 |
| CGTTCAATCC TCAGTGGGTC AGTGTGACCT ACGGCATCTG GNATCTGCCT GGAGTGCTCG | 240 |
| GGGNGNACAC CGCGGGTTTG GGGTTCACCT NCAGGTNCAG TGTCTGCCG CTCTGGGTTC | 300 |
| T | 301 |

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

| | |
|---|-----|
| TGGCAAGCTG GGGCCCGGCC TGCGGGTGCT GGACGCGTCC TGGTACTCAC CAGGCACCCA | 60 |
| AAAGGCTCGN AAGAGTACCT CGAGCGCNAC GTACCCGGCG CCTCTTTCTT TAANATAGAA | 120 |
| GAGTGCCGGG ACACGGCGTC GCCCTACGAG AATGATGCTG CCCAGCAAGG CTGGNCTTCG | 180 |
| CCGAGTATGT GGGCCGCTG GGNATNCAGC AACCACACGC ACGNGTGGTG TATGAATGGT | 240 |
| GAAACACCTG GGNCAGCTTC TATGCTCCCC GGGTTTGGTG GATGTTNCCG TGTGTTTNGC | 300 |
| CACCGCACCG TTTTCAGTGC TTCAATGGTG GNTTCCGGA ACTGGTTGAA GGAGGGCCAC | 360 |
| CCGTGAACNT CCNAGCCTTC AGNCCAGAA CCGGCCTTTT TCAAAGCCAC ATGGGACCGT | 420 |
| NNCTGNTTCA AACNTAGAG TCAGTGTTGG AGNAACTTGA ATTTAAGAGG TTTCCACTGG | 480 |
| TG | 482 |

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

| | |
|--|----|
| GGCAGAGCGG GGGTCTNGGG AGGCAAGTC CNTGGCAAGC CGTCTTCTGC TCAACAACGG | 60 |
|--|----|

| | |
|---|-----|
| AGNCAAGTTG CCCATCCTNG GGTGGGAGC TGGTNGTCCC CTCCAGGNCA GGTGNNCTGA | 120 |
| GGACGTGAAA GATGGCCATT GNACGTCGGG TACCCCCACA TCGACTGTGC CCCATGTNTA | 180 |
| CCAGNTTGAG CNTGAGGTGG GGGTGGCCAT TTCAGGTGCA GCTCAGGGNG NAGGTGGTTG | 240 |
| AAGNGTGAGG TNGCTTCTTC ATCGTCCAGC AAGNTGTGGT TGCACGTTAC CNTGGAGAAA | 300 |
| GGGCCTGGGT TGAAGAGGAG CCTTGCCCCAA GAGNACCANT TCANGGGACC CTG | 353 |

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

| | |
|---|----|
| GGCANAGGTT NTCCCTTCGC GNCCCAAACC ACATCCTGGA GCGCACTCTC CAGCGTGGCT | 60 |
| GGNAGCGNGG ACT | 73 |

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

| | |
|---|-----|
| TCCAGCCTNA CTTCTGGGC ATAGAGTCCT ATGGNATGCA CGAACTACC TTCACTCCA | 60 |
| TCATNAAGTG TGNACGTGGT ACATCCGTAA ANGACCTATA CGCCGTCACA GTGCTGTCTG | 120 |
| GNGGCACCAC CATGTACCNT | 140 |

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

| | |
|---|-----|
| AAAAGAAAGT TTCCCAGAC AAGATGNTTN AANTGCAAGC ANAANTTGAT GAGGAGAGAA | 60 |
| AAGCACTTGA AACAAAGCTC GACATGGAAG AAGAAGAAAG AAACAAGGCT AGAGCTGATT | 120 |

| | |
|---|-----|
| TAGAGAAACG GGAAAAAGAT CTTCTTAAAG CCCAACANGA GCATCANTCT TTGCTGGAAA | 180 |
| AATTATCTGC CCTGGAAAAG AAGGTAATTT TTGGTGGGGT TGACTTGTTG GCCAAAGCTG | 240 |
| AGGAACANGA GNANCTTCTT GAAGAATCTA NCATGGAAGT GGTGGNAAGG AGGAAAAGNG | 300 |
| CAGNGCAACT TNGCAGAGAT CTTGAGGAAA AGAGCAAGNN CGCTTGGATA TTGANGNAAA | 360 |
| TATACCCGTT TGCAAGTGGT AGCNCGGGN AAGTCCAGA AGTTAAGGAA GTTTGGCCCT | 420 |
| GCTGATGGTG CAAATCCNGG TNGGTTGTCT CCACCAGACC TTCGGGGNAT T | 471 |

(2) INFORMATION FOR SEQ ID NO:1213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

| | |
|--|----|
| TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTNGGGGG GGNTTTTTTT TTTTNNC | 58 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

| | |
|---|-----|
| GGCAGAGCGG CACGAGNCCT TGCACCTGGN CTTCGCGTCT CAAAGGTGGG ATGCAGATCT | 60 |
| TCGTGAAAGA CCCTGACTGG TAAGACCATC ACTCTCGAGG TGGAGCCAGT GTNCACCATT | 120 |
| GAGAATGTCA AGGCAAAGTA TCCAAGGNCA AGGGAAGGGC ATCCCTCCTG ATCCAGGCAG | 180 |
| AGGTTGATNC TTTGGCTGGG NAAACACTGT GTANGATGGG ACGCACGGTG TCTTGACTAA | 240 |
| CAACATCCAG TAAAGAGTTN CACNCTGGCA CCTGGTG | 277 |

(2) INFORMATION FOR SEQ ID NO:1215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

| | |
|---|-----|
| NTGCGGGGAC TNGCTGGAGC AGCGGTAGGG GGAGCNTGTA GANCCGCTGC GTCCCTTCAC | 60 |
| AGTCCGGAGC CCGGCCGTGC GCTGNCCGTA GGAACATGA CACTTTTCCA TTCCCGAAAC | 120 |
| CGANTCCCGC AGGGGGTACA GCGNMNGTCT GCC | 153 |

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

| | |
|---|-----|
| GANNNCATCA ACAAGGAAAA TANCACTAAG TTGAACATTG TAAACCTCCA GATCACGGAA | 60 |
| GACCCTGGCG AGTATGAATG TAATGCCACC AACGNCATTG GNTCCCCTCT TTTGTAACTG | 120 |
| TCCTNAGGGT GTGGNGGCAC CTGGGCNNNA CTNTGGCNTT NNTTGGGAAT TCTGGCTGAA | 180 |
| TTATNATNNT TGTGGTGATC ATTGTTGTGT ATGANAAGAG GAAGAGGNCA GATGAGGTTT | 240 |
| TGAACGATGA TGAACCAATT GGACCAATGG | 270 |

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

| | |
|---|-----|
| GGCCTTTAAG GCTTNACCCA ACGTNATCAA TCACCGATTT CCACGGTAGC AGACGCGCAT | 60 |
| CCTGAAACAT CATTGCTTG TTTTCCTGAN TTTAAGCCAG CGGTGTGGTG CCCGCAAACA | 120 |
| CATCGCCTGN GGTTGGCGTT TCCANACCTG CCAGCAGGCG NCACAGGGGT ACTTTTGCCA | 180 |
| CCACCGCTGC GGCCACCAC CGNCACAAAC TGACCTGCCG GAATATGTAA AATCCAGTTG | 240 |
| GTTCCAGGGA CGATATTTTC CGCGTNAATG TTTGCTTTAC TGCATTGAGC AACAATGGTT | 300 |
| TGNCCCTGGT TTCAAACGGG GCAGTTATTN CATACCGTGG GCCTCCTTTC AAATGATTAA | 360 |
| GCCGGGTTTC CCAACGGNAA CCCNNGG | 387 |

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

| | |
|---|-----|
| CCAACCTACG GTTGNTTCGT NCTTTAACCC CTACACGTTT CCCATTATGC CGTTGGNGAT | 60 |
| GAGTGGGANG ATTGTTTGNT TCGGGTTTAA ACTGTTGTGC CCGT | 104 |

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

| | |
|---|-----|
| AGGGAGAAAN TGGCCAGATG ATGAGCTGCA CATGTTTTGG GAAACGGAAA AGGAGAATTC | 60 |
| AAGTTTGANC CCTCATGAAG GCAACGTNTT ACGATGATGG GAAAGACATA CCACGTAGGA | 120 |
| GAANCAGTGG CAGAAGGNAA TATCTCGGTG CCATTTGCTC CTGCACATGC TTTGGAAGGG | 180 |
| CAGCGGGGCT GGCGCTGTGA ACAACTGCCG CANACCTGGG GGGTGAAACC CAGTCCCGAA | 240 |
| GGCACTACTG GGCCATCCCT ACAACCAGTA TTCTTCAGAG GNTACCATCA GGGGACCAAA | 300 |
| CACTAATGTT NAATTNNCCC CATTNAGTG CTTTCA | 336 |

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

| | |
|--|-----|
| GGCACGAGAG AAAACTCATT CTGGAGAAAA ACCCTATGAG TGTAAGTAAGT GTAAGAAATC | 60 |
| TTTTGTGCAC CTGTCTTCCC TGATTGANCA TTGGAGAATT CACACTGGAG AAAAACCATA | 120 |
| TCAATGTAAG GNCTGCAAAA AGACCTTTTG TCGTGTGATG CAGTTCCTC TGCACAGGAG | 180 |
| AATTCATACT GGTGAAAAAC CCTATGAATG CAAGGAATGT GGAAAGTCCT TCAGCGCCCA | 240 |
| TTCTTCTCTT GTTACTCATA AGAGAACACA CAGTGGGGGA AAAACCGTTT TAAATTGCAA | 300 |
| GGAATNTGGG NAAAGCCTTT CAGTGGCGGA CTTTTCCCT TGTTTACTCC NTANGGGGAC | 360 |
| ACACATTGGG GNGGAACCCT TTACNTGGCC TGCCCTNGGG GAGGGCCTTT AATATTTCCCT | 420 |

CCCCATTTT

429

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

| | |
|---|-----|
| GGCACGAGCC ATAGTGGTNA TCAGTGCCTC TNATGATGAC GTGGGTGAGA ATGCTCGTAT | 60 |
| CACCTATCTC CTGGAGGACA ACCTNCCCCA NTTCCGCATT NANGCAGACT CAGGNGCCAT | 120 |
| TACATTACAG GCCCCATTAG ACTATNAGGA CCAGGTNACC TACACCCTGG NTATCACAGN | 180 |
| TCGGGNCAAT GGNATCNCAC AGAAGGCAGA CACTACTTAT NTGGAGGTGN TGNTCAATNA | 240 |
| CGTGANTGGC AATGCTCCAC AATTTNTGGC CTNCCACTAT ACAGGGNTGG TNTCTNAGNG | 300 |
| NTGCCCCANC TTTCACCACT GTCCTTCAGT TCTCAGCCAC TTGCCNGGCT GCTNATGCCA | 360 |
| ATGAGTCCGT GTNCAGTACA CTNTCCAGAA TGGTGTATAG ATTGGGTGTG GTAGGTNTTT | 420 |
| AA | 422 |

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

| | |
|---|-----|
| GGCAGAGTGA AGCCTCCTGA CCTCCAATAC GGTGCACTCT GGTGAGGGAC AGTGGGTGGG | 60 |
| GTGGGCCAAG GAGGGGCCAC AGGGTGGGGG CAGATGCTGG AGTGTCCCTC ATATGCCTGC | 120 |
| AGACACCCGG GAACTACATC TGTGAAGTTC TGCGCCCGGT CTTTCCGCAC TAGCAGCAAC | 180 |
| CTTGTCATCC ACAGACGTAT CCACACTGGA GAAAAACCCC TGCAGTGTGA GATATGCGGG | 240 |
| TTTTACCTGC CGCCAGAAGG TTTCCCTGGA ACTGGGCACC AGGGCAAGNT TGCAGAGACG | 300 |
| GTGGGTTGCC TTGCGNTTTC CCCTGTGAAT TTTTNCGGGN AAGGCTTTTN AGGAAGNCCA | 360 |
| GACATTTTTT GCAGCCCACC TTGGCAAAAT TTAACCCNGC CTGTTTTTAG GCCCTT | 416 |

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

| | |
|---|----|
| GGCACGAGGN TGGCTTTTGC CTGTAGTCCC AGCTACTCGG GAGGCTGAAT GAGGTGGAAA | 60 |
| AATGGCTTTT TTTTTTTTTT NNNGNG | 86 |

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

| | |
|---|-----|
| GGCACGAGAA ATTATGGATT CTTTCAAAGA GAAAATGGAG AATATTGACT ACAGCAACGA | 60 |
| GGAGCACATG ACCCTGCTGA AGATGATTTT AATAAAATGC TGTGATATCT CTAACGAGGT | 120 |
| CCGTCCAATG GAAGTCGCAG AGCCTTGGGT GGA CTGTGTTA TTAGAGGAAT ATTTTATGCA | 180 |
| GAGCGACCGT GNAGAAGTCA GAAGGCCTTC CTGTGGCACC GTTCATGGGA CCGNGGACAN | 240 |
| AGTGGACCAG GCCACAGCCC AGATTGGGT CCATCCAAGT TTGTGCCTGN TCCCAATGTT | 300 |
| TGAAACAGTG ACCAAGCTCT TTCCCCATGG TTGNNGGNGG TTCATGNTG | 349 |

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

| | |
|---|-----|
| GGCAGCCGAG GTGGCAATGC TACACCTCAT TTTTATGCG GGTTTGCCAG GGCAAGCCCG | 60 |
| GCACTCGACC GATAGTCAAT GAGGATTATG TCAGCCACCA GCGCACGCNC ACCACCAGAA | 120 |
| CCACGACCAG AATCAACCAG ACCCAGTGCT TCAAATGCTG GTCGAGATTG TGCCACCACG | 180 |
| GNGCAATCAC CTGACCACCA GCGTAACCAA TAGTGGTAAA AATCAACGCC CAGGCAAATG | 240 |
| TGCCGAGNAT TTTCAGCGGC AGAANATTTT CGGCGGCACT GGTGGNAC CATTACGCGT | 300 |
| TGGGCCATTC ACCCGAAAGC CTNACTNAAN GGGGTTACCA TGACAAACAG TTACGGNTGG | 360 |

NGTTGGNTNA GTTTTTGN GN CCCGTTTCATT TTGTGCNGNT GTTTTGGGGA AACGGNGTTA 420
ACATGCCTTG TTTCAGTTAG TTAGATTCTT GCCGTNATNT TTGTTTCAGGC GTTGNACGGT 480
CNGGCCAGGT TAT 493

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

GGCACGAGCC ACAATGGCTG AGCACTTCCT GACGTTGCTG GTAGTGCCTG CCATCAAGAA 60
AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTNTGGAAC ACACCATGAA AGGGCTCAAG 120
TGCTGTGGCT TCACCAACTA TACGGATTTT AAGGACTCAC CCTACTTCAA AGAGAACAGT 180
GCCTTTCCCC CATTCTGTTG CAATGACAAC GTCACCAACA CAGCCAATGA AAACCTGCAC 240
CAAGCAAAAG GCTCACGAAC CAAAAGTAG AGGGTTGCTT CCAATCAGCT TTTGTGTGAC 300
ATCCGAAC TAATGCATTAC CGTGGGTGGT GTGGCAGCTG GNATTGGGGG CNTGNGNTGG 360
NTGCCTG 367

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GGCANAGAGT TAACGGAGGC AAGTTGGATG TCGGGAATGC TGGGGGGAAN TTTTGGGAAG 60
AGAACAGGAG CCTGGAAGGC TGAACCTGCA GAAGCTAAAG NACGAGCTGG CCAGCACTAT 120
GNCAAAAAC AGAGAAAGCT GAAAACCAGG TTCTNGGCCA TGCGGGAACA GTTCTNAGAG 180
GCCTCACCAA GNGTTACGN ACCGATTTC TGGAGGAGGC AC 222

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

| | |
|---|-----|
| GGCAGAGCTG CAGGGCCCCC AGGAGCATCC CTGNTCACCC CTCTGCNCCC TCCCCACCAG | 60 |
| AGCTGAAGAT CCCTGAAAAC GCCAACGTCT TCTATGCCAT GAACTCTACT GCCAACTATG | 120 |
| AACTTTGTCC TGAAGNAAGC GGNCCTTCAC CAAGGGAGTG AAAGGTCAAG CCACGGTAGG | 180 |
| CCAGCTTCCA CCCTCCCTTC GCATGGAAGC AGAAAGGGAC TCAAGATTGC CAAGGGCATC | 240 |
| TTCCTGAGGG GCATCCTCCC AGGGTCTGGC TGGCTGGTTA GCCAAGCACT TATGGGACCA | 300 |
| GAGTGGGCCC AGGCCAGTTG GGGGGCCTTT CTTCCCAACT GNNCAGCCCA GGGTACCCCA | 360 |
| GATTTCANTT TCANCCCGGA ANTTTT | 386 |

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

| | |
|---|-----|
| TAACGGCGTC GAAACCTATT TTNAAGTCTA TGTTAACGGT CAGTATGTGG GTTTCAGCAA | 60 |
| GGGCAGTCGC CTGACCGCAG AGNTTGACAT CAGCGCGATG GTTAAAACCG GCGACAACCT | 120 |
| GTTGTGTGTG CGCGT | 135 |

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

| | |
|---|----|
| GGCAGAGCGA AGTTTTTTTT TTTTTTTTNA GGNGGTTTTT ATTNAAAGTN CTTNTTTTTT | 60 |
| TGGGGT | 66 |

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

| | |
|---|-----|
| GGCAGAGNAA CGAACATTTA ATCTGCTGAT TGGCAAGAGA CAAAGACCAA TCCATTTAAG | 60 |
| TTTTGATATT GAATGCATTT NACCCTACAC TGGCTCCAGC CACAGGGAAC TCCTGTTGTG | 120 |
| GGGGGACTAA CCTATCGAGA AAGGCATGTA TATTGCTGAG GAAATACACA ATACAGGGTT | 180 |
| GCTATCAGCA CTGGGATCTT GTTGAAGTC CAATCCTCAG TTGGCCACCT CAGAGGAAGA | 240 |
| GGCGAAGTCT TACAGNTAAC CTGGNCAGTA GATGTGNATT GCTTCCAAGN TTTGGTCCAG | 300 |
| ACAAGNGAAG GGGGGGCATA TTTGTTCTTT GGGCCAACCT NCCTACTTCC CAGTTTCACC | 360 |
| AGTTGGATTC AGAAAATTCA AGCACGTGTG NAGAANTTTN GGNGACA | 407 |

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

| | |
|---|-----|
| GGCAGAGGNA CGAACTCATG NAAAGATACT GTCCTAATTC CGTATTGGTC ATCATTGATG | 60 |
| TGAAAGCCGN NGAACTAGG GCTGCCTACA GAAGCGTACA TTTCAGTGGN AGNAAGTCCA | 120 |
| TGNATGATGG GAACTCCAAC CTCGAAAACA TTTGAACACG TGAACCAAGT AAATTGGAGC | 180 |
| AGAGGAAGCT GAGGAAAGTT GGAGTTGNAC ACTTGTTACG GGATATCAAA GACACGACGG | 240 |
| TGGGGCACTT NGTCCCAGCG GATCACAAAC CAGGTCCATG GTTTTNAAGG GGCNTGAAAC | 300 |
| TTCCAAGCTT CTGGGTNTTC AGGNGCTACC TGGNAAAAAG TCGCCACAGG CAAGNTGNCC | 360 |
| CTTCAACCAC CAGTTCCNTT TACCAGTTGC AGGACGTTTT TCAACCTGTT GCCCAATGTT | 420 |
| CAGCTGCAGG GGTTCNTCAA GGCTTTTACC TGANGGCCAT GGCCATTGTG GTAGTTTATT | 480 |
| GGCNCGTTAT C | 491 |

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

| | |
|---|-----|
| CAGGCCTTTG CGCCTTCATA CTGCACCGAG TTTTGCCCAT CAATGGCTTT NACCACGTCT | 60 |
| TGGTAAGTTC ATACGTNAGA ACCCAAGCAT CGATCTGCGA ACTTTAAGCC AGCACAGAAT | 120 |
| ATGCACGTTT TGAACAGGGA TGATTTTAAA TCTEGATATA GTCTACGGTG NAACCCCGTC | 180 |
| CATCACCTTA TGAGAAAGAT CCCGCTTGCT GTTGAAGAAC TTACGCCACT GTNTTCTCCC | 240 |
| CAACTGGGCT GAGCGGCTAA AGAAACCAGA GGATCTCTAT GCGTTGGACA TTGGATTGAG | 300 |
| TGCGGTGTTG CAGTTTGTTA CCCNTNGGAA AAGGNNGTTT TAGGGGGGNT AAAAT | 355 |

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

| | |
|--|-----|
| GGCANAGNNG GAGTAGGAAA ATCTTGCTTG CTTTCATCAAT TTACAGAAAA AAAATTTATG | 60 |
| GCTTNTTGTC CTCACACANT TGGTGTTGGT TTTGGTACAA GAATAATCGA AGTTAGTGGC | 120 |
| CAAAAANTAA AACTGCAGAT TTGGGNTACG GCAGGNNCAG GAGCGATTTA GGGCTGTTAC | 180 |
| ACGGGGCTAC TACAGAGGTA GCTATCGGGG AGCCCTTNAT GGTNCTAT | 228 |

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

| | |
|---|-----|
| AGACTGCCCT CATCCACGAT GGCCTAGCAC GTGGNAATTC NCGAATTGCC AANGCCTTAG | 60 |
| ACAAGCGCCA AGCCCATCTT TGTGTGGCTT GCATCCAAC NTGGTGTGCC TATGGTATGG | 120 |
| CAAGTTGGTG GTGGCCCTTT GTTNCTNNNC ACCAAATCAA CCTAATT | 167 |

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

| | |
|---|-----|
| CCAGGNTTGC TGATTTGGCG AACGGTAGCA ATGATCATCA ATGAAGCCCT TGAATGCGCT | 60 |
| TCAAAAAGGC GTGGCCTCTG AACAGGATAT CGATACCGNC ATGGTNCTTG GGGTGAATTA | 120 |
| TCCATATGGC CCACTTGCCT GGGGAGCGCA ACTTGGCTGG CAGCGNAATA TTAAGGCTCC | 180 |
| TTGAAAATCT ACAGCATCAC TATGGCGAGA AACGCTATCG CCCATGTTCA TTGCTGCGCC | 240 |
| AACGGGGTTT NCTGGGAGAG CGGTTATGAA GTCATAAGGC CTGGCAAAT GCCCATGCAA | 300 |
| TGTATGAGAA CGATGCCTGC GCCAAAGNTT TGGCNGGACC ATTATCTTCA ATGGATGAAG | 360 |
| GCTTTGCTGT TAGTGGACCN GNACCTTCAT TGCACAATGC TTAACGGTTC NTCAAGTTGC | 420 |
| CAGGGGGGCA GTATTTTTC TGGGTGATAN NGCTTTGCNA CGCTGAATAG CCAGGGTTGC | 480 |
| ACNGTACCAT T | 491 |

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

| | |
|--|-----|
| AACCACTGGT ATCACATGGN CATGAACCTAC CGCGGGATGA TCANTATGCT GATCTNCTGC | 60 |
| GGTTGTTTCG GGCAAAGCGG TGGCGGCTGG GCACACTATG TCGGCCNGGN AAAAAGTGGC | 120 |
| CCCCACAAAC CGGCTGGTTG CCACTGGCCT TTGCGCCTCG ANTGGNAACC GACCACCGCG | 180 |
| CCAAATGAAC AGCACCTCGT TTTTCTACAA TTCATTCCAG CCAATGGCGC TTATGAAAAA | 240 |
| GTCTCTGCTC CAGGGAGTTN ACTTTCACCG CTGCGCGATG CCATAAAGTT ACAGCGGTCA | 300 |
| TCTGATTGAT TTCAACGTTT GNGCCCGAGC TATTGGGCTT GGCTANCTTT TTGNGCCNTG | 360 |
| ATTGGGGGGT TAACCCGTTT GGNATTNAAA GTTGAAGCCG ACAAGGCCGG ATTTTTCCTCC | 420 |
| CACAG | 425 |

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

| | |
|---|-----|
| GGCANAGGTG ACGTGCGNCC AGTACACAGC CCTGAGTTGG GATGTTGAAT TTNTCGATCA | 60 |
| CGCCATAGAT GGTATCCAAC ACGCGGCTTA AGTTTTCCAC GTCGTCAGTC ACCGGGTTAN | 120 |
| CGCCGATCAC CGCATCGCCC ACCCCGAAGG AAAGCCCTTC GTAGATTTGC GCGGCGATAC | 180 |
| TTTGACGTC GTCACGGGTG TCATTTGGCT GCAAACGGGC GCTAAAGGTG CCCGAAATAC | 240 |
| CGATGGTGGT ATTGGCCTTT TTGGATTACC GGCATTTTCT TCGCGCCGTA GGATTCAGGT | 300 |
| CCGCGTTGGG AGCAAAATCT TTCGTTANCG CCGGGGACCA TTTCCGAGGT TCANCCCTT | 360 |
| TGCGGGTNAA AGGCAATGTC GTTCCACGTT GGTTCANCG TTCAGCAACA TATTNAAGGA | 420 |
| TTCGTNGATG CTTCCATTTT TAANCTGGTT TAAGGCCTTT GTTAAAANGG TCC | 473 |

(2) INFORMATION FOR SEQ ID NO:1239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

| | |
|---|-----|
| GGCANAGGNN NAAATGGATT GATTATGTCA AGNGCCAGG CATGGTAAGG AGCAAAGAAG | 60 |
| GTTCACTCTG GACAGCACTA AGGAACTTTG GTTTAGGAAA GAAGAGCTTA GAGGAACGCA | 120 |
| TTCAGGAGGA GGCCCAACAC CTCACTGNAG NCAATAAAAG AGGAGGAACG GNACAGCCTT | 180 |
| TTGGACCCTC ATTTCAAGAT CAACAATGCA GTTTCCAATA TGCATTTGCT CCATCACCTT | 240 |
| GCGGAGAACG CTTTGAGTAC CAGGATAGTT GGTTTTCAGC CAGCTGCTGN AAGTTNACTG | 300 |
| NGATGNAAGT NCACATTACT TTGGGGGG | 328 |

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

| | |
|---|-----|
| GGATCCCCCG GNCNGCAGGA ATTCGGCACA GGTCAAAGNC CACGGCGAGT ACACGATGGA | 60 |
| AGCAAACAAG GACTANAAGG ACTATAAGNA CGATGAGCTG CCAGCCAAGG AATGACCCAA | 120 |
| ATTCCCCNCT GCAGCCCGGG AACACCCCTG CAGCTGTTTG AAGGGTCGGA GGAACCGCCG | 180 |
| CAGTAGNNTA GNACGCCCAA AGTGGTGGAG GAGCAGGAGT GCCANGGNGC ACTACACCGT | 240 |

GTGCCAT

247

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

| | |
|---|-----|
| GGCANAGGGA CCTTCCCACC TCAGTCTCCC AAGGTGCAGG GATTATAGGC GTGACATCTN | 60 |
| TCTGGCACCA GCCCCAGNAG CTTTCAATG AATGTGTTCT ATGTGGGAAG TGGGTATGTN | 120 |
| GTGGATTTTT GTAAAGCTTA TCCTNTAGAT TTCTTGAAC CTGNGATGNN ATATCTCTTC | 180 |
| TCAGTTTTTG AAAATTCTCA GCCATTATCT CTTTACACAT TTCTTCTGCC ACATTCTTTC | 240 |
| TGTTATTNCT CCTTCTGGGG GCTNCAATTT ACANATNACG NTA | 283 |

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

| | |
|--|-----|
| AGATGAACGA NCAGACTCAG GCGATGTGCT TTATGGCAGG CGCAAACCTCG ATTTTTTACG | 60 |
| GTTGCAAACCT GCTGNACCAC GCCGAATCCG GAAGAAGATA AAGACCTGCA ACTNTNCCGC | 120 |
| AAACTGGGGN TAAATCCGCA GCAAACCTGCC GTTNTGGGCA GGGGGATAAC GGAACAACAG | 180 |
| CAACGTTTTG GAACAGGCGC TGATGAACCC CGGACACCGA CGGNATTTTT ACAACGCGGC | 240 |
| ACATTTATGC NGCTGGGCAA GNNGAAANTT TAAACGGGGG | 280 |

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

| | |
|---|----|
| NCCGACCNTA ACCATATCGG TAANTTTAAN CTTATCGGCC TTAAGCCACT GCCCAACCAC | 60 |
|---|----|

ATAGCTGGTC ATAATTTTAG TNAGGCTCGA GGGTTCCATT TTN

103

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

NATTCTCAAA GGNCTCAAGT TCAACCTCAC GGAGACTTCT TAGGTCAGAA ATTCACCAGA 60

NCTTCCANCA CCTTCCTNCG CCACCCTCAA TTCAGTCCAG GGANTGAGCT CNAGCTGA 118

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

TTGGCACCAA AATNCTGCAC CTAACCGTTG NACAGGCACG TGGCTTTAAT GCTGAACACG 60

AATGGAAAAC CNTTTTTTAA TGGTNTGGTT GANTTCATGA CCTCNGGCCC GATANGANGT 120

TTCCGTGNCT GGAAGGTGAA AACGCCGTTN AGCGTNACCG NAATCTGCTG GCGCAACCA 180

ATCCGGCAAA CGCACTGGCT GGTACTCTGC GCGCTGATTA CGCTGACAGC CTGACCGAAA 240

ACGGTTNCCA CGGTTCTGAT TCCGTGGAAT CTGCCGCTCG GAAATTCGCT TATTTCTTTG 300

GCGAGGCGAA GTGTGCCCGN GGACCCGTTA ATAATTTCTG AATNGCCGNT GCAAAGTNGG 360

TTTCCGTGCG GCCAAATTN 379

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

AAAGGAACGA CCTGGCTTNT AAGCAGGACG AAGGGCCCCCT AGACGGCAGG CACGGTCCAA 60

AGTCCAGCCC CTAAACNAG GTGGTGTNTA AAGCCTTTTT CCGCTTCTTC CGTGAAGAT 120

| | |
|---|-----|
| TGTGGGAACA TGACTCTTTG TTCCTAACGT CGGGCGAGCN TAAGGAGAGA ACCCTGCAGC | 180 |
| GGGAGGCCTT CCGCAAAGCT GTCTCCTCCA ANAGCCTCCG NNACTTCCTG GAAGGTTTTT | 240 |
| CATGGAGGAC TTCAAATGTT TTCGGGGGCT TTCATTCCAG GAGCGGGAAG TTGCGNCCGG | 300 |
| CAGGTATGGC CAAAGGGTCT GTTTTNNAGG TTCCGNAGGN CCCAGAAGTT ATTTGGGGAA | 360 |
| AACAATTTCC CCA | 373 |

(2) INFORMATION FOR SEQ ID NO:1247:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

| | |
|---|-----|
| TTAATTCANG CGTACCATCG TACCGAAGTA TGCGTCCGA TCAAAACCAA AGCAGGCACC | 60 |
| GTGTTTGGA TATTCGTAGC GTTCCAGGCA GGAACCTCCG CNAGCTCCTG GNATGGNCTT | 120 |
| CACTTAGTTT AGCGGCCGTT TCCAGTGAAT AATCCGGTTT CCGGCGGATG TAACACATTC | 180 |
| GGCTGGCGCG CGCTTTCTGG TAGATTCGGG ATTGGGNCGA GTAGCGCAAC CGAAAGCGCA | 240 |
| TCCAGCGGCG TTCATCAACA CCACGGGCAG CAACCGATTT TAGGCAATCC TGGGCCACNG | 300 |
| ACCATGTACG GTTCAGAAAT CCAGCTTTTG TTTGGTCGTT TTCGGTTTTG CAGGCGGACC | 360 |
| NTCCNTCTGG TTTNTTAACG GNTTTC | 386 |

(2) INFORMATION FOR SEQ ID NO:1248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

| | |
|---|-----|
| ATCTGGNAAG GCGATAAAAA GCCGATGCAG GGGCGGNAG ATATTCAGGC TCGTCGACTG | 60 |
| AAACTAAAGA NCTGATGCCC GATGTGGAAC TGAATGCAGA AGACGCTGGG GGAAATGAAA | 120 |
| CGGTGACGCG NNACTACGCG GTAGCGTNAG ACTGCGGTGG CGGCACTTTT AGGCAACANT | 180 |
| AACGGCAACC TGGAAACTTT TGATGAATGA CGGGCTGGTG AAGCCGCAAC CTGATGGGAG | 240 |
| ATTGTTGGGC TGAATGTCGG CAACTTACAT TGTCGGTGCG ATATTTGGTT GATGATGAGG | 300 |
| TGCGGGTGAA ACTNCGNCGG CGGGGGAATT CTGAAATAAT TGCCACGGG GTTGGGCGGN | 360 |

GCCCCCAAAA TTTTGTGCTT TTCGNTAACT GAGAACNCGT TTTGATTNAA TNTTAACCCG 420
GAAGGCAA 428

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GTTTTNCCTG ACGGGAGANC GACTGCNAGA ATTCAGGAAT ATACAGCAAC GAAGGCTGAC 60
GTGGATCGAA GGAATCGCC CCGACCATCA CCGGATTTTT AATGCCCTGC CCTTTGGCAT 120
CGGCAACAG CGCGGCGAGT TTTTCCTGGN AGGGAAGTGT GCGGGCGAAT CCCC GTTCCA 180
CAGCCGGTTN CATCGANGCG GGCAGAAAACA TCCTGAACGT GCGTGAAAAC TCGGGGTANN 240
GCGGACATTA ANGGA AAAA 259

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

TTTGCGTGCA ANGAAACGTG AACTCGCGAA ANTGGNATAT TTGCTAATCT ACTCGCCGCA 60
TTTTTAATTG ACGACATAAT CCAGCCATCG CTGATTGCG CCCCCAGAAG TGCCGGATCC 120
GAAAAGAAGA ACTGAACTCG TTGTGGAGAA TAACAAAAAT GGTCTCTGG AGCTTACAGG 180
TGGCCATTCG TGGGNACAGT NATCCCTGAA CAGCCTACAA AACGCAATTG AAAGAACGCG 240
AAGGGCATCG TGCTTGAACG NGGGCACCGA GGCGTCGCAT TGTGTCAGAT GGTTC CAACC 300
CTTGAAGTTA AGCGCTTTAT GGGNTAAATT CCCCCGCATA TNCCGGTTTG TCCAAGTTCA 360
NGGATGGGTT AAGGGCANCN GG 382

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

| | |
|---|-----|
| GGGCACAGTG TNCTGAGATC TGAGTCAGTA TCATTNATAT AAATGTCCTT CATAATGTTT | 60 |
| AGCACAGTGG GTTATCCGTN ANCCCAAGTA TCCTGTGAAT AGTCAAATTG GCTTTGTCCT | 120 |
| GTGTTGGGAA TATGGNGGGA TAGTGAAATC CATGTGGTTA TGTCCTCTTA TGTGCCGGAT | 180 |
| GAAAAAACT GATTAANCAG ATGTGTGTAA TTGCGTTCCC AAGTTCCAGA TAGCAAGGGA | 240 |
| TTTATCGAAT CCAGCTCATT TCTGAGTATA CACAGATTCA ANGAAGANTT GAGATATTTA | 300 |
| AGAGNTACCN ATATTTGNAA AA | 322 |

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

| | |
|--|-----|
| AAGCTTATCG ATACCGTCAA CACCCTGAAA NAAGTGGCTG CCCAGGTTNN CTGAATCAGC | 60 |
| AACTGGAAAC TCCCCGCTTC CCCTTCCCGT ACAACACGCC AACCTCTAAA GAAGTGTA CT | 120 |
| TGTATCGGGA GATCTTTGAA AGAACTATTC CCGNTTCCAA GNGCCGNTGA AGTGCGTGCC | 180 |
| GGGCGGTCCT TCCATCGCTT GTTCTTCCGC TAAAGCGAAT NCGNTTGGGA ATGCAAGCGT | 240 |
| TTCAAGAAAA ATGGGACGGT TCCGTCTGGT NCGCGNGGTT GGTGTTCCAC CAGTTCGGCG | 300 |
| TATTAGGTTA AGAAATNCGG NAACCGCCCC CGGTGGAATT CCGGGGTCCG GTTACCCAAT | 360 |
| TTCGNCCTNT TAGTTGAGTT CGTTTTTACA TTTNCATTGG GCCT | 404 |

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

| | |
|---|-----|
| GGCAGAGCCA AAGTGCAGAT ATTACAGGTG TGAGCCACTG TNCCTGTCCA TTTTCTAAGT | 60 |
| TATTTTATAA ATAATTAACA CAAGTAAACA ATGAAAAACA ACCTTATTAG AACTTTAAT | 120 |
| AAGAATTTAA CCATAGCAAA CCCAATTTTT TTTATCCTGT AAGTTCCTTG GTTTTGAAGA | 180 |

| | |
|--|-----|
| CACATACATA TTCAAAATGA GAAAAAGTCC TTTGGANTAT AATCATCANT TGCTATATAC | 240 |
| AAACCTGTAA ACATATACAT TATATAAATC CTGATTTNCC CGGTTTAAAA TGGAAATCTCT | 300 |
| TAATATGGTC CGGGGGTTAN CCATNANTTC TGGGTTTTTG GCATTNAAT TGTTCCAAAG | 360 |
| GGCCGTATTT TTGGAAACT TTGGATGGGC TAGNATTTT | 399 |

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

| | |
|---|-----|
| GGCANAGCCA AAGGGNCGGC ACAGCACGGT GCAGCGCTCC AAGTCCTTCA GCCTGCGGGN | 60 |
| CCAGGTGAAA GGAGACCTGC GCCGCCTGCC AGAAGACCGT GTACCCCATG GAGCGGCTGG | 120 |
| TGGCCGACAA GCTCATTTTC CACAACTTTT GCTTCTGCTG CAGACTGTCA CACCAAGCTC | 180 |
| AGNCTGGGCA GCTACGCCGC GCTGCACGGG GAGTTCTACT GCAAACCCCA CTTCAGCAG | 240 |
| CTGTTTANGA GCAAAGGCAA CTACGNACGA GGGGTTTGGC CGCAAGCAGC ACAAGGAGCT | 300 |
| TTGGGCCCCAC AAGGAGGTGG ACCCCGGCAC CAAGACGGCC TGAGGGCTCT TTAACTTTC | 360 |
| CANCCCCTTT NNGGAAGGTC TTGTAGCCGN CAGGGGAAAG TTGGGAAGGA GGTGAGCTT | 420 |
| GGGGTTTNTT TGGGGGNCC AGTTGGNAAG GGGTTAGGGT TTTTCAGGGT AGGGGNCCAG | 480 |
| GNAAGGTTTT TTCCAGGATT | 500 |

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

| | |
|---|-----|
| CGANATGCCG CCACCGCCAC CTGCCCTTN AGCGCATCTT TNACCCCAAC CACCGCCACT | 60 |
| TCGGCAACGN CCGGAATGGC TGGAGATACT CTNTTCAATC TCGCGGTCC CCAGCCGATN | 120 |
| TNCCNGCAAC GTTAAATTAC ATCGTCAGTG NCGCCCGAGA ATAAAGTGAA TAACCGTCAG | 180 |
| CNTCACGGAT GCCCCAGTCA AAGGTGGCGT ACACCGNGCG GGAAAACAGC GACCAGTAAG | 240 |
| TTTTACAAA GCGGCCGTCG TCGCCCAGA TGGTCTGAAT ACACCCCGGC GGCAGGGCCC | 300 |

TTCACCACC AGCATCCCTT TTTCGTTGAN GCCAAAGGTT TGCCGGTGGA TTTCATTAAG 360
CAATGCAAGT TATAGNCCTT ANATTGGNAA AACGGGGNTT TCCAAAGGGT TGGNCTTTTG 420
TTCAGACGGG GGAATGGCC 439

(2) INFORMATION FOR SEQ ID NO:1256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

CAACAGATGG GTAATGGCAC CAACGAGAGC CTGATGAAAG GGAGGGCGAT CCTCCAGTTC 60
AAATATAAGG TCAGAACCTG CATGGTTTAT ATCAGACATC CCTTCACTCC TTTTAAAGTA 120
AATTTGAATC ATCTGAATTA GTAAAATAAA TTCCACGAA TTTGGGGCGC AGGACGCCTT 180
GAGAACGGCT TATCTCATTT TCGCA 205

(2) INFORMATION FOR SEQ ID NO:1257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GGCAGAGGGA AAATNAAGTA CTCTTTTCAG TTGTGGATCG CAATGATGTC AGCAAAGGGA 60
CATGATGGGA AGGAACCTGT GAAATTTGTA GATTTGCTTG GTGACCATGG GAAACATGTN 120
CAGTCCTCTG TGGGAGTTGA TCAAATGGTG CCTGGGTCTG TCAGTGTACA CCATCCCTTC 180
CATTGGACTG GCTTTGTTGG AAGAAAAGCT CAGATATAGC AATGAGAAAT ACCAAAAGTT 240
TAAGGCAGTG GAAGAAAGCC TGCGTAAAAG AGCTGGTGGA TATGCTAGGT GATGATGGTG 300
TGTTCTTATA TNCCCTCACA TCCACAGTG GGCACCTAAG CATCCATGTN CCTTTAACA 360
CGGGCCTTTC AACTTTGGNT TACAACAGGT GTTCTTTCAN TGNCTGGGT TTGCCNGTNA 420
ACCCCATGCC CATNGGACTG AATGCCAAGG ACTCCTTTAG GCATCCAGTT GTNGGNGTAC 480
CCTTAAGGTC ATTTGCCCCG GTG 503

(2) INFORMATION FOR SEQ ID NO:1258:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

| | |
|---|-----|
| AGNTGAANAN NCCACAACCC TGACTCCCC GACGTCCACC GTGAATCCAC ATCCGCANCG | 60 |
| AGACCTCCGT GCCCGACCAT GTGTCTGGTC CCTGTTCAAC ACCCTCTTCA TGNAACCCCT | 120 |
| GCTGNCTGGG NTTCATAGCA TTCGNCTAA | 149 |

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

| | |
|---|-----|
| AGCTAAAAAA CGTCGCTGCG GTAATGGTGA CAGNGGCANT GTCTCCGTTT GGNACGNCAT | 60 |
| GGGCAAACCA TCGATGTGGT GGTTTCTTCC ATGGGAAATG CCAAAGCTT NCGTGGAGGT | 120 |
| ACGTTGTTGN ATGACACCGC TTTAAGGGNC GTTGGACAGT CCAGGTGTAT GCGCCTNGCG | 180 |
| CATGGGCAAT TATCTGGTT GCGGNCGCA GGAAGCCTCC GCTNGCGNNT ACAGTGTTC | 240 |
| AGGTAAACCA ACT | 253 |

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

| | |
|---|-----|
| ATATGCCGCA GAAATTTGGT CTGTATGAAG ATCTCACGGT GATGGAGAAC CTCAATCTGT | 60 |
| ACGCGGATTT GCGCANGTNC ACCGGCGAGG CACGTAAGCA AACTTTTNCT CGCCTGCTGG | 120 |
| AGTTTACGTC TCTTGGGCCG TTTACCGGAC GCCTGGCGGG CAAGCTCTCC GGTGGGATGA | 180 |
| AACAAAACT CGGTCTGGCC TGTACCCTGG TGGGCGAACC GAAAGTTTGT CTGCTCGATG | 240 |
| AACCCGGCGT CGGCGTTGAA CCCTATCTGC ACGGCGCGAA CTGTGGCCAG ATGGTGCATG | 300 |
| AGCTGGCGGG CGANGGATGT TANTCCTCTG GAGTACCTNT ATTTTCGACG AAGCCGAGCC | 360 |

ATTGCCTGNA CGTGTTAATT GATGAACGAN GCGNATTGCT GTTTTCAGGG NNGAACCAAA 420
AGCCTGNACA CAAACCNGGC CGGACGCAGT TTTTGATGAC CATTACAGG AGGGCAACNC 480
AAANNTTGC 489

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

GGCANAGGGA GAAGCAGGAG CTGTCGGGNA GATCAGANGC CAGTCATGGC NTGACCAGCG 60
NGACCTTAT 69

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

GGCANAGGAG ACAGGCAGTA TACAAATACT ATAAATACAC TGGAGGAAAA CATAGTGGGG 60
CTGATTATAG TCGATTTTTG CTCTTTTATT TCCGGTAACA GTAAAACAAC TCTGNATAAG 120
AAAAGGTTTG AACATGAAGG CAGACCTGAA GCGNGTNAGG NNAGTGAGCT ATGCAGCTAA 180
CCAGGGTAAG AGTTCCAGGT AGTGGGGATA GCAAGTGCAA AGGCACTATG GNAAAGGNTC 240
ACATGGNNAG NGGTGTCAGC AAGAAGGGCC ACTGTAGCCA GAG 283

(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

GGCANAGCAA GAAGGCAGGC GAAACAAACC GCCGTCAACA GATCCCAGAC TACCGTACTC 60
CTCCNANTNT TTNAGAAGGA TCGCTTTCAA GACATTGCCA CCAGGGAACA GCTGGCCAGA 120

| | |
|---|-----|
| GAAGACGGGC CTCCGGGAAG TCCAGGGATT CAAATCTGGT TTCAGAATCG AAGGGCCAGG | 180 |
| CACCCGGGAA CAGGCTGGCA GGGTACTTAC CAGGCAGGCG GGCTTGATTG TTGGGCCCCA | 240 |
| GGCGGGGTTT TAACCCTGNT TNCCTNGTGG NTCNGTTTT | 279 |

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

| | |
|---|-----|
| AGCNTGGGNT ACGACGTGGA GAACGACCGG NAGGTGAGGC CGANTTCAAC CGCATCATGA | 60 |
| GCCTGGTCGA CCCCAACCAT AGCGGCCTTN TAACCTTCCA AGCTTTCATC GACTTCATGT | 120 |
| CGCGGGAGAC CACCGACACG GACACGGCTG ACCAGGTCAT EGCTTCCTTC ANGGTCCTAG | 180 |
| CAGGGGACAA GAACTTCATC ACAGCTGAGG AGCTGCGGAG AGAGCTGCCC CCCGNACCAG | 240 |
| GCCGAGTNAC TGCATCGCCC GNTATGGTGT CCATNACCAG GGGCCCTGAA CGCCGTGGCC | 300 |
| CGGTGGCCNT CGAA | 314 |

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

| | |
|---|-----|
| GGCAGGAGGA GACAGGTCTT AGTCAATTTG GTAAGTTTAT TTTGCCAAAG TTAAGGACGT | 60 |
| GCGCCTGCAA CACAGCCTCA GGAAGTTCTG ATGACACGTG CCCAAGGTGG TCTGAGCGCA | 120 |
| TTGGNTTTTA TACATTTTAG GGAGATATGA CACATCAATC AATATACGTA NNATGAACAT | 180 |
| TGGTTTTGGT CTGGGAAAGG TGGGACAAC TGAACAAAG GCAAGACAAC TGGNAGTAGG | 240 |
| NAAGGGAGCT TCCAGGTCAT AGGTAGNTTA AGAGACAAAT GGTTGCATTG CTTTTGAGTT | 300 |
| TCTGNTTGGG CCTNTCT | 317 |

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

| | |
|---|-----|
| GTCGTTGNTG TTGTTGTTGT TGNGTATGCN GCAGAATTTN ACCAGNTGAT CTTAAAACCA | 60 |
| CACAGTGATA ATACAAGTTA CCAGCTATGG TCAAACAGTA TTGAAAAAGA NGATCAAAGT | 120 |
| TGGAGGACTC ATATTTNCCA ATTTNAAAGT TGCTTTAANG CTNCTNTAAT CAAGATGCTG | 180 |
| TGGTACTGGC ATAAAGAAAG ACATATATGT TGGTGAATA GAATTGAGAA TCTAGNAANC | 240 |
| TTTACATTTA ATNAGTCAAT TGATTTTCCA GNNGAATGCT ATTAAGACGG TTA | 293 |

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

| | |
|---|-----|
| GGCAGAGGGN CCTCTCAAAG TGCTGGGATC ACAGGTATGA GCCACTGCAC CCAGCCAATA | 60 |
| CTGTATATAT TTTTTTTAAT GGACCAAGGC CACCACAATG TGAGCAGAAA GGTCAAATAG | 120 |
| TCTGTTATGT GGGAGAAATG TGTACAGTGN ACTTTGTTTT TTAATTTCCC CCAGTTTTCT | 180 |
| AGTTTTCTGT TTTAGAAGAC ATGCTGTCAC AATTAACAAC TCTTACTNAA TAAGNACTTG | 240 |
| NTCAATTTGA AATGGTCTAT ACCAATTATG NAAATATGGA GGAAAGTTAG GGCATTAGGA | 300 |
| CTTACAAGCA CGTACTTCN TCTTAAGTGG CTTAGGATTC CCAAGCTGT NAACANTGCT | 360 |
| TTTTTTCAGC TGTTNCCN | 379 |

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

| | |
|--|-----|
| GGCANAGCGN ACAGGGGGCG CTGTTTTCGT GGAAATCCCC CGGCTGCGAA CCTGGGATCC | 60 |
| CTGACCTGGA TCAAGTCTCC GAAGCTGGCA GAGTCCATTC TGCATCACCG GTCTTGGGCT | 120 |
| TTGAAGAAGC TAGGAGAAAT TCCGCTTCGG CCATCACGCT ATGGAAAAGT GGATTTTTTTT | 180 |

| | |
|--|-----|
| TTCTTAAGTC AATTTTTTTTT TTTTGAAAAT ATGAGACTTA GTAGGTTTGG GAAGTGGGCT | 240 |
| AAAAGAACAT TTGATATTGT AAATTGGACC CCCCCTTTGA AGGTGACAGT GTTTTTCCCC | 300 |
| TACTTNAAAG CGCCAANTTT TTTTNTGGCA CTATNAAAAG CTATTTACTA N | 351 |

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

| | |
|---|-----|
| GGCANAGGGA ACTAGTTCTC TCTCTCTCTC TCCATGACCC CGCAGCTTCT CCTGGCCCTT | 60 |
| GTCCTCTGGG GCNANCTGCC CGCCCTGCAG TGGAAGGAAA GGGGNCCCCA GNAGCTNCTG | 120 |
| AACACTG | 127 |

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

| | |
|--|-----|
| CAGTTTNAGG CGCAGAATAT CTNNGGAGGC GCTGCGCCCC GGTAAAGGTG CCGGAGAAAAG | 60 |
| TAACGNGGGC GGCGGCAGTT GAACGACGTG ATTCTGCCCN GAATGCCGCA TCACGCTGCC | 120 |
| AGGCTTCGNT TTCGCGGTAT TGCTGGTACT CTTCCACTAC ATCANCNAAA GCGTNAAAT | 180 |
| GGCGAANAGG NCGTTGGTTC GCCACGCAGC CATGTGCAGT NAAATATTGG CGATCTGGCG | 240 |
| GGTAATGGCC GGGAAACTA AAAGCCATCG NACCAGCAAA TGGTGATAAC GCTGNTTACC | 300 |
| ANTACCAGCG GTTTATNCGC CCACCTGTTN TCAGCTGATG AAAGACCATG GTTTTACCGT | 360 |
| TATCGACGGG CNATTCTTGT TGCAAATCCG CCTGGTATTA ATGCCTGGGC CATTACCNTG | 420 |
| CGGGNTCATG TTTGGTTCNT AGGGTCGTTA ATTTTGGCN ATTCGAACGT TNAA | 474 |

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

| | |
|---|-----|
| GGCACGAGAA AGAACGAATT GGCAGCCCTG TCTACACTGG CCCTCTCTCA GGTGCATCAT | 60 |
| AACCTATTCC ATTCAGGCTT TTNACTCTCA GCACTTAGGG GCAGTTATGC TTGGCATAGT | 120 |
| TTCCAAAAAC TTCCATTTGC CAAATCTAAA AGTCAGTCTT CTGTTCTCAT CTTGAAAATG | 180 |
| AATTATTAAA TTATGTATAT TTGGGCGGAG GCACTTGTTT TCCCTTTGAA GTCAGGGACC | 240 |
| CCCTGTTTTA TACCCTATGA TTATTGTTAA TGTTTCTGTT TCTCTCAGTT TTAAGACAAT | 300 |
| TATCTCCTAT ATTGATGAGC AATTTGAGAG GTACCTGCAT GACGAGAGCG GCTTGAACAG | 360 |
| GCGGCACATC ATTGATAATT AGGGTGCATT GTTGCTTTTA CTTTATTTCA CCTTTTGGAC | 420 |
| ATGGGTAAGT AATTGTTTAT CGTGGAGAAA TGCTTTACTA CATGGGGTTG TAAGTTTACC | 480 |
| CAAAC TGGGG ATTTTAATAT | 500 |

(2) INFORMATION FOR SEQ ID NO:1272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

| | |
|---|-----|
| GGCACGAGAA GAACGACATC AGAGATGAGG ACAGCATTCG TGCTCCTTGC AGCCCTGGNT | 60 |
| GTGGCTACAG GGCCAGCCCT TACCCTGCGC TGCCACGTGT GCACCAGCTC CAGCAACTGC | 120 |
| AAGCATTCTN TGGTCTGCCC GGCCAGCTCT CGCTTCTGCA AGACCACGGA ACACAGTGGN | 180 |
| AGCCTCTGAA GGGCTTCCCC GAAAGTTNTG GGNACCAGGT CCAGGTGGGC ATGGAATGCT | 240 |
| TGATGACTTG GGAGCAGGCC CCCACAGACC CCACAGAGGA TGAAGCCACC CCACAGAGGA | 300 |
| TGCAGCCCCC CAGTTNCATG GGAAGGTTGG AGGGACANAA GCCCTTTGGG TTCCCCGGGT | 360 |
| TTTCAAATTN CTTNNGGTTT TT | 382 |

(2) INFORMATION FOR SEQ ID NO:1273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

| | |
|---|-----|
| GTTCGCCTTC CGCTTTNAGG ATTTGCAACT GTTTTTAACC TTCGGCTTTA AGGATTTCCG | 60 |
| CCTGACGGAT CCCTTCCGCT TCAAGAATGT AAGCNCGTTT GGNACGTTCC GCTTTCATCT | 120 |
| GCGCGTTCAT TGAAGAGATA AGCTCTGCCG GTGGGCGCAC GTCGCGAATT TNAATACGGG | 180 |
| TNACTTTAAT CCCCCACGGG TTGGTGGCTT CATCGACAAT ACGCAGCAGG CGTGAAGTTT | 240 |
| GATGCTGTCTG CGCTTGAGAG AGCATTTTCGT CAAGTTCCAT TGAACCCAGC ACGGGTACGG | 300 |
| GATGTTAAGT NCATGGTCCA GGTTTGATGG TTCGCCAAGC TTCCAGATTG CTTGACTTTC | 360 |
| ATAAGNCNGC GCGCGGGGGG GGTTNAATTC ACCTGGAATT AAAAGGCACA CGGGCGTTTCG | 420 |
| ATTGGTNACC GTTTGGCGGT TATCCTTTTC GGGGATAACT TTCCCTGGGG AAGGGGNTAT | 480 |
| TCGAG | 485 |

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

| | |
|--|-----|
| CGGGGGNGAA TCANTTTNTG GAATACTTTG GTGAGGCGCT GTTCCGTGCC GACTTGTGCA | 60 |
| CGCCGACGTA GCGATGGGCG ATCTGCTGAT TCACGAAGGC GCGCCATGCA TTGCACAGCA | 120 |
| ACATGCGGCA AAAGTNTTTA ATGCCGATAA AACCTACTTC GTTTTAAATG GNACTTCATC | 180 |
| TTCTAACAAA GTGGTTTTAA ACGCNC'TGCT AAACACCGGG TGATCTGGTG CTGTTTGATC | 240 |
| GCAATAACCA CAAATCTAAC CACCACGGGG CGTTGCTACA GGCTGGTGGC AACACCGGTT | 300 |
| TTATCTGGGA AACGGCANTA AACCCGTNTG GCTTTATTTCG GTGGGCATTT GATGCGCACT | 360 |
| GTTTTNNAAG AAAATTTACC CGCNGTGAGT TGATTCCGGG AAGTTCCAGG GGGGGGGCCC | 420 |
| GTTACCCCAT TTGGNCCNC | 439 |

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

| | |
|---|----|
| CAAGGGGCGC CACAGCNGAG GGAGCTGGCC GAGGTGGATG TGGACTGGCT GATCGTTTCT | 60 |
|---|----|

| | |
|---|-----|
| GGTCGCGGCG CAGTGGTGTG CGATAACACC GAATTCCGCG TGGTGAAGTC ACGTACTCAG | 120 |
| CNGNAAGCGT ATGTTTTTGC ACCGGCTACG CTGTCCAACA TTTACTACGG TTTCTCGCC | 180 |
| GTAACAGCC GTTCAATGC TTTCGGTGAT GGTGTGGCGC AACTGGGCCG CTCGCTGGAT | 240 |
| GTTGATGCCA ATACCAACGG TCAGGTGGTG ATCCGTGGAT AGCGCCATCA ACGGAAGTTT | 300 |
| TNAACACGGC TGAAACCGTG GGGCCGATGC GGTGTTTCTC TNAATCGTGC CNNTTNNGGG | 360 |
| GNAATAACCG GCANCGTAGN TGATTAACGN ACGAAATACC AGCGCAATCT GGAATNGNCA | 420 |
| CTAANTACAA CCGCATGTGG GGGATTACAN TAAACCCGGG CGTTGGGTAA TAAAATGGGT | 480 |
| TNNCAAGGGC GAGAAATTAA GGGCAATTN | 509 |

(2) INFORMATION FOR SEQ ID NO:1276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

| | |
|---|-----|
| AAAATTGGTC ATCTGTTTGA CTACATCCTG TTTGANTCAG CATGGGTCGG CTATGAACAG | 60 |
| TTTATTCCGA TGATGGCGGA CTGTTGCGCG CTGTTGCTGG TTCTTAATGA GAACGATCCG | 120 |
| GGTATTCTGG TTACGCAATC TGTGCATAAA CAACAGGCTG GTTTTTNTCA GACTTCACAA | 180 |
| ATTCATAAAA AAGACAGCCA CATCAAAGGG CAANAGCGTT ATGTACCGCA CAAACGCATG | 240 |
| AACAACGCCT TTNTGAATGC ACGCCTCCAC CAGCCCGTTT CTATCCGCTG TTTGCCGCAC | 300 |
| TGNANTATCC AACGCCAAN TGNCATGGAA GGTGTTGAGC GGTTCGTAAT NATGTGGGAT | 360 |
| GG | 362 |

(2) INFORMATION FOR SEQ ID NO:1277:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

| | |
|---|----|
| TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTCNCCAGA TGGNGTCTCT CTCTNT | 56 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1278:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

| | |
|--|-----|
| CGGTTCCANA CTGTAATTGG TTTCCATCGC CACTTTGCCA CGCAGCACTT TGCATTTNCA | 60 |
| GGTCGCACAG ACGCCGCCTT TGCAGGCATA GGGCAGATCC GCCCCCTGGG GCAATGCCGC | 120 |
| ATCGAGAAAT GCTTTCATCG TCGGCATTAA GCACGATTTC CCGATCCCGC CCATCCTGAC | 180 |
| GTACAGTCAC TTTTNTCCG TNACTTTGCA CGTTAAACGC TACGTTTGAA CGCGCGTGCC | 240 |
| AGGGGTATTA AACCGCTCCA AATGAATGGT TTTTCTGGG CATTCCCAGT GGCTTTTTAA | 300 |
| GGCGGTTTTTC CGGGTNCATC CATTCAATCG NCGNCGGGNC CACAAATAAA ATGGCCTCNT | 360 |
| CCTTAAAGAC | 370 |

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

| | |
|---|-----|
| GGTTTCGCCA GTGAACGAAC TGCTCACCCA TCAGGCGCAT CGNCATATCC ACACCTTTGC | 60 |
| GGNTCAGCGG TTCACCNTTN TTACCGATAA TGCGGTTTCTAG CGAAGCGGGA GAGGCTGGCT | 120 |
| TCGTTATGGG TGGAAACCAG TTTGCCAGTA AACAGCAGCC CCCAGGTGGC GGCATTAACA | 180 |
| AACAGTGACG GGCTACGAAC CAATGTNTGA CTGCCAGTTA ACCGTTGCTG ATTTTTTCGC | 240 |
| GGAATTAAAC GCGTCGGGGG TGGGCTTTGT CGGGGAATAC GCAACAACGG TTTCCGCCCA | 300 |
| GACACATTCN GCGGCCAAGG CTTTCCTGCG NATTGACCAG CGGAAAAATT CCTGGCAATT | 360 |
| AANCCCTTGG GACCATAACC TGGGNGGACC CATTGGGNAT TTTTTTGNAT TACGGCGTTT | 420 |
| TTTTCCGGCC CANTTG | 436 |

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

| | |
|---|-----|
| TGGCGCAGGC NCTGTTTGCT GATCCGGATN TTCTCCTGCT CGACGAACCG ACCAACAACC | 60 |
| TCGACATCGA CACCATTTCG TGGCTGGAAC AGTGCTGAAC GAGCGTNACA GCACCATGAT | 120 |
| CATCATCTCG CACGACCGTN ACTTCCTTGA ACATGGTCTG TACCCACATG GCGGATCTGG | 180 |
| ATGACGGCGA GCTGCGNTTT TATCCGGGTT NTTGNCGNAT GGAGTACATG ACGGCGGCGA | 240 |
| CCCAGGCGCG TGAAACGTNT GCTGGCCGNT TAACGNCAAG ANGAAAGCGC AGATTGNTGA | 300 |
| GTTGCAATCT TTGGTTTAGC CGCTTTTAGG GC | 332 |

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

| | |
|--|-----|
| GGCCATCCNC TGGGCCTGCA GGTGCATGAN GTCGCTGGTT TTATGCAGGA TGATAGCGGT | 60 |
| ACGACCTCGC GGCACCGGCA AAATATCCGT ACCTGCCCTG CACCCGTNTT CTCCAGCCGG | 120 |
| GCATGGTGTT AACCATCGAA CCGGGTATCT ACTTCATCGA ATCGCTACTG GCACCGTGGC | 180 |
| GTGAAGGGCA GTTCAGCAAG CACTTCAACT GGCAGAAAAT TGAAGCACTG AAACCGTTCG | 240 |
| GCGGCATTCTG TATCGAAGAC AACGTGGTGN TCCACGAAAA CAACGTGGGA AAACATGACC | 300 |
| CGGGATCTGA AACTGGCGTG ATGGAAAGCT GGTTAATTCC TGCGGCACCG GTCACGTTCTG | 360 |
| TTGGNGAGNT CAAAAAGAGC CGGTTTCATA ACGATGTTGG GNGCATACCG TGGCGTTTTA | 420 |
| GGCGGCGAAA GNTTTTTTTT GAATCGGTTC GGGAAGAAAA CCCCNTTN CCGGAACATT | 480 |
| TTTTTTGGGT TGTTTC | 496 |

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

| | |
|---|-----|
| TAATGAAGAA AACTCCNGGN TGTGGATNTA CCGCAAGCTN GCGGCGGGC TACTCGGAAT | 60 |
| TTTAATGGTA CCGGTGCTCG CGGCCTATAC CACCTATNCT NTGGNAGATA AACCGGCGTT | 120 |

ACGCCAGGCT TTGCGGCTGG ANTTGCNGCC AACATGATCG GCTCCGGGTT TNTCGGCGCG 180
GTCGTTGGCG GNTTGATANC CGGTTACTT 209

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

TACACACAGG CCAAAGAATC CTGGGAGATG GATACCAAAG AAAAATTGGA GCAGGCTGCC 60
ATTGTCAAAG AGAAGGGAAC CGTATACTTC AAGGGAGGCA AATACATGCA GGCGGTGATT 120
CAGTATGGGA AGATAGTGTC CTGGTTAGAG ATGGAATATG GTTTATNAGA AAAGGAATCG 180
AAAGCTTCTG AATCATTTCT CCTTGCTGCC TTTCTGAACC TGGCCATGTG CTACCTGAAG 240
CTTAGAGAAT ACACCAAAGC TGTTGAATGC TGTGACAAGG CCCTTGGA CTGACAGTGCC 300
AATGAAGAAA NGCTTGTATT AGGAGGGGTG AAGCCCAGCT GGTTCATGAA ACGAGTTTNA 360
GTCAGCCAAG GGTGGACTTT TGAAGGAAAG TGCCTNGNAA GTAAAACCCC CAGANTTAAA 420
GGCTGCAAGA CTGGCAGATC TCCCATGTGG CCAGNAAAAA GGGCCAAGGG NGCACAACGG 480
AGCGGGGANC CCCAGGATTT T 501

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GGAGCCGGGG AATCTGCGCC ANTTGATGAT CCCGGAACAG CAGAGNCCTG CTGGAGACGT 60
TTACGCTGTT AGTCGCCAAT GCCCTTNAGC GGCTGACGCT AACCGCCAGC NANGAACAGG 120
CGCGGATGGC AAGCGAACGT GAACAGATCC GCAACGCCCT GCTGGCGGCG CTTTCGCATG 180
ATTTACGCAC GCCGCTTACG GTGCTGTTTG GTCAGGCAGA AATCTTAACG CTCGATCTGG 240
CAAGCGNANG ATCACCCAC GCCCGCCAGG CCAGCGAGAT CCGTCAGCAT GTGCTGAACA 300
CTACCCGACT GGTGAATAAT CTA CTG GATA TGGCGCGAAT TNCAGTCCGG CGGCTTTNAT 360
TTGAAGAAAG AGTGGTTAAC GCTGGAAGAA TAGTCGGCAN GCGCTGCAAN GCTGGAACCG 420

GT'TTTNNNTT GCCCNTCATG TTTNNTTNNN CAGAACCNTG AACCTAATNC CAGTTGAANG 480
GGCCATTNTT NNAACGGGTG CTGATTAATC TG 512

(2) INFORMATION FOR SEQ ID NO:1285:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 485 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

ATTGTTTTTAA AAAAGATTAT ATCTTTACGT CCGTAACCGG AGATTTCCCG CAAAGCCAAT 60
TTACCGATAA TGAAATATCG TCTTTTATAA GGATATCTAA GATGCGTAAA ACAGTGGCTT 120
TTGGCTTTGT CGGTACCGTA CTGGATTATG CCGGGCGCGG CAGTNCAGCG CTGGTCAAAA 180
TGGCGTCCGA CACTCTGTTT ATGCCAGCAA GAATCGTTGG TCATCGATCG ACTGGAATTG 240
TTGCACGACG CCCGCTCCGC GCTCGCTAAT TTGAAACGCT TAAACGCGAT TATCGCCAGC 300
NTTTCGCCAG AAACAGNAAG TGGTGAGCGT TGAGATTGAA CTGCATNAAC CCTGGGATTT 360
CGAAGAGGTC TACGCCTGTC TGCATGATTT CGCCCTGGTT AAGGAGTTTT CAGCCAGAAA 420
AGGAAGANCT TTTATTTTAC NTCACCACCG TTACCCAGTG GNNGCNATTT GCTGGTTTTN 480
GCTGG 485

(2) INFORMATION FOR SEQ ID NO:1286:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

TATAAGCAAC GTGATGCCCT TGTGGGTCGC GCTTTTAAA GATCCCCTAC TTGNNGANCT 60
CTTCAAACGT TGGCAGTTCA GGAATNGCTT CCCGCGACTG GGCATACAGA TGCCGNATCC 120
ACTCTTCCTG GGTACGGCCT TCAGTAAACT GTTGCTCAAC GCCAAGACGT TTNCCANTT 180
CGCTGGTTCA TTTCATAGAT GGTCTTACAT TCAAAGCGCG GNTTAATCAC CTGATCGTTG 240
AAAATCACGT AAGGCNTATN CCCGAGTAT GCATCCAGCG NAAAGTCCAT CTGTTNCGGA 300
AGCGGTNCAG TCAGGCAGCA GGATGTCCAG CATA 334

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

| | |
|--|-----|
| TGACTCACTG CTTTGCAACA CTCCGTGCTC TCATCGCCAA GTTTGGAGAC TTACTCTTCG | 60 |
| AAGTGGAGGT GGAACAGTGT TTCGACCTAT GTCACCAAGT CCTGCANCAC TGCAGCAGCA | 120 |
| GCATGGGATG TCACCCGGAG ACAAGCCTGT GCCACCCTTT ANCTCCTCAT GAGGTTTCANT | 180 |
| TTTGGGGCCA NCCAATAATT TTTCAAGNTT AAAGATTCAA GTAACCCAAG GCCCN | 235 |

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

| | |
|--|-----|
| GGCACGAGGG AGCCGGCGCC CGNGGAGCA AGAGGAGGAG GAGGAGGAGA GGTCGGAGCC | 60 |
| GTCTCCAGGA GCCCTTAGAG ACCGAGTCCC GGCGGCGACG GCGGGGCAGC GCACCGGCAG | 120 |
| GCGGNTTCAT TCCACTTAAA ACCTGAAAAC ATTGGACCAC ACAAAGTCTT ACTGATTTCA | 180 |
| GGTAAAAACA ATAATTGAAG ATGTCCAGCA AAACAGCAAG CACCAACAAT ATAGCCCAGG | 240 |
| CAAGGAGAAC TGTGCAGCAT TNAAGATTAG AAGCCTCCAT TGAAAGAATA AAGGTTTCGA | 300 |
| AGGCATCCAG CGGACCTCAT GTCNCTACTGT GAGGAACATG CCAGGAGTNA CCNTTGCTGA | 360 |
| TAGGATTACC AATTTTCAGAA AACCNNTTCA GGNTAAAAAA ATTGCTNCTN TTNTATGGAT | 420 |
| NGAGAAACAG TTCTTGGCTT TTTCCCAACA NGGCAATTAT GAGCAGTCTT GAGGGGTTTA | 480 |
| CNTCAGTTAT TTGGTAACCA TGTT | 504 |

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

| | |
|--|-----|
| AGCGAGGCAC GCAGCCTACT AGGTGTGGCG GCGACCCTGG CCCCAGGGTTC CCGTGGCTAC | 60 |
| CGGGNGCGGC NAACCCGCGC GNGAGCCGAA ACGCCCGGTG GNCNAGACCC CGAGGACCTC | 120 |
| | 120 |

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

| | |
|---|-----|
| GGCAGAGCTT CACAATAGAA GTGGAAAGGG CCCTGAGAGT NTTGGATGGT GCAGTCCTTG | 60 |
| TTCTCTGTGC CTGTTGGAGG GGTACAGTGC CAGACCATGA CTGTCAATNG TCATTGANGG | 120 |
| CGCTACAACG TTCCGTTTCT AACTTTTATT AACAAATTGG GACCGAATGG GCTCCAACCC | 180 |
| AGCCAGGGNC CTGCCAGCAA ATGAAGGTCT TAAACTTAAA TNCATAAATG CAGCGTTTTA | 240 |
| TGCAGATACC CATGGGNTTT NGGAGGGTAA ATTTTAAAG GTNTTGTTAG GATCTTTATT | 300 |
| NGAGG | 305 |

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

| | |
|---|-----|
| GGCAGAGGNC GCTTCCTGGG CCGCTTTGGT CTGCAGCCCC AAAAAACCAA ACTNNTTGGG | 60 |
| GCAACCACCC TGCGCCTTTT TAACATTCCG CAGCGCTGCA GAGAGGGACA AGGCCCTGCG | 120 |
| CCGTTTTGCA TGGTGCCCTC TGGGAAAGGC CGCCCACTCA GTGTGCGCCT GTCCCCGGCC | 180 |
| CAAGGGCAGC CCCATGGCCA GGAGGAGGCG ACAGGAGGGT GAGAGTNAAG CCACCAGTGA | 240 |
| ACACGAGTGG CCGACGTGGT GACCCCTCTA TGGACAGTGC CCTATGCTGA GCAGTTGAGC | 300 |
| GGNAGCAGCT GGAGTNCAG CANGTGCTGC AGAAATTGCC AAGAAATCGG GAGCACCAAC | 360 |
| CTGCCTTGTT GCCTGGTTGT TGAGCAAGGC ACAAGCACAA CAAGGCTGTN NCCGTTGAGG | 420 |
| GGGTCAGNCT TANCCCNCAA TT | 442 |

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

| | |
|---|-----|
| AAAAAATGGG ACCTCGGCGA CATCCTCGGC GCGAAAGGTA AGCTGTTCAA AACCAAAACC | 60 |
| GGCGAACTGT CTATCCACTG CACCGAGTTG CGTCTGCTGA CCAAAGCACT GNGTCCGCTG | 120 |
| CCGGATAAAT TCCACGGCTT GCAGGATCAG GAAGCGCGCT ATCGTCAGCN TTATCTCGAT | 180 |
| CTCATCTCCA ACGATGGAAT CCCGCAACAC CTTTTAAAGT GCGCTCGCAG ATCCCTCTCT | 240 |
| GGTATTCGCC ATTCCATGGT GAACCGCGGC TTTATGGAAG TTGAAACGCC GATGATGCAG | 300 |
| GTGAATCCCT GGCGGTGCCG CTGCGGTNCC GTTTANTCAC CCACCNTAAC GGGTTGGATC | 360 |
| TTNGACATGT TACCGCGTTA TCGGGCCGGA ACTGTAACTT CAAGGGTTTG GTGGTTGGTG | 420 |
| GNTTCGAGCG TGTATTCGAA TCAACCGTAA NTTTCGTAAAG AGGTNTTTC GTANGTN | 477 |

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

| | |
|---|-----|
| TTAATGGTAC CGGTGCTCGC GGCCTATACC GCCTATTCTN TGGCAGATAA ACCGGCGTTA | 60 |
| GCCAGNNTTT GCGGCTGGAC TTGCCGCCAA CATGATCGGN TCCGGGTTTC TCGGCGCGGT | 120 |
| CGTTGGCGGN TTGATAGCCG GTTACTTGAA TGCCTGGGT GAAAAATCAC TTGCGTCTTA | 180 |
| GCAGTAAAT TCAATGGATT CCTGGACTTT TTATCTCTAC CCGGTGCTCG GTANTTGGGA | 240 |
| GCGGGCAGTC TGATGCTGTT TGTGGGTGGG GGAAGTGTTC GCCTGGGATC AATAACTCGT | 300 |
| TTAACCGCCT GGCTTGAACG GTCTTTTCAG GAAGTAAACG GGCTGTTTGC TTGGGTGNCC | 360 |
| ATTCTCGGTT TTAAGGGGTT CCCTTTGAAC CTTGGAGGGG CCATGAATAA AAGCCGTAA | 420 |
| GCANTTCTGC CCGGGGGNAA TGGGGAACGG GGTTTAAGGN CCNTATGCCA TTTGGGCTCC | 480 |
| GTNAAAA | 487 |

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

| | |
|---|-----|
| AGCTCAATCC CGNCNCCGAC AAGACCCAGC GGNTTGGTGC CGGACTGTNG CGATTTTCCG | 60 |
| TCCTNTTGCT TCGCGACCAA AGCCAGGCAG TGTTCAGCAC GTCGTGGGCG ACCNNGNCCT | 120 |
| CTCAAGTCGT CCGTGGTATT ATCACCCGNA CG | 152 |

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

| | |
|--|-----|
| GGCAGGAGCC GGCNTCCCCC ATCCCCCGGT TCGGACCGNC GAGCGCCGGC TCTCCCCCTCC | 60 |
| CTGAGCACCG ATCCCAAGTT CCAGCTAGAG AAGGTGGGCG GCACGCAGCC CGGCGGCCCC | 120 |
| TCCCAGCTCC CAGCGATTG AGAGGGAAGA TCTGATCTCC TAGAATTAGA GTTGGTACAG | 180 |
| AAACCATTTC AGCTCCAAAA ATGTTGGAGG AAGATATGGA AGTCGCCATA AAGATGGTGG | 240 |
| TTTGTAGGGA ATGGAGCAGT TGGAAATCA AGTATGATTC AGCGATATTG CAAAGGCATT | 300 |
| TTTACAAAAG ACTACAAGNA AACCATTGGA GTTGATTTTT TGGAGCGGCC AAATTCAAGT | 360 |
| TTAATTGATG ANGATGCAGA CTTATGTTAT NGGGCACTNC AGTCAAGGAG GAATTTTGNT | 420 |
| GCAATTACAA AGGCCTACTT ATCCGGGGAG CCCAGGCTTG TGGTGCTCGG TNTTCCTNTA | 480 |
| CCACAGGTAG GGGATT | 496 |

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

| | |
|---|-----|
| AGCGGTTCAT CCCCTTCCGG CGTCAGAGGA AAAGGTTAAT TTCTCTCCCA CCACCTGGGT | 60 |
| TTCGACGATT TGTCCGTTGT CCATAACCGT TACCCGCTGG CAAAAGCGTT CTACCAGGCG | 120 |

| | |
|---|-----|
| TGAATCGTGG GTGAATGAAC AGGCAGGCGG TGCCAAACTG TTNNTGTAGC TTTTTCAGCA | 180 |
| GGCGAATGAA CACCCGCCTG TGAACACGAG ATCAAGGTTA GAAACGGCTT CATCCAGAAT | 240 |
| CAGTAGTTTC GGTTCGACCT TCANCGCGCG ACCAGGCAGA CGCGCTTGTA GCTGGCCGCC | 300 |
| GTTTAACTGC GGTGGGNCTT TNTNGAGAAC GCTGTTTATC GAGATCGACC GNCTTCAGNA | 360 |
| NTTTCGTTGG CGGGCGNCAT TTGTTCCGGA TTTTTCCTCA TGATTAGCAA GTTGGCGCAT | 420 |
| CGGTTTCAGGN AGNTTTTCGG GAAGGTTTTT CGGGAATTCA GGGGTTNTGG GNT | 473 |

(2) INFORMATION FOR SEQ ID NO:1297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

| | |
|--|-----|
| GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA | 60 |
| CCTTCACGGT AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTTAG CTGGATAAGC | 120 |
| GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGGTGTAATC CTGCATACGC | 180 |
| GGANATNCAT CAACATCCGG GTTATAGCGA TAAATTNANA AACTCGAGTC TCATTTTCCT | 240 |
| GTCTCCGCAT TAGTTAAGTA CGGAATCTTN GGTGCGGGGAT TGCCNGGGCG GCATTTTCGG | 300 |
| GTTTCCCATG TTTGAACGTT TTCGGNGGCG TTCANNGGAT TTCCCGAACT T | 351 |

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

| | |
|---|-----|
| TGCATAGTCT GGCAGGATCG CTGGATGTNG CCGATCGCCA AATGGTGGA ATCGTCNGCG | 60 |
| GGCTGATGCG CGACTCGGGN ATTCTGAATN CTCGATGAAC CTACCGCCTC GCTTACCCCT | 120 |
| GCGGAAACCG AACGCTTGTT TAGTCGCTTG CAAGAGCTGC TTNCTACTGG CGTGGGTATT | 180 |
| GTTTTTATCT CGCATTAAAG TGCCGGAATA TTCGCCAGAT TGCCGNATCG AAATTAGCGT | 240 |
| GATGCNCGAG CGGGAACCAT CGCCTTNAAG GGGGCAAAAC CAGCGGAACT GTTCTNACCG | 300 |
| ACGACATTTA TTTCAGGCCA TNCACCCAG CGGGTAGNGG GAAAAATCGG TCTTNTG | 357 |

(2) INFORMATION FOR SEQ ID NO:1299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

| | |
|---|-----|
| GGCANAGCCT GATCCGACCC CGTCCCGCNG CGCGCCCGNC AGCCATGAGC TCNACGCATT | 60 |
| GCAACAAGGG CCCCTCGTAC GGGCTGTCGG CCGAGGTCAA GAACCGGCTC CTGTCCAAAT | 120 |
| ATGAACCCCC AGAAGGAGGC AGAGCTCCGC ACCTGGNTCG AGGGACTCAC CGGCCTCTCC | 180 |
| ATCGGCCCCG ACTTCCAGAA GGGCCTGAAG GATGGGAACT ATCTTATGCA CACTCATGGA | 240 |
| ACAAGCTACA GCCGGGCTCC GTCCCCAAGA TCANCCGCTC CATGCAGAAC TGGCACCAGC | 300 |
| TAGAAAACCT GTCCAAC TTC ATCAAGGNCA TGGTCAGNTA CGGGCATGAA CCTGTGGACC | 360 |
| TGTTTCGAGGG CCAGGAACTG TTTTAGAGTT GGGAAACATGA NGCAGTTGCA NGTGTTTTTT | 420 |
| TTTNGNCCTG GGTGGGAAG GNCAAGATTA AGGGGTTG | 458 |

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

| | |
|---|----|
| GGCAGAGCAA CAAAGGAGCC AAGGGNGACC GAGGCTTGCC TGGNACCCAG AGGCCCCCAG | 60 |
| GGNAGCTCTT N | 71 |

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

| | |
|---|-----|
| TTNGCAACCA CGATTTTCGC GTCGGTTGGG TTTTCCAGCA GGTATTCTGC CAGCAGTTGC | 60 |
| TTCATCTCCT GTTCAACCGC CGATTTCACC TCAGAAGAAA CCAGTTTGTC TTTGGTCTGG | 120 |

| | |
|---|-----|
| GAGGAGAATT TCGGGTCCGG CACTTTCACG GAAACAACCG CAATCAGGCC TTCACGCGCA | 180 |
| TCGTCACCGG TGGCGCTGAC TTTGGCTTTT TTGCTGTAGC CTTCTTTGTC CATGTAGGCG | 240 |
| TTNAGGGTTA CGGGTCATCG CCGCACGGTA AGCCTGCCAG GTGAGTACCG CCGTNCACGT | 300 |
| TGCGGGATGT TGTTGGTAAA GCAGTNAGAT GTTTTGCNTG GGANGCCN | 348 |

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

| | |
|--|-----|
| GGNAGAGCGG GATCAGAACA AGTACAAGGA GGCTGCCCAC CTGCTCAATG ATGCTCTGGC | 60 |
| CATCCGGGAG TAAACACTGG GCAAGGACCA CCCAGCCGTG GCTGCGAACA CTAAAACAAC | 120 |
| CTGGNCAGTC CTGTATGGCA NGAGGGGCAA GTACAAGGAG GCTGAGCCAT TGTGCAAGCG | 180 |
| GGGCACTGGN GGTTCTGGGAG AAGGTCCTGG GCAAGTTTTC ACCCANATGT GGGCCANGCA | 240 |
| GTTTAGGAAA NNTGG | 255 |

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

| | |
|---|-----|
| GGCAGAGGAG GAAGGGGTCT CGTCGGAAGG CGCTGGACGG GGGTGACCGG GAATCGGGNA | 60 |
| CAGGGACAGA GATAGGGACA NGGACAGGTC ATCCAAGAAG GNCCGNCCCC CCAAGGAGTT | 120 |
| CGGCGNCTTC CTCAGGG | 137 |

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GGCANAGGTA AACAGGGTG AACCTGGTGT GGTGGTGCT GTGGGCATGA CTGGTNCATC 60
TGGTCCTAGT GGACTIONCCAG TAGTGAAGGG GTGCTGCTGG CATACTGGT AGGGCAANGG 120
NAGTTAAAGG GTNAACCTGG T 141

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

GCATATTGTT GGCGGTAGTN AGGCAGTCCT GGAACNNCGN CGGCGCTTTC TTGAAATCCG 60
CTGGTTAAGN CACCGGCGTC GCTGGCGAAT CTGGTATTAC TCGGTTGGTT ACTCGGCGTG 120
CAATATGCCC GTGCGNCATA AATATTNTTA GTGGTCGGCA ATATCCTCAA CATTGTGCTG 180
GATGTCTGGC TGGTGATGGG GCTGCATATG AACGTGCAGG GCGCGGCGCT GGCGACGTTT 240
ATTGCGGAAT ATGCAACATT GCTGATTGGT CTGCTAANGG TGCCTAANAT CCTCAAACCTA 300
CGCGGAATTT TCCGGCGNAA TGCTGAAAAC TGCCNTGGCG AGGNAACTTN CNTTGGTTTG 360
NTGGGGGTTT AACCGGGATA TCAAGCTGCG TTCNCTGTTG TTGCAANTNG TTTCGGGGGG 420
ATCANCTACT TGGGGCCNAC TGGGGGGTGC CTTATCNTTT TAACGGGTT 469

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GGCANAGCGT TTGCGNAGGC TGTTCCACCG CCCTGGGAGG CAGCAGCTTC TTCGAGAAGG 60
AATGGAGCCC NNTTTTGCCC CGAGTGCTAC TTAAAGCGCT TCTCGCCAAG ATGTGGCTTC 120
TGCAACCNGC CCATCCGACA CAAGATGGTG ACCGCCTTGG GCACTCACTG GCACCCAGAG 180
CATTTCTGCT GCGTCATTGN GGGGAGCCCT TNGGAGATGA GGGTTTCCAC GAGCGCGAGG 240
GCCGCCCTA CTGCCGNCGG GACTTCCTGC AGNTGTTTCG CCCCAGGTTG CCAGGTTGCC 300
AGGCCCCATC TTGGTTAACT ACATCTNGGN GTTCAGGGNT TCTGGGACCC GGANNTTTTC 360
GTTTNCANGG NAATGTTTGG GGCCTTTTTN GGGGGGNATT TTTTNGAGC AANAAGGCN 420

CCCTTTTGG AGAAACCATT TCCAGGAAGA AGGGGTGTT TTGNCAAGT TTGGTTCCC 480
TNTAANC GCC TTTGTT 496

(2) INFORMATION FOR SEQ ID NO:1307:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

TCCGGTATGT NCAAGCTGG TTTNCTGGG GACGACGCTC CTGAGNTGTG TTTCTTTCCA 60
TCGTCGGGTG CCCNAGNTAC CAGGGCGTCA TGGTGGGGCA TGGGCCAGAA GGACTCCTAC 120
GTGGGNNACG AGGCCCAGTG GCAAGCTTGG CATCCTGACC CTGNAAGTAN CCCATTGAGC 180
ATGGGNATCG TTAACCAACT 200

(2) INFORMATION FOR SEQ ID NO:1308:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

CCGCAGTTTC GCTTCGGCGA GNGTGTGTG AACCACTTAG CGTCCGTTGG ATCAGCGCAT 60
CCAGCTGCGG GTCATTGAGT TGTTTCCACC ACTGCGCCTG AGNCCAGCCG GAGCTGCANA 120
GAATGAATAT CGTCGGCCAG TTTGAATTTG TTCCGGTTTG AGCTGTCAGT GGCATAGGGG 180
CAGCGCGGGT TAAAGCAGGC AGCCGTTTCG GCGGTTTCGTA CTTGCCGGGA ACGACACCTG 240
GCAACGACGC CAGACGTTCT TTGTCCTGAG CAAATTCTGG CAGCGCACGC AGCAATGCCT 300
GAGTATAACG GGTGACGCG GCGCATGGTA AGATGGCGTG CCGCATTCAC CGGTTTTCCA 360
CCAACTGGGC TTGCATAACA TCACGATGAT TTTANTGTTG CCCGTTTCCG NCAACAAGGC 420
CAGTTCATGG GTAATTAAAC ANCAGGGCCA GTTNTTTTTT TGGTTTNAGT TCCCACA 477

(2) INFORMATION FOR SEQ ID NO:1309:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

| | |
|--|-----|
| AGCCACCAGN GCTGGGACGC GCGGGCANGG CGGCGGCGGC GGCCCTCCGG CAAAGCGAAG | 60 |
| GCTGGNAGNT AGGAGAAAAGC GGTCATCAGT ACCTCTCAGA TGGTTTAAAA ACCCCCAAGG | 120 |
| GTCAAAGGAA GAGNTGCACT ACGNNGTTCC AGATAGTCCA AAAACTCCAA AATCTCCCTC | 180 |
| AGAAAAACG CGGTATGATN ACGTCTCTTG GTCTGNTCCA CCAAGNAAGT TCATTTTCAGC | 240 |
| TTCCTGCAGC CAGTTCACCC GATGGGGTAT TGGNATTTGN AACAAGGTCA GNCAGNNGTG | 300 |
| CTNAAAAGTG CAAAAGAGGN AGGTTTTTTG NTTATNCACC AACGTTTTTG TAAGGNCTNC | 360 |
| CACCTGNITT AAGAAGTAGT TNTAAAAACA ACGTNCCAAT GGGTGGGGTT GCATTCTGTT | 420 |
| CTGAGGTTGG GGGNATGTTT NGCCCATTTT CAAGGTCTGT TCAAAGGAGT NACCCGGTTC | 480 |
| AGTCAGGAG | 489 |

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

| | |
|---|-----|
| TTTTTCTGG GCGGCCGCTG CGACACGGGA CTGACTTNGG GATGGGAAGT GGAGTNCCCG | 60 |
| GAGCTGCTAC CGTGGCGGCG GCGCTGTGAG GAGCAGCCAG GGGGAGGCAG CTGCGGCTCG | 120 |
| CCNNTGAAGT ATCCGGGAAA GCGCCACCAT GGGGCTCCGT GAAGAAGAGC ACCAAGAACC | 180 |
| CCCCGTTCT CAGCCAGGGA ATTCATCCTG CAGAAATCATG CGGACATCGT CTCCTGCGTG | 240 |
| GGGATGTTCT TCCTGCTGGG GCTTGTNTTC GAGGGAACAG CAGAAGCATC CATCGTGGTT | 300 |
| TCTCACTNTT TCAGCACANT GTTTGCTGTA CCCTGCAGCA GAGGGAACAA GCCACGGGGT | 360 |
| TCAAAGNCCC CCTNTTTTTT ATGGTGTTC AAGATTNNGG CCACGGTTTT TTTNTTACAA | 420 |
| GGTGGTGGGC AATCATNTT CATGNCACAT TTCAGGAATA NGTGTGTTGGN TAAATTAAC | 480 |
| AAGAGAATGC | 490 |

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

| | |
|---|-----|
| GGCACGAGGT TGGGCTCCCG CTGGAGTNTG CGTTGGGGGC GGACCAGGAG CGGTGGTCTC | 60 |
| NAGGGAGGTC GAGGCTGGGG CTCCCACCCG GATTTGGAGC AGGGTCGCCG CGGCCAGCT | 120 |
| GAACCCGCCG GCNTTTGTAC GTTGTGTGCC CACTCAGGGA GCCATGGACA ACTGTTTGGC | 180 |
| GGCCGCAGCG CTGAATGGGG TGGACCGACG TTCCCTGCAG CGTTCAGCAA GGTTGGCTCT | 240 |
| AGAAGTGCCT GGAGAAGGGC CAAGAGGAGG GCGGTGGACT GGGCATGCCC TGAAGCNTC | 300 |
| CCAAAGGCTG CATGGGGGTC CTTGCCCGGG AAGTGCCCCA CCTAGNAGAA ACAGCCGGCA | 360 |
| NCCGGCCCCG ANCGGTTTTT CCCGGGGGNA AAGAGAAGAG AGACCCCAA CCTTTAGTGN | 420 |
| TTTCCTTTCA GAACAATGGC TGAATTCAT GGATTNTATT TCAATTCANT NTGGGAATA | 480 |
| NTANTTCATT GTGGCC | 496 |

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

| | |
|---|-----|
| GGCTGCTGGG TCACGGCGAT TCGCCGCCAA CCGTACCCGC TGGTACTGCG CGACTGNTTN | 60 |
| AACGCTTAAC CGCTGCGCAT GAAATCAGGN ATATCGACCG TTTGCTGGAG GTGCTGCATG | 120 |
| GCAACGGTTA ATAAACAAGC CATTGCAGNG GCATTTGGTC GGGCAGCCGC AACTTATGA | 180 |
| GCAACATGCA GATCTACAGC GCCAGANTGC TGACGCCTTA CTGGCAATGC TTNCACAGCG | 240 |
| TAAATACACC CACGTTACTG GACGCGGGTT NTGGANCTGG CTGGNTGAGC CGCCATTGGG | 300 |
| GNAACGTTCA CGCGCAGTGG GCG | 323 |

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

| | |
|---|----|
| ATGGCGATAT CGGCGGCGAG ATCGNGATCC GCATCATCGA AAACGATCAG CGGTGATTTA | 60 |
|---|----|

| | |
|--|-----|
| CCGCCCAGTT CCATGGTCAC TTCTTTCAGG GAAGAGGCCG CCGAGTTAGC CATCACTTTT | 120 |
| TTGCCGCTGG NGACACCGCC GGTAATAATGA ACACTTTGGC AATGCCCCGA TGCTCGGTCA | 180 |
| GATAATTGCC CCGGTNTNCG GGGCCCAAGN CCNGGCAACA AGGTTAAATT ANGG | 234 |

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

| | |
|---|-----|
| CAGGAAAGAC TATGGAACGG AGCGTCANCG TGCCTTTATC AATGCCGAGA ATATCCAGCC | 60 |
| ACTGCTGCAC CAGTTTTTGC TGGCGATCCG AAACGGCCTG ATAAATGCCA ATCGAATCAA | 120 |
| AATAGCCAGA AAGAATCACA TTACGCACGG TAGTCTGAAC CCGTAATCC AGATGCAAAC | 180 |
| TACTGCTGAC GTAACCGATA TGCTTTTTGN TATCCCAGAT GGTTTCGCCG CTGCCGCGAC | 240 |
| GTACGTCCGA AAAAGCGTCA AATCGTTGCT GTTAACCTTG CGGATGATNC GNCAGTTAAC | 300 |
| CAGGGTTAAT AAACGTGGNT TTTTCCNGCA CCATTGGGC CCGACAATTT GN | 352 |

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

| | |
|---|-----|
| GGCACGAGCT GCGGCGNCAG NAGCAGCAGC AGCAGCGNGN GGNAGAGGNG GTGGCGGCGG | 60 |
| GGTGGACAGC ACGGCCGAGG CTGCCAGAG GCGCCTCCTC CACACCCCCC GCTGCGGCAG | 120 |
| CACCGNGAA CAGATTTTTT AAAAAATGGA TTTGGCCAAC CATGGACTTA TTCTACTGCA | 180 |
| ACAGTTAAAN GCTCAGCGAG AGTTTGGTTT CCTGTGTGAC TGCAAGGTTG CAGTCGGGGA | 240 |
| TGTATANTTC AAGGGCACAG TAGATNCAGT TACTTANCTT CATTGCTACC AATTAACTTT | 300 |
| TANNATGTTG TTTGTA | 316 |

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

| | |
|--|-----|
| TGTCACTGGT CCAGTCTCGG AAGGCAGGAA TCACTTCTGC AATGGCTACA CGCACTTCTC | 60 |
| TTAAGGACGA NGAGCTGAAA TCCCACGTNT TTAAGGAAAC CCTGCAGGCC TTAATCTACC | 120 |
| CCATTTTCGTG CACCACTCCT CATAACTTTG AAGGTCTGGN NGGCCACTAC CCCAACCTAC | 180 |
| TGCTATGAAG TGTGAAGGNC CTGCTCTGGG GCATTGTCCG GCAGGATGNC GCCTGCAGCG | 240 |
| AAATGTGGAG TCAAGTGCCA TGNGAAGTGC CAGGTATCTG GTTCAATGNT GGACTIONCTG | 300 |
| CCANCGGGNT GNANATAAGA GCTGTGAAAC ATGGAGCTGA GGGACCGGTA CCCAGAACNT | 360 |
| NNNCNTGGGC CNGGAAGGNA CCGCATGGAA GATCCGAGTG GGGAATTAAN GNCAGAGATN | 420 |
| NTTTGNAAAG TTTTTCGGG GANTNTTTTC ACAGTGGAAC AAAGTTGCC NGTGNCAGTA | 480 |
| GNTTG | 485 |

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

| | |
|---|-----|
| GGCAGAGCTC GGCNAGANAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 60 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANAAAGNNG | 100 |

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

| | |
|--|-----|
| GGCANAGAGA AGGAGAAGGA GGAAC TGGAC AGGGGCTGCC GCGAGTCCAA GCGCAAGGTG | 60 |
| GCCGAGTGCC AGAGGAACT NAAGNGCTG GAGGTGGCCG AGGGCGGCAN GGCAGAGCTG | 120 |
| GAGCGCCTGC AGGCCGAGGN CACAGCAGCT GCGCAAGGNG GAGCGGACTG GGAAGCAGAA | 180 |
| GCTGGAGGAG ATGCGCAAGA AGGAGAAGAG CATGCCCTGG NAACGTGGGA CACGCTTCAG | 240 |

| | |
|--|-----|
| CAAAGACGGC TTTCAGCAAA GAGCATGGTT AATTACCAAG CCCGAGAAAG TACGGTAGGA | 300 |
| GGATTCANAG GAGGTTGAGG GGAGCAGAAA CACAAGACCT TTCTTGGGAA AATTACGGGT | 360 |
| AAACAGNTTC AAGCATTTTG GGCATGTTTT CGCCGTTGGG GTTGACAGCC AAAATTACCT | 420 |
| TTTCAGACAAN TTCCACTTGT TTTTCGAGGA GACAGCCCTT TACCTGGTCN TTTGGTGCTT | 480 |
| TGACCTAGAG TTGGAGGGAA TT | 502 |

(2) INFORMATION FOR SEQ ID NO:1319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

| | |
|---|----|
| GGCAGAGTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TNAANAANA | 50 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

| | |
|---|-----|
| GGCAGAGCC ATGATGACGC CCACGGGNNC TTCCAGTACG ACCATGAGGC TTTCTTGGGA | 60 |
| CGGGNAGTGG CCNAGGAATT CGACCAACTC ACCCCAGAGG AAAGCCAGGC CCGTTTGGGG | 120 |
| CGGATCGTGG ACCGCATGGN ACCGCGCGGG GGACGGCGAC GGCTGGNTGT CGCTGGCCGA | 180 |
| GCTTCGCGCG TGNGTTCGCA ACGACGCAGC AGNGCACATA CGGGNNTCGG TGAAGCGCGG | 240 |
| CCTGGGACAC GTACGA | 256 |

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

| | |
|---|----|
| GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTCATGTTCA GACCGTCGGA ACCGCACACA | 60 |
|---|----|

| | |
|---|-----|
| CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGAATCT TTCTCTTTTA GCTGGATAAG | 120 |
| CGCATCCAGC AGCATCATGT CGCGACCTTC ATCCGCTTCC AGGGTGTAAT CCTGCATACG | 180 |
| CGGANATNCA TCCAACATCC GGGTTNATAG CGGATAAATT GAAAACTCGA GTCTCATTTT | 240 |
| CCTGTCTCCG NATTAGTNAA GTACGAATCT TCCGGNGGGA ATGNCCGGGC GCATTTNCGG | 300 |
| TTCCATGTTT GACGTTCCGN GCGTTCATGG GNTTCCGAAC TCTGGGCAGA TACAGGGNAN | 360 |
| TGGGCACANC CATTTTTTCA TCATCAAGAT TCGGGGAAGT CGA | 403 |

(2) INFORMATION FOR SEQ ID NO:1322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

| | |
|---|-----|
| GGGGTAATAC AGGCCAGACC ATTCTTGCCG TTNATGTTCA GACCGTCGGA ACCGCACACA | 60 |
| CCTTCACGGC AGGAGCGGCG GAANGACAGG CTGGGATCTT TCTCTTTTAG CTGGATAAGC | 120 |
| GCATCCAGCA GCATCATGTC GCGACCTTCA TCCGCTTCCA GGGTGTAATC CTGCATACGC | 180 |
| GGANATGCAT CAACATCCGG GTTATAGCGA TAAATTMNA AACTCGAGTC TCATTTTCCT | 240 |
| GTCTCCGCAT TAGTAAGTAC GAATCTTCGG CGGGAATGCC NGGNCGCATT TTCGGTTCCA | 300 |
| TGTTGACGCT TCGGGGCGTC ATGGGTTCCG ACTCTGGNCA GATACAGGGA GTGGCACAGC | 360 |
| AGTTTTCATC ATCAGTTCC GGAAGTCGAA GCGGTTNTGG CGCCAAGGTT TTTCGTANGG | 420 |
| AATTTTGCAG AACAGCNTTG CNTAGGCGTT TCCNTCAGTT ATCCATTCCA G | 471 |

(2) INFORMATION FOR SEQ ID NO:1323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 429 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

| | |
|--|-----|
| GGCANANAGA AAGATCCACG ACTTGGCCCT GGAGCTCTAC ACGCAGAGAT CGCTGCTGGT | 60 |
| GATGGGGCGG GGCTACAACCT ACGCCACCTG CCTGGTAAGN AGCCCTGAAA ATTAAAGAGA | 120 |
| TAACCTACAT GCACTCAGAA GGCATCCTGG CTGGGGAGCT GAAGCACGGG CCCCTGGCAC | 180 |
| TGAATTGACA AGCAGATGCC CGTTNATCAT GGTCATTATG AAGGATCCTT GCTTCGNCAA | 240 |

| | |
|---|-----|
| ATGCCAGAAC GCCCTGCAGC AAGTTNACGG CCCGCCAGTG GNCCCCCATT TNTACTGTGG | 300 |
| NTCCAAGGGA CGATNATTGA AAGTTTCCCA AGTTTGCGTA TTAAGNCAAT TCGAGGTTGC | 360 |
| CCCCACATTG TGGGAANTGC CTTCCNGGGG ATTCTGAGGC GTTGATTTCG GTTGCNATTG | 420 |
| NTGTTTCCTT | 429 |

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

| | |
|---|-----|
| GGCACGAGCN CGCGTGGNTC GCGCACACGC AGCAGCGGCA CATACGGGAC TCGGTGAGCN | 60 |
| CGGCCTGGGA CACGTACGAC ACGGACCGCG ACGGGCGTNT GGNTTGGGAG GAGCTGCGCA | 120 |
| ACGCCACCTA TGGCCACTAC GCGACCGGTG AAGANTTTCA TGACGTGGAG GATGCAGAGA | 180 |
| CCTACAAAAA GATGCTGGCT CGGGACGAGC GCGGTTTCCG GGTGGCCGAC CAGGATGGGG | 240 |
| ACTCGATGGC CACTCGAGAG GAGCTGACAG CCTTCCTGTA CCCCAGAGAG TTCCCTCACA | 300 |
| TGCGGGACAT CGTGATTNCT GAAACCCTGG AGGTCTTGGA CAGAAACAAA GATGGCTATN | 360 |
| TCCAGGTGGA GGNGTACATC GCGGATCTGT ACTCAGCCGA GCCTGGGGAG GAGGAGCCGG | 420 |
| CGTGGGTTCA GACGGAGAGG CAGCANTTNC GGGACTTNCG GGATCTGAAC AAGGGTTNGG | 480 |
| CACCTTGATT GGGA | 494 |

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

| | |
|---|-----|
| GGCANAGCGG CAGANCANCC ACACAGAGAT GGAACATGAA GTGGCTTGCT TTGGACATCA | 60 |
| CCCCATTAGG TAGACAGCAA TGGACTGTCG CCTCTTTGTN CCATTGGCCT CTGGGACGGT | 120 |
| ACATCTCGNN CTCGTGATCT TGAAAGTTGC CCTNTTTTGN | 160 |

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

| | |
|---|-----|
| GGCANAGGCA AGAGTGTCTG GAACAGGNTC GGCTGCTTGG CTTGCTGATG CCATTTAGGG | 60 |
| CATTTNGTGG TGTAAGTTC AAATGGAGCA TTGACCTTCA AAAGNGAGTG ATAGAATCTG | 120 |
| GGCCAGACCA GTTGAATGA CAATGAGATA TACCAAGTTT ATTCCTCCTG AATTATCACA | 180 |
| CACCTCCTTA TCTCACTGGC TGAGGCANAG GTAACCTACC ACCGATTGAA GGCCACAGGA | 240 |
| TGAAGTTTCT GGTGTTGGCT ACTGGATGGG TTGTGGGAGA CTGATGTCAN GGGGCAGGNT | 300 |
| GTGGTTAGGA TTNTGGGTGA GTACCTAACT GGGCATGGNA TNC | 343 |

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

| | |
|---|-----|
| ACGAGCAGGC TATTCTTTGG AGAAGGTATT TGGGCTTCAA TTNAAGGAAA TTGATAAGAA | 60 |
| TGNCCANTNT TACANTCTTA TCAGCACCTT AGAGCCCACT TATGTCAGGN CATTCTCGGA | 120 |
| ACGNNCTAAG GTACTCACCC AAGCTGGGTC TGCTCATGGT GGCTTGCTTA AGCATCATCT | 180 |
| TCATGANNTG GTAAATCGGT CCNGTGGAGN CTGTCATGTG NGGAG | 225 |

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

| | |
|---|-----|
| GGCAGAGACT GACCACAGCC CATGAGCAGT TCAAGGCCAC CCTCCCTGAA TGCCGACAAG | 60 |
| GAGCGCCTGG CCATCCTGGG CATCCACAAT GAAGGTGTCC AAGAATTGTT TAGACCTACC | 120 |
| ACGTGCAATA TGGCGGGCAC CAACCCCTNA CACAACCATC ACGCTCAGG AGATCAATGG | 180 |
| CAAATGGGNA CCACGTGCGG CACTNGTGCC TCGGNAGGGA CCAAGCTCTN ACGGAGGAGC | 240 |

ATGCCCCGNCA G

251

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

| | |
|---|-----|
| GGGNGAATTT CAACAGNCAA CAAAAGAACC TTTCAGTGAG CNGTGCNGCT GCTTCTNTGG | 60 |
| CCAGTTCACG CTCTTCTGTA TTGAAAGACT CGGAATATGG NTGTTTGAAG TTTCCACCAA | 120 |
| GATGTANGTT TGATCATCCA GATGCAGATA AAACACTGAA TCACCTTATA TCGGGGTTTG | 180 |
| AAAANTTTGA AAAGNAAATC AACTACAGAT TCAAGANTAA GGCTTACCNT CTCCAGGCTT | 240 |
| TTACACATGC CTCCTACCAC TTACAATACT NTCAGTGNAT TGGTTNACCA GCGCTTTAGT | 300 |
| AATTCCTGGG TNGATGCGAT TT | 322 |

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

| | |
|--|-----|
| AGTTGTTCCG AGGTGACACA GTGTTGCTGA ANGGAAAGAA GAGACGAGAA GCTGTTTGCA | 60 |
| TCGTCCTTTC TGATGATACT TGTNCTGNAT GAGAAGATTC GGAATGAATA GAGTTGTTTCG | 120 |
| GGAATAACCT TCGTGTACGC NTAGGGGATG TCATCAGCAT CCAGCCATGC CCTGATGTGA | 180 |
| AAGTACGGCA AACGTATCCA TGTGCTGCCC ATTGATGGAC ACAGTGGTAA GGGCATTACT | 240 |
| GGTAAATCTT CTTNCGAGGT TATTACCTTT AAGCCGTNAC TTTCTGGA AGCGTTATCC | 300 |
| GACCCCATCC GGNAAAAGGN GACCATTTTT TCTTNGT | 337 |

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

| | |
|---|-----|
| TGCAACAAAT GGTTTATAAC CTGCCGCCAG ACATTACGCT GGTGAAAGCC ANAGTCTTGC | 60 |
| TGATATGAAN CCGCAGTGNA TAACTTCTAC ACCGCCGAAA AACGCTGTGC CTGAATGCAC | 120 |
| CGCGTAATCC GTTCCGTGGC GTGAAAGCTG TGCAAACCGA NTAAACCGAT AGAACCTGTT | 180 |
| TATGCTAATC GCTTCTTTGA ANGTATTAAG CGAAAAGCAT TCAGCCAGAG CACGCTGATG | 240 |
| CGTTTACTTT CCAGCATCAG TGGGCAAGGC TGGGGGCAAN CAGCCCGANG CGGCGGAAGT | 300 |
| TTTANCGGTT AGCGCCAANT TAAAAGGCGT TACGGGTAAT GGAATTGTT GCGGACCN | 358 |

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

| | |
|---|-----|
| GGCAGAGCAA CCACGGTGTC GCAGGCCAAG GNAGTNCTGA GCGCCGAGCA GCTGCCAAGC | 60 |
| GAGGAGGTGC ACGCCGGCCT GGGCGAANCT GCTGTCCTCA CTCAGCAACT TGACGGCNCG | 120 |
| CAACGTGAAC CTGGATGCTG GGCAGCCGAC TGTTCNCGGA CCCAGCTCAN TAAGCTTTCG | 180 |
| CTAATGAACT TCNTGNG | 197 |

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

| | |
|---|-----|
| CNTGGTNAAC CTGCTCCATN AAACAGGTCC GTNAAAATNT TTAATGTGCG CAATGGAAGG | 60 |
| GCAGATCCTT ATCGCCGACC TCAGGGGTCA TGAAGGTCC TGTTTGGCAA GTGGCCTGGG | 120 |
| CTCACCCCAT GTTACGGCAA CATCCTGGCA TCGTGCTCCT NTGAACCGGA AATCATTATN | 180 |
| TGGAGANAGG AAAACGGCAC TGGGAAGAAG AGCCACGAGC NGGGGGGACA CGANTCCTTC | 240 |
| ATTGAAANTC GGTGTGCTTG GG | 262 |

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

| | |
|--|-----|
| CTCTGGAAGC ATTACTTCCA GANTNNCCCA GGGTCTTATT TTTTGGTAG ATAGCAACGA | 60 |
| TCGTNAAAAN TTTCAGGAAG TAGCAGATGA CCTGCAGAAA ATGCCTTCTG GTAGGTGNAT | 120 |
| TTGAGNAGAT GGCAGTCCTG CTGACTTTTT NCAAAACAAAC AGGNTTTGNC CAAATGCTAT | 180 |
| GGCCATCAGT GGAAATG | 197 |

(2) INFORMATION FOR SEQ ID NO:1335:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

| | |
|--|----|
| GGCACAGGNA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AANNANN | 57 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:1336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

| | |
|---|-----|
| GGCCCCGTCC CGCCGCCCGC CCGCCAGCCA TGAGCTCGAC GCAGTTCAAC AAGGGCCCCT | 60 |
| CGTACGGGCT GTCGGCCGAG GTCAAGAACC GGCTCCTGTC CAAATATGAC CCCCAGAAGG | 120 |
| AGGCAGAGCT CCGCACCTGG NTCGAGGGAC TCACCGGCCT CTCCATCGGC CCCGACTTCC | 180 |
| AGAAGGGCCT GAAGGATGGT AACTATCTTA TGCACACTGC ATGGAACAAG CTACAGCCGG | 240 |
| GGTCCGTCCC CAAGATTCAN CCGGTACCAT GTCAGNAACT GGTCACCAGC TTAGTAAAAC | 300 |
| CTGTNCCAAC TTTCATTCAA GGNCCATGGT GCAGGTTGGG GGATGNAACC CTGTGGAACC | 360 |
| TGTTTCNAGG NCCAAGAAC | 379 |

(2) INFORMATION FOR SEQ ID NO:1337:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

| | |
|---|-----|
| GGCACGAGGA CCCGAGTTCA CCAGCATCCC TGCCTGCTAC TGGTGGGCTG TNATCACCAT | 60 |
| GACGACGGTG GGCTATGGCG ACATGGTCCC CAGGAGCACC CCGGGACAGG TAGTGGCCCT | 120 |
| GAAGCAGCAT ACTGAGCGGC ATCTGCTCA TGGNCTTCCC AGTCACCTCC ATCTTCCACA | 180 |
| CCTTCTCCCG CTCCTACCTG GAGCTTCAAG CAGGAGCAAG AGAGGGTGAT GTTCCGGAGG | 240 |
| GCGCATTCCT CATCAAAACC AAGTNCGCAG CTGAGCGTGT CCCAGGGACA GTNAACATCT | 300 |
| TGTTACGGAA GTGACCTNCT NCGGNACACC AG | 332 |

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

| | |
|---|-----|
| GGCAGAGCCA GTNTCCGCGC CTCCACCCAG CTCAGGAACC CGGGAAACCC TCTNTTGACC | 60 |
| ACTATGAAGC CTCCCGTCCA GCCGCGCGTC CCGTGTCCCG GGTCCTTCGG GCTCCTTGTC | 120 |
| CGCGCTGCTC GGCTGNCTGC TCCTGCTGAC GCCGCCGGGG CCCCTCGCCA GCGNCTGGTC | 180 |
| CTGTCTCTGC TGTGCTGACA GAGCTGCGTT GCACTTGTTT ACGCGTTACG CTGAGAGTAA | 240 |
| AACCCCAAAA CGATTGGTAA AACTGCAGGT GTTTCCTCCG AGNCCCGCA NTGCTTCCAA | 300 |
| GGTGGGAAGT GGTAGCCTT CCCTGAAGAA CGGGGAAGCA AGTTTGTTTT GGACCCGGAA | 360 |
| GNCCCTTTTT TTAAAGGAA AGTGCATNCC AGNAAATTTT TGGGACAATT GGNAACAAAG | 420 |
| AAAAAATTGG GTNAACCAAA AAAGG | 445 |

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

| | |
|---|-----|
| GGCAGAGGGN AGCTCTTGGG GAGCCCGGAA AGCAGGGATC TCGGGGAGAC CCNGTGAATN | 60 |
| CAGGACCCCN TGGAGACTCT GGTACAGCCA GGCCCCAAGG GNAGACCCCG GNCAGGCCTG | 120 |
| GTTTCANCTT ACCCAGGACC CCGAGGNGCA CCCGGTAGAA AAAGGCGGAG CCCGGTNCCA | 180 |
| CGNGGCCCCG AGGGAAGGCC NAGGCGAACT TTGGTTTGAA AGGAGAACCT GGGTAGGTAA | 240 |
| AGGAGAGAAA GGTAGAGCCT NCGGTATTCC TGTTCCCCC TGGTGNAGCC AGTTACCTTC | 300 |
| GGGGGGGCCA AGTAGGTAGT TCCCANGGAC CTCGNAGN | 338 |

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

| | |
|--|-----|
| GGCANAGTGA ACGCCACCT GCCGTTTGCT GTCATTGGCA GCACAGAAGA ACTGNAGATA | 60 |
| GGCAACAAGA TGATGAGGGC GCGGCAGTAT CCTTGGGGCA CTGTGCAGGT TGAAAACGAA | 120 |
| GGCCCACTGN GAACTTTNTG AAAGCTGCGG GAGAATGCTG ATTCGGGTCA ACATGGGAGG | 180 |
| ATCTGCGGGA GCAACTCCAC ACCCGGGCAC TATGNAGCTG TATCGCCGCT GTANCTGGNA | 240 |
| GGAGATGGGC TTCAAGGACA CCGACCCTGG ACAGCAAACC CTTCAATTGA CAGGTGGACA | 300 |
| TATGNAGGCC AAAAGGAACG AGTTCCTAGG GGGGAANTCCC AGNAAAAAAG AAGAGGNGAT | 360 |
| GNGGACAGTT GTTCGTTCCA GCGAGTTCAA AGNGGAAAGG AAGCGGGTTT CCAAAGG | 417 |

(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

| | |
|---|-----|
| GGCANAGNAA ACACCCCAT ATCAAAATGG TGATGGAAAG TGGGGACTGG ACTGGTTGGT | 60 |
| GGAGACCTTN AGGTGCTGGA GAAAATAAGA TGGAATGATG GGCTGGACCA ATACNTCTG | 120 |
| AACACCTCTG GAGCTCNAAC AGAAATGTGA AAGGAAATGT AATNCTGATN CGGTGTTTGC | 180 |
| ATTCCAGTTG CGCAATCCTG TCCACAATGG CCATGNCCTT TTTGAATGCA TGACACTCGT | 240 |
| CGNAGTTCNC TNAGTAGAGG GGGCTACAA CACCCGGTT | 279 |

(2) INFORMATION FOR SEQ ID NO:1342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

| | |
|--|-----|
| GGCANGAGGG ACAGCTAGCC CTGCTGCCCC GCTCCACTGT GCTTCTGCCC TTGGCCTGGG | 60 |
| CTGCTACGTG GCTGCCGCTG ACATCCAGGA CCTGGTCTCT TGCCTTGCCT GCTTAGAAAG | 120 |
| TGTTTTTCAGC CGGTTCTATG GCTTGGGGGG CAGCTCCACA AGTCCTGTGG TTCCTGCCAG | 180 |
| CCTGCACGGC CTGCTCTCTG CTGCCCTGCA GGCCTGGGNA TTGCTGCTCA CCATCTGCCC | 240 |
| TAGCACCCAA ATGNAGCCAC ATCCTTGACA GGCAGCTGNC CCGGCTGCCC CAGNTNCTTG | 300 |
| TGCCAGTGGA AAGTNTGAAC CTGCGGATNG TTGCCGGTGN AAACATTGGC ACTGCTCTTT | 360 |
| GAAGCTTGCC CGGGAACCTN GAGGAGGGAT TTGTTTTTAG GAGGACATGG AGGNCCTTTG | 420 |
| CAATGTTCTG GGGGAATTTGG GCCATTGANA NTAACAATAC CTTGNCAAGG TTGATTCGTT | 480 |
| GGGGGCAAGG TTNTA | 495 |

(2) INFORMATION FOR SEQ ID NO:1343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

| | |
|---|-----|
| GGCAGAGGGC TCTGTCATTG ATTATNAACT GATTGACCAA GATGCTCGGG AATCTCTATG | 60 |
| AACGCTGGAG TGAAGAGGAA AGGAACTGAN TGTTCCCAAG TGGATCAGCA TCATGAACCG | 120 |
| ANCGGANGGN CCCACCTCC AGAAAGTATT TGAATAGGTA CAAGAGTTAC AGCCCTTATG | 180 |
| AACATGTTGG GAAAGCATCA GGGAAAGAGG TTAAAGGAGA CCTGGGAAAA TGCTTTCCTG | 240 |
| AACCTGGTTC ATGGCATTCC AGAACAAGCC CCTGTGNTTT GCTGATCGGC TGTATGACTC | 300 |
| CATGGAAGGG NCAAGGGGAC GCGAGATTAA GGTCCNTGAT TCAGAATTCA TGGTCTTCCC | 360 |
| GCATTGAAGT TGGNCCTGTT TGGAAATTTA GGTCTGGATT TCAAGGGNAA GTANGGGCAA | 420 |
| TTCCCTGTAC TTTTATNTTC CNGCAAGGCA | 450 |

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

| | |
|--|-----|
| GGCANAGCCC CTTTNTTGAA GCCAAGAAG AGTTTGCTCA TAAGACCCTG GCAATGGATG | 60 |
| TNATGAAACC CCGGAGAAAT GATCCTTTGT TGA CTGTCCT TACTCAGGAG AGTTATGTAC | 120 |
| TGTGGNAAGA TGTAGAGACC ATAATCAGTG GAACCACTTA CAGTGGCTTC CCAGTGGTGG | 180 |
| TATCCCGGGN AGTCCCAAAG ACTTGTGGGC TTTGTCCTCC GAAGAGATCT CATTGATTTC | 240 |
| AATTGGAAAA TGCTCGAAAG AAACAGGGTG GGGTTGTTAG CACTTCCATC ATTTATTTTC | 300 |
| ACGGGGCATT CTCCTCCATT GCCACCATAC AATNCACCCA TTNTAAAGNT TTGGGAANAT | 360 |
| NCTCGG | 366 |

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

| | |
|---|-----|
| GGCAGAGTAA AAGCAGACAA CCAGAGGCTA AAGGNTGAAA ATGGGGCCTT GATCAGAGTT | 60 |
| ATAAGCAAAC TTTCCAAATA AAAAAAAAAA AAGCAGCANG NAATGGTGTT GCACATATTA | 120 |
| GTAACCCAGT GGAACCATAN TTNGTN | 146 |

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

| | |
|---|-----|
| GGCAGAGCNA GGNGCCAGTC GTGTGAGTCC AATCCTAACC TGGGCTATCC CTGCAATCAT | 60 |
| GTCATGCTCT CCTGCTGTGA AGGGTGAAGA GCCTCTCATA GTACCTGAAG GTTCGCCGAC | 120 |
| CTCCAGAGNC CGCAGNTGCA CCACGGAGAG TTTCAGAGGC AGAGATGGCG GGCCGAGAGC | 180 |

| | |
|---|-----|
| TCGNTTCACT GGGCACAGAG GCCGAGCTGC CGAACAGNCT GCCGGGCGAT GTACCAGGAT | 240 |
| GAGTGCCTTC TCCTNCCGGG GNGAGCTGTG CCAGCACCTT TGGCATCAAT AATTGTGGGT | 300 |
| TTTTTACCAT GTGGCTGGTT TTTCCTGGGT TTTTCAATGG CAGNACGNTG GGCCGCAATT | 360 |
| NTNCGNCCA | 369 |

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

| | |
|---|-----|
| GGCAGAGGNA GGGGAGGCTC CAGCCCTCGG NAGTAAATAT CTTCCCTTCC AACCTGGTGT | 60 |
| CAGCAGCCTT TCGCTCATAC TCTACCACCT ATGAAAGAGA GGAATATCAC CGGAACCAGG | 120 |
| GTGAAGGTGC CCGTGGGGCA GGAAGGTGGA GGGGATGAAC ATCCTGGGCC TTGGTAGTGT | 180 |
| TTGCNATCGT CTTTGGTGTG GCGCTGCGGA ACTGGGGGCC TGAAGGGGAA GCTGCTTNTC | 240 |
| CGCTTNTTNA ACTCCTTTNA ATGAGGCCAC CATGGTTCTG GTCTCCTGGA TCATGTGGTA | 300 |
| CGNCCCTGTG GGCATNCATG TTTCTGGTGG CTGGCAAAT TCTGGAGATG GAGGATGTGG | 360 |
| GTTNATCTTT TGCCCGCCTT GGNAATAACA TTTGTGCTGC CGTTGGTNAA GGCATCCNGG | 420 |
| GNTCC | 425 |

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

| | |
|---|-----|
| GGCAGAGTG GAGGCCTTTA ACTTTAACGA GTACCAGCCA GAAATGCTCG AAAAGTTCCG | 60 |
| GAACATGCNC NGCAGCACCC CTACGTCCTC ACGGAGGACA CCCTGAAAGG TCTACCTGAA | 120 |
| NCAAGTTCAG ACAGTCCTCG CCGGACAGNG TGAAAGGTGG TCATTNNATT TTNCTGNTGG | 180 |
| AGCAGACGGA GAATCTGGCT GATTACACA GNGGCATCTG AGAAACCTCC GCCAAGAAAG | 240 |
| GAGTCCGTGC CCTTGAATCC TGGTGGGCCT TGAAACGANN TGGTTCAACT TGGAAGCGGC | 300 |
| TTAATGCATC TGGNGTTTGG GNGAGGGTTT ATGTNTGA | 338 |

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

| | |
|---|-----|
| GAACCCACTN AGGNGACACC AATCTTNGAC TTCCAGATGG AACATGACAT CNATAAAAAG | 60 |
| GNAAGTGAT GGCATCTATA TCATAAATCT CAAAAGGACC GGGAGAAGNT TCTGCTGGNC | 120 |
| AGC | 123 |

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

| | |
|---|----|
| GGCANAGCCT GGNTTAAANG GACACAATAG ATTTCAAGGT CTACCTGGTA TCGCTGGTCA | 60 |
| CCATGGNGAT TTATGGTGCT NGTGGTTCCG TGGGA | 95 |

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

| | |
|---|-----|
| GATACTCTAA CCGTTTTAGT AGTCGCAGCC TCGAAATGAT AGACGAAATG CTCCACCTGT | 60 |
| AAGANCAGAA AATCGTCTTA TAGTTGAGAA ATTTATCCTC AAGAGTCAGC TGGGCAGGTT | 120 |
| TGTTGAAATA CAGTTTTGAA GTTATTTTGN ATGTGGCTTT TTAATAAAGT TTANTGGGTA | 180 |
| GCTCAATGTT GTATTGTTTT ATTAAANGTA GTTTTGAANT TAATGGGTTT NATGGG | 236 |

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

| | |
|---|-----|
| GGNACGAGGT CTGGCTCCCG TCCCCGCAAG CAACCACCCC GGAAGCACAC TCGTNCCTGG | 60 |
| NCTGTCCTGA AGCTGCTGCT GCTGCTGCTG CNATTTGGTG TGGCGGGAGG GCTGGTTGCT | 120 |
| TGTGGGGTGA NAAAGCTGCA GCAGCACCCC CTCTGCNACC AGCNTGAAAC ACCATCTTAT | 180 |
| GAANAATGNG GGTCCAGGGT CTACGCCGCC ATNAGATTCC TCCAGTGGGT CCTCCAAACC | 240 |
| GAA | 243 |

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

| | |
|---|-----|
| AAGGAACCTC TGAGAACTT AAGGTTGACA GNTNTNTCCA GCCCTNNACC TGCCTAGTCC | 60 |
| TGGGCCCTGG CCCTTTTTTT TGGTGAAGGG TCTGCTGTGC ACCATCCCCC ATNCCTAACG | 120 |
| TGGGCCCACC TGGCCTACAA ATTTCGGGGT GAGNGGTGTT TAAGNCAGGT GGCGGAGGGT | 180 |
| TTCCAAGGGA CCGAAANGTG GTTTTTTCAA CCNTNTG | 217 |

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

| | |
|--|-----|
| GGCACGAGCG GACCTTCATC ACCATTGGAG ACAGAACTT TGAGGTGGAG GCTGGTGA | 60 |
| TGGTGACCAT CTCAGAACTG GGCCGTGGAG CCTATGGGGT GGTAGAGAAG GTGCGGCAGG | 120 |
| CCAGAGCGGG CACCATCATG GGNCGTGAAA GCGGATTCCG GGCCACCGTG NAACTCACAG | 180 |
| GAGCAGAAGC GGCTGCTTCA TGGGACCTGG NACATCAACA TGCGCACGGT TCGGACTGTT | 240 |
| TTCTAACACT GNTCACCTTC TNACGGGGTC ACTTATTTC A GAGAAGGGTG GACGTGTGGG | 300 |
| ATCTNNCATG GNAGCTTCAT G | 321 |

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

| | |
|---|-----|
| CGGTTGCGCA ATGGGNGAAT ACTTCCGTGA CCGCGGTGGA AGATGCGCTG GATCATTTAC | 60 |
| GATGACCTGT CTAAACAGGC TGTTCGTTAC CGTCAGATCT CCCTGCTGCT CCGTCGTCCG | 120 |
| CCAGNNGAGA GAGGGATTCC CGGGNCGAAC GTTTTCTACC TCCACTCTCG TCTGCTGGAG | 180 |
| CGTGCTGCAC GTGTTAANCC GGAATACGTT GAAGCCTTCA CCAAAGGNAG ATGGGAAAGG | 240 |
| GGAAACCGG TTCTNTGNAC CGCACTGCCG ATTATCCGAG ACTCAGGCGG GTGACGTTTC | 300 |
| TGCGTTCGTT TCCGACCAAC GTAAATCTTC CATTANCGAT GGTTTCAGANC TTNCTGGGAA | 360 |
| ANCAAACGTGT TTCAAGGCCG TTATTTCTGTC CTGNGGTTTA ACCCGGTTAT TTTCCGTATN | 420 |
| CCGTGTTTGG TGGGTGCAAG NAAAGNCCCA GGTTTCATGGA AAAAAATGTT CCGNGGGTAT | 480 |
| TCCGTA | 486 |

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

| | |
|---|-----|
| GGCANAGGGA TACACTCCCT TGATGGAAGC TGCCCGGGAA GGACATGAAG AAATGGTGGC | 60 |
| ACTACTCTTA GCACAAGGAG CAAATATAAA TCCCCAGACA GAAGAACTC AAGAACTCC | 120 |
| TCTTACTTTG GCTTGCTGTG GAGGATTTCC TGGAAGTTGC AGACTTTCTT ATTAAGGCAG | 180 |
| GGGCTGATAT AGANCTTGGC TGCTCCACAC CTCTGNATGG AGGCATCTCA GGAGGGACAC | 240 |
| CTGGGAATTG GTTAAATATT TCCTGGCTTC TGGCGCTAAA TGTGCCATGG TNACAACAGC | 300 |
| AACAGGGGGA CACAGCCTTN AACCTATGCT TGTGNAAAAT GGGACATACG GATGTTGCAG | 360 |
| ATGTTTTACT TCAAGCAGGG GTTGNTTTTA GACAAGCAGG NGGGNCATGA AGACTATTTT | 420 |
| GGAGGGCNAG ATCCGGCCAG NTCAGTG | 447 |

(2) INFORMATION FOR SEQ ID NO:1357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

| | |
|---|-----|
| GGCACGAGCT CAACTCAGCA GGCAAGATGG ACAAATGAG GTTATTGAAC ATCCTAATGC | 60 |
| AGTTGNGAAA ATGTTGTAAT CATCCATATC TCTTTGAATG GAGCAGAACC TGGTCCACCT | 120 |
| TATACAACAG ATATGNCATC TAGTAACCAA CAGTGGGCAA AATGGTGGTT TTAGACAAGC | 180 |
| TGCTCCCTAA GTTAAAAGAA CAAGGTTTAC GAGTACTNAA TCTTNAGTGC AAATGACAAG | 240 |
| GGTATTGGGA CATTTTGGAA GGTTATTGGC ATGTGGGNGA AATTNTGAGT ACTGCCAGGT | 300 |
| TGGGATGGTT CAGACANCCC ATGATGNNGA GNCAAGACTC CTTCAATGCC TTACAATGG | 359 |

(2) INFORMATION FOR SEQ ID NO:1358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

| | |
|--|-----|
| AAATCCCTGN CCAGAACCAC CATTGTAAAC ACGGCAAGTT TGGCAAGTTG GGNTGNNGGAA | 60 |
| CAACACCCCC ATGTGGCGTT TNCCCAGGAC CCCACCANTT G | 101 |

(2) INFORMATION FOR SEQ ID NO:1359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

| | |
|---|-----|
| ACGTGAAAGC ACCGTAAAGC CGCTGCCNCC NCGCCGTTGG AATTTCCCTG AGGGGCAGGN | 60 |
| TACATCAAGG GCATCGTNAA GNACATCATC CAGAACCCGG GCCG | 104 |

(2) INFORMATION FOR SEQ ID NO:1360:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

| | |
|---|-----|
| AGCGCGGCCG GCCGGGNGCT TCGTGGCGGG GCTTGGNAAG GTGCGGCCCT ACTCCGTCTA | 60 |
| CCTCTTCAGC TTCTCCATGT TCTTNAACGG CCTCGCGGAC CTGGCGGGCT CTACGGCGGG | 120 |
| CAACTACGGC GGCCTCGTGG TCTTCTGCAT CTTCTTTGGC ATCTCCTACG GCATGGTGGG | 180 |
| GGCCCTGCAG TTCGAGGTGC TCATGGCCAT CGTGGGCACC CACAAGTTCT CCAGTGCCAT | 240 |
| TGGGCTGGTG CTGCTGATGG AGGCGGTGGG CCGTGNTNCG TCGGGCCCCC TTTCGGNAGG | 300 |
| TAA AATTCCT TGGATGCAAC CCAAGTTTTA CANGTAAGTN TTTCAATCTT GGCGGGGGG | 359 |

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

| | |
|--|----|
| GGCAGAGCCC NNNGGGCAAG AAGTGGCAG NGGAGCACTT TATTTGTCCC AANTGTAAGT | 60 |
| AGCCATTC | 68 |

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

| | |
|---|-----|
| TGCANAGGTC CAGGGCCCTA GCTGTGACCG CTGTGCCCCC AACTNCTGGA ACCTCACCAG | 60 |
| TGGCCATGGT TGCCAGCCTT GTGCCTGCCA CCAAGCCGG GCCAGAGGCC ATCCTGCAAC | 120 |
| GAAGTTCACA GGGCAGTGCC ACTGCGGTGC CCGGCTTTTG GAGGGNGGAC TTGTTCTGAA | 180 |
| GTGCCAAGAA GCTCCACTGG GGAGACCCTG GGTTCAGTG CCATGCCTGT GAATTGTGAA | 240 |
| CTCTGGTGGG AATTAGGATA ACACCTTCAG TNTGNAACCG NTTTCACAGG TTCAATGNCN | 300 |
| A | 301 |

(2) INFORMATION FOR SEQ ID NO:1363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GGCACAGCTT GCCTGCCCTG TGTCGTAAAA TGGGGGTCCC TTACTAACAT TATCAAGGNN 60
GNAGGCANGA CTGGGACGGC TAGTCANNAG GAAGACCTGG CACCACTGTC G 111

(2) INFORMATION FOR SEQ ID NO:1364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GGCACGAGGT TTTTTTTTTT TTTTTTTTTT TNAAAAAAAA NAANCCCTTT TTTNAANG 58

(2) INFORMATION FOR SEQ ID NO:1365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 428 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

NAGCTTGCTG ATGTAAACAA CATTGGA AAAA TACAGATCTG CAGGAGCATG TACAGCTGCA 60
GCATTCCTGA AGAATTCGT AACTNATCCT AAGTGGGCAC ATTTAGACAT AGCAGGCGTG 120
AATGACCAAC AAAGAATGAA AGTTCCTAT CTACGGAAAG GCCATGANTG GGAAGGCCCA 180
CAAGGACTCT NATTGAGTTC TACTTCGTT TCAGTCCAAG ACAATGCTTA GTTCCGATTA 240
CTCCAAAATG TCTTCACTCT GTNTTAAATT GGNCA GTTGA CTTAAAGGTT TTTGATTAAN 300
TGGGTTGGAA ATTTTTTTTAA CGGGGGCCAA GGGTTGGTTT TTTAAAAATT TGGGGCCCCC 360
ATGAAATTGG TTGCCCCGAT TTTTTTTTTN CCATTTNCCC CCCGGTTTTT TAANGGNAAN 420
GTTAATTC 428

(2) INFORMATION FOR SEQ ID NO:1366:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

| | |
|---|-----|
| GGACTTTTGC CGTCAGNTGA AAAGTGTGAT TATTACTTTA GTGTGGATGC AGATNTTGT | 60 |
| TTGACAAATC CAAGGACTTT AAAAATTTTN ATTGANCAAA ACAGAAAGAT CATTGCTCCT | 120 |
| CTTGTAATC GTCATGGAAA GCTGTGGTCC AATTTCTGGG GAGCATTGAG TCCTGATGGT | 180 |
| TACTATGCAC GATCTGAAGA TTATGTGGNT ATTGTTCAAG GGAATAGAGT AGGAGTATGG | 240 |
| GAATGTGCCC ATGTTATGGG CTNAATGTGT ACTTGAATTG ANNGGAAAGA CACTNCGNTT | 300 |
| CAGAGGTGA | 309 |

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

| | |
|---|-----|
| TGACCGANAA NGGACAAGTC GTGTCCCCCG TGTGCCGTCA GACTANGGAC CCGGGTGCAG | 60 |
| AATCGGCANA GGTCGGGGTT CCTGNTCAAC AGTGCTTGGA CGGACCCGCG TCGTCCCCAC | 120 |
| CCCGGCCGCC GCCATAGCAG CTCCGNACCT CTTCACCGAC CCTCGGCTGC CCAAGCCCCG | 180 |
| NGCGTCCAGG NCGCGANNAC CGCGCGCGCG CTCTCTTAGT CGCGCATGAC GCCGCGCCAC | 240 |
| CTCGCAGTGC GCAGAACTAC CACCAGACTC ANAGGCGCAT CACCGCAGAT CAACCTNGAG | 300 |
| TCTACGNTCT ACGTTACTGT CATGTNTACT ACTTAACGGA TGATGTGCTT GAGACTTGCA | 360 |
| ATANTTCTCA CATCTATGAG AGAGGACATC TAGAACTGTG AGTNAGACCA CGAGTGNCGA | 420 |
| TCTCTTCAGN TACAGAACAG CTGTATGCTG GAGGGGGTGA TGATGAGTTG ATAATTGAAA | 480 |
| ATGTATNANC ANTATGACTG AAAC | 504 |

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

| | |
|---|-----|
| CCNAGGTCAT CTTGAATTNG ATGCGCTACA NGCAGACGGT TGGNCATCTG GTCNTGGGC | 60 |
| TGCATCATGG CGGAGATGTT CACAGGCAAG ACGCTGTTCA AGGGGCAGTG AANCACCTGN | 120 |
| AACCAGGTGN AAGGT | 135 |

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

| | |
|---|-----|
| TAAAGCTCNT CACAGTTTTA CAGCAGAGAC CAGTNATGAC TTATCATTCA ANAGGGGNGA | 60 |
| CCGGATCCAA ATTCTGGAAC GTCTGGATTC TAACTGGTGC AGGGGCAGAC TGCAGGTACA | 120 |
| GGGAGGGGAT CTTCCCAGCA GTGTTTGTGA AGGCCCTGCC CAGCTGAGGC AAAAAGTATG | 180 |
| TTGGCCATAG TTACCGAAGG GNTTGAAAGG CCAAAGCCTT ATATGAATTT CCGAGGGGNG | 240 |
| ANTGANGATG GAACTTTTCC TTTCAAGGGC TTGGGGGNTG | 280 |

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

| | |
|---|-----|
| AGGGATGANT TGTTTACCTC TAAAATCTTT AAATGGAGC TGCAGAACGT NCCTCGCCAC | 60 |
| GCNAGCTTCA GCAACGTCCG GCGCTTCCTG GGCCGCTTTG GTCTGCAGCC CCACAAAACC | 120 |
| AAACTCTTTG GGGCAACCAC CCTGTGNCCT TTTTGAACAT TCCGCAGCGC TGCAGAGAAG | 180 |
| GGACAAGGCC CTGCGNCGTT TTGCATGGTG CCCTCTGGAA AGGCNGCCCA CTCAGTGTGC | 240 |
| GCCTGGCCCG GCCCAAGGCG GACCCCATGG CCAGGNGGAG GCGACAGGNG GGTGAAAAGT | 300 |
| NAAGCCACCA GTAACACGAG TGNGACGACG TGGGTGAACC CTTCTTGGG NCA | 353 |

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

| | |
|--|-----|
| AGCGGCGCGT GCCCAGCAAN TTNCAGCGCC CGCGGCTCGT GAAGCAATAT GTTCTTCGTT | 60 |
| AAGGATGTGC TCAAGCTGAT GGCGAATTTC CTCGANATCC AGCGCCTTGA GATGAAATTN | 120 |
| CAGACAGCGT GACAAAATCN TCACCGGCAA TTTCTNTGGA TCGGTCGTCTG CCAGCAGAAA | 180 |
| CTTAACGTGC TCCGGCGGCT CTTCAAGGGT TTTTAACAGT GCCGTAAAG CTGTGGCGCG | 240 |
| GACACATGAT GCACTTCGTC GATNCAGATA AACTTTGAAA CGACCACGCG CCGGAGCGTA | 300 |
| ACTGGGACGT TTATCCAGCA GGTTCGCGGG TTTCTTTCAA CTTTGGTGCG CGAGGCGGCG | 360 |
| TCGATTTTCA ATCCAGATCG ACAAAGCGGC CCCTGCTTCG TTTTCACGAC ATTATTCGNA | 420 |
| CAAGTCGNAA GNGTCGNGGG TNAATGCCCG TTTT | 454 |

(2) INFORMATION FOR SEQ ID NO:1372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

| | |
|--|-----|
| CCCAAGGNGC TCCAGGTNTG GTTGCAGGAN TACCGCCNCG ATAGTGGAGA GGAGGCCGTA | 60 |
| ACCCTTGAG AAGACTTGGA AGCTTAATTT ATCAGGACAA CAGGTCCCAG GTCAAGTNCA | 120 |
| TGGACCTNAA ATGCTCGNAA GGGGGATGGT GCCTCTGGAT CCATTTTCAGG AGTCCTCNAG | 180 |
| CTTTAACCTT CATCACGAAG GCCACCCAGT CCCACTTCAA ACATTTCGTTT CGGAAAACCC | 240 |
| CGCCTTTTAA CAGTNCACNA GCTCTTGCTT GCTTGCCCAC ATNCCTGCAC CCCNGCATGA | 300 |
| AGGGTANTTC CCAGAGAACC AGGCGATGGG CATTGCCANT ATTTACACAGC GGATTTCCCA | 360 |
| GGCATGGTGG AAGATCGAGG ACNGGCTGTT NTCCTCANTC TGGAGGAATG GGGATTNAAG | 420 |
| ANTTGGGTTC GGAGGNATTT TCATAGGGGN CAACAGGCAG AGATTA | 466 |

(2) INFORMATION FOR SEQ ID NO:1373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

| | |
|--|-----|
| AAAAAGAAAG ACTCACATTT ACAAGAGGCA GATNTCCAAG TAGAGCAGAA CCGGCAACAC | 60 |
| TTCTATNANC TGTCTCTCGA GTATGTNTGT AAGCNGCAGG AAATCCAAGA AAGAAAGAAG | 120 |
| TTTNANTTTG TGGAACCTAT GCNGTCATTT TTNNAGGGGA TGTTTACCTT CTATCATCAG | 180 |
| GGCCATGAAC TTGCCAAGAA CTTCAATCAC TACAAAATGG AACTACAGAT CAACATTCAG | 240 |
| AATACACGGA ATCGATTTGA AGGAACAAGG TCAGAAGTGG AAGAGCTCAT GANCAAAATC | 300 |
| CAGNCAGTTC CCAAGGNCCA CAAACGAGCA AGTCAGTTTA CAGCCGAGTT ACCTGTTTGT | 360 |
| GCCAGGAAAA AGGCCTGCTC CNTTTGGTTC CATTGGGTTC AANCATTTTT GCCNGTTTTTC | 420 |
| GAAAGCAGCA AGGNAGTTCC ANCTGTTCCC CTTTTAGGCA CCGTTTGGT GGGGAATTNG | 480 |
| GGGNCGGNGA GGTGTTCTTT | 500 |

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

| | |
|--|-----|
| NTACGTCGCT CCNACCTNCT GGCTGNCTAG GGGGAACTCT CCCCCAGCGA AAAGGACATC | 60 |
| AAGAAGATCT TGGACAGNTG GGTATCGAGG CGGACGACGA CCGGNTCAAC AAGGTTATCA | 120 |
| GTNANTGAAT GGAAAACNTG AAGAGTCNTG CCAGGTTTGG CANCTTGNN TTTACCTCTG | 180 |
| GTGGGGTGTA GCGTNTNGCT GCCCCGGTCTG CAGCCTGTGT GGTNTTCCCT GCTGCAGANA | 240 |
| GGAGAGNAAG TGAGAGAGGA GGAGTCTGAA GGTCACTGTG ACNNGGATTG GCNTTTGATT | 300 |
| ANNTCTGTCC CTGCAATAAA GCTTTTACAC TCTCAAAAAA AAAAAAAAAA T | 351 |

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

| | |
|---|-----|
| GGCAAACGAC GTGGGCAGCG TGGATGGAGA AGTCGTCATC GCACACGGTG CCCCANTGGC | 60 |
| CATCATAGTA CACCTCCACC CGGCCCTCGC TGTGCTTCCT CTTCTGCCCA GCCAGGCGCA | 120 |

| | |
|---|-----|
| NTNAATATCT TGGCCACGTT GCGGGTNTC TNGGAGCTGG TGAATACTNA GGAAGCCGGT | 180 |
| TGCTGGAAAT NACTCGGGGT AAATGGGNGC CAGCTGTAAA TACTGTGCCA GGTTCAGGGG | 240 |
| GGACAGGNGG GCCAGCATT GCCAGGCANT TGCAGAGGTG GGGAGCACAG AGGCCTTTTC | 300 |
| CATCCCTGTT TTTCGGGCTG ATGATTCCCA CGNAANGGNC CCTGCGCATT GAAAGGGGGN | 360 |
| ACAAGGCGGG GGTACAGAA GCANCAGGGG TTTTTTT | 397 |

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

| | |
|---|-----|
| CANCAAAAC TAAAACTGNN GGTCCAGATC AAACAGAAAT GANCTATTGA GGGCTTGCGA | 60 |
| GCNCACAGTG GAGTATGTGG TTAGTGTCTA TGCCTCAGAA TCCAAGCGGN GAGAAGTNAG | 120 |
| NCTCTGGTTC AGAACTGNNG TAAACCAACA TTGAATNGGN CTAAAAGGN ATTGGNATTT | 180 |
| CACTGATGTG GGATGTGGGT TTNCATTNAA AATTGCTTTG GGAAAGNCCA CAGGGGCAAG | 240 |
| TTTTCCAGGT TCAGGGTGAC TTATTTGAGC CCTNNGGGTT GGG | 283 |

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

| | |
|---|-----|
| GCCANCCAG NTTCCGNAA CNTGCCAGGA GCTCAAGTA AGCCATCAAG AGCCTGCAGT | 60 |
| GGNTGGCGGG CGGTCACCTT CACGGGGGAG GCCCTGCAGT ACAGGGGGAA CCAGNTGTTG | 120 |
| NCGNCCCAGC CCGAACAACC GTNTCGCCCT GGTCATCATT GACGGGCGTT CAGACANTCA | 180 |
| GAGGGG | 186 |

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

| | |
|---|-----|
| CTNCCGGATT CGGCGTGGTC AGCAGCCGAA AAGAATTTC CCGCTTATNC GNACCTTCCA | 60 |
| TAATAAGCAA GCNATCTNCT GGCTGAAAAA AGCTGCCCTA CAAGGCCATA CTTTGNCTTC | 120 |
| CAACGCCCTT GGCTGGNACA CTGGATCGTG GAGAAGCCCC CATTATGAA AGANGCGGTT | 180 |
| GTTTGGTATC GAATAGCCGC GGAGAGCGGA ATGTNTTATG CGCCAAAATA ATCTTGGGTG | 240 |
| GATGTACANA ATGGCAACGG AGTCGCAAAG ACTNTGCGCT GGCTTTTNTT GGTNCAAACA | 300 |
| GTNGCTTACA GGCCTT | 316 |

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

| | |
|---|-----|
| TGTNNCAGGG AACTTGCTAC TACCAGGCAC CATGNCCTAC CAATATCCAG CACTGACCCC | 60 |
| GGAAGCAGAA GAAGGAGCTG TNTGGGNATC GGTACCGGA TCGTGGGACA CCTGGGCAAG | 120 |
| GGACATCCTG GCTAGCAGAT NNANTNCCAC TGGGAAGCAT TGCCAAGCGG CTGCAGTCCA | 180 |
| TTGGTNACCG AGAACACCGT TGGTGAACCG G | 211 |

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

| | |
|--|-----|
| GGCAGANANA CCTTGGCACC CGNNATCAAC TGGTTGCTTT TNNTCAACAC CATCTTCTAC | 60 |
| CCCGTGGAGA TCAGTNAATC CAAGCCTATT GTGGTCTATG ACAAGGNAAT ACCTGAAGC | 120 |
| AGATCTCCAC TCTCATCAAC ACCACCGACA GATGCCTGCN CAACAACCTAC ATNATCTGGA | 180 |
| AACCTGGTGC GGAAAACAAG CTCCTTCCTT GAACCAGNGC TTTCAGGACG CCGATGTGAA | 240 |
| AGTTCATGGG AAGTTNATGT ACGGGNCCAA GAAGACCTGT TTTCTCGCT GGGAATTTNG | 300 |
| CNTTGGTGAT CACAGTAAAC ANCCTGGG | 328 |

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

| | |
|--|-----|
| GGCAGAGCCC TGGTCCGCAT CTNCTNTGGC CGCCACCCGA TGCTGTTCAG TTACCAGCGC | 60 |
| TCCCTGCCAC GCCAGCCCGT GCCCTCTGTG CAGGACACCG TGCGCAAGTA CCTGGAGTCG | 120 |
| GTCCGGCCCCA TCCTNTCCAA CGNAGGACTT CGAACTGGGA CCGGGGTCTG GGCGCAGGAA | 180 |
| TTCCTGAGGC TGCAGGCGTC GCTGCTGCAG TGGTACCTGC GGGCTNCAAG TCCTGGGTGG | 240 |
| GGCGTCCAAT TATGGTCCAG TAACTGGTTG GNAGGGAATT TTTGTNACCT GNGGATTCCC | 300 |
| GGAAATTCCG NTTG | 314 |

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 488 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

| | |
|--|-----|
| GGCAGGAGCN AGCCTCAGCC TTCCCTGGCC AAGAGCTCAT GCTTTCCTTG CTCTCCCCAG | 60 |
| GGTCCTGCTG GTCCCCCGCG TCCTGTCGGC CCTGTGGCG CCCGTGGCCC CGCCGTAAAG | 120 |
| TACCCTGCTG TNTCCCCCAT GCCTTCANAA CTCTACAGAT GCAGACAGTG CCCCCTCGA | 180 |
| TGCCAATGGA AACTTCCGCC TGAAAGTTTG TCCCTTTNTC TCTTCTAGGG GACCCCAAGG | 240 |
| NCCCCGTGGT GACAAGGGTG AGACAGGCGA ACAGGGCGGA CAAAGGCATA AAGGTCACC | 300 |
| TTGGGTTCCTT TGGGCCTCCA GGGTNCCCCT TGNNCCTCCT GTAAGTTATG GTTCAGNCCT | 360 |
| TNCCCAGTCC CCTGNTGTTG TGTGGGTTAG NAAGGGGGAG TTTGGNCTNA ATTTTCCCTT | 420 |
| TGGGTNGTTN ATTNTTTCCC TTCCTNATGG GGATTGGGGG TNTNAAGATT TNTGGGGNAT | 480 |
| TTCCAAGT | 488 |

(2) INFORMATION FOR SEQ ID NO:1383:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

| | |
|---|-----|
| GGCACAGCAG GGTTCACACC GGTGAAAGCC CTNACGTGTG TGGTGA | 60 |
| CTGTGACTGT GGGAAATTCT | |
| TCAGCCGAAG CTCCAACCTT ATTCAGCATA AGAGGGTTCA CACTGGTGAA AAGCCATATG | 120 |
| AGTGCCAGCN ACTGTGGGAA GTTCTTNAGC CAGCGTTCCA ACCTCATTCA TCATAAGAGG | 180 |
| GTTCATACGG GCAGAAGTGC CCATGAGTGC AGTGAATGTG GGAAATCTTT CAACTGCAAC | 240 |
| TNNGAGCCTA ATTAAACAT TGGAGAGTTC ACACTGGAGA AAGACCTTAC AAGTGTAANA | 300 |
| NATGTGGGGA AATTTTTTAG NCCACATTGT NCAGNCTTCA TTCCAAC | 347 |

(2) INFORMATION FOR SEQ ID NO:1384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

| | |
|---|-----|
| AGCAACGGCG ATCATTGTAA CTTCAATTCT GGTGCCAATT CTNACCTCTA TCTGGNCACG | 60 |
| TAAAGTCAAA GCCAGAGCAG CGAAAAATCG AAATTTTAGG TACGGTGAAA TAAACCTGCT | 120 |
| TCCTTAATCC CCACNGTCGG ATGANCTAAC GTTCGTCCGG TTTGCTATTG AGTTCCTGCC | 180 |
| TGGAATACTT ACCGAGAAAA ACAGCACGNC TGAACATTAA AATAAAATNT GGGTACTAAA | 240 |
| TGGGGGAAAT TTTCTGCGTG GGAGAGGGAA ACAGATGNCG ATTATTCCGN TTGATTGTNT | 300 |
| NACACAGGAC AAGGTTTCCG GGATTTTCC CGGANGG | 337 |

(2) INFORMATION FOR SEQ ID NO:1385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

| | |
|---|-----|
| GAGGATAAAA AGTACATATA CAGTTCATAC AATAATCTTA TGTATGTANA ACCCCGTTAC | 60 |
| GATGTCGGCG ACGGGGCCCA TCAGTAACTA TTACGTGGAC TCGCTCATCT CTNACGACAA | 120 |
| TGAAGACCTC CTAGCGTCCA GGTTCCTGGC CACCGGGGCT CATCCCGCCG CCGNCAGACC | 180 |

CAGCGGTTTG GTGCCGGNCT NTAGCGATTT TCCGTTCTTG TGAGCTTCGG GNCCAAGCCG 240
GN 242

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GGGGACCCCC AGGAGGTGAC CCTGCAGCTC TTCACAGATG GAATCACAAA TAAACTTATT 60
GGCTGTTACG TGGGAAACAC CATGGAGGAT GTAGTCCTGG TGAGAATTTA TGGCAATAAG 120
ACTGANTTAT TAGTCGATCG AGAATGAGGA AGTAAAAGAG TTTTCGAGTG TTGCAGGCTC 180
ATGGGTGTGC CACCACAACCT NTACTGTTAC CTTCAATAAT GGACTATGNC TNATGGATTT 240
TATACAGGGA GGAAGCACTG GGATCCAAAG CCATGTTCTG GCAACCCCAG CCATTTTTC 300
GGGCTAANTA GCTTCGTTCA GTTTGNTTAA AAATCCCATG NCTTATTTCC ATGGCACCAC 360
CAATTGGGCT GGGTTTCCCC CAAATTNTAA TTCTTTTGGG NTTAAAGATT GGGGGNAAGG 420
TTATTTTNTT TT 432

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

TCCTCCTGGC CATNATCTTC CTGCTGGGGA AGATCTGGAA GGTNCAAGTG CTGCAGGGCA 60
TCTTTGGGAN GAGCCAGNTC CTGTTTGCNC TCGTTTTCAG CAC 103

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

| | |
|---|-----|
| ATGGCTGTGC CACCCACGTN TGCCGATTTT NGCAAATTTG CCAGGGAATN TTTTCACCAA | 60 |
| GGGCTATGGT TTTNGTTTAA TAAAGCTTNA TTTGGAAAAC AAAA | 104 |

(2) INFORMATION FOR SEQ ID NO:1389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

| | |
|---|-----|
| TGAGGGACTT NACCCAATNA ACTACCTGGG CATTANNACC AACATTCAAG GCCAGGTGCC | 60 |
| TNACGTCCCA GCAAATTTAA CAGTCCACAT CTCTCCCTAC AAGGAGCTGT ACCACTACTC | 120 |
| CAACTCCACT GTAACCTCTA CAAGTNCCNG TAGACTACTC TNTAACTTTT GGTGCAATCA | 180 |
| ACCAAACATG GTGCTACCGC ATCCACCAGA ACATCACTTA CCAGGTGTGC AGGTACGNCC | 240 |
| CCAGACACCC GTCCTTCCNC ACCACCCAGN AGNTTGAACG TGGACCGGGT TTTTTCCTT | 300 |
| TGTNAT | 306 |

(2) INFORMATION FOR SEQ ID NO:1390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 466 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

| | |
|---|-----|
| GGCAGAGNCT TGGAAGAATT TATTTAGATA TGCTTAATGT ATACAAGTNC CTCAGTGAAA | 60 |
| ATATTTCTNC AGCTATCCAA GCTAATGGTG AAATGGTTAC AAAGCAACCA TTGATTAGAA | 120 |
| GTATGCNAAC TGTAAAAAGG GAAACTTTAA AGTTAATATC TGGTTGGGTG AGCCGNTCCA | 180 |
| ATGAATCCAC AGATGGTCGC TGAAAATTTT GTTCCCCCTC TGTGGATGC AGTTCTCATT | 240 |
| GNTTATCAGA GAAATGTCCC AGCTGCTAGA GAACCAGAAG TGCTTAGTAC TATGGCCATA | 300 |
| ATTGTGCAAC AAGTTTAGGG GGACATATTA CCAGCTGAAA TACCTCAAAT ATTTGATGCT | 360 |
| GTTTTTGAAA TGGCACCTTG GATTATGGTA AATAAGGACT TGNAGGATTT TCCCGNACCT | 420 |
| GGACGGACTT TTCCTTACTA CTCNNGGTGT TCAATTNNCC TTGTTT | 466 |

(2) INFORMATION FOR SEQ ID NO:1391:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

| | |
|---|----|
| GGCAGAGAGA NGCTGCGTCC CGGAGTAATC TGAAGCGGGT NACGCTGNAG CTNGGGGGGG | 60 |
| ANGAACCCCTT GC | 72 |

(2) INFORMATION FOR SEQ ID NO:1392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

| | |
|---|-----|
| AANAAACCAT CTGGTTCANG TTCCTAATTG GGCCAGCAAG TAAGGATGGC CAGGCCTCTG | 60 |
| GAGCAGGCGG TACTGCNATC NTTTGCACCT TCCAGGTAAT ACGCAGGTGC TGTGGGGACA | 120 |
| AATACAAGCN CTGCCAGGCG GACTCAAGGA GCTGCTGCAG AAGGAGCTGG CCACCTGGNA | 180 |
| CCCCGANNAA TTTTCGGGAA ATNTAACTAC AACAAATTCC ATGANTNTTC CTGGGACACC | 240 |
| ANCAAGGACT GCAAGGTGGG ACTTTTTTGG GAGTATGTGC GCTCACTTGC TCTGNTCGCN | 300 |
| TTTTCTACTG CC | 312 |

(2) INFORMATION FOR SEQ ID NO:1393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

| | |
|---|-----|
| AAACNTNTN TTNTCCTGTA AACAGTGGCC AGCCCCCAA CTATGAAAAT GCTCAAGGAG | 60 |
| GAGCACGAGG TGGCTGTGCC TGGGGGCGCC CCANAACCCT GCTCCCCGA NGTCCACNGT | 120 |
| NAATCCANAT CCGCAACGAA GACCTCCNTG CNCCGACCAT NTGGTNTGGT CCCTNTTCAA | 180 |
| CANCCTCTTC ATGNAANCCC TGCTGCCTGG GNTTCATAGC ATTCGCCTTA NTCCGTGAAA | 240 |
| GTTTTAGGGA CAGGGAAGAT GGTGGGGGA CGTNAACCGG GGGNCCAAG NCTTATGGTC | 300 |
| TTCCAACCG | 309 |

(2) INFORMATION FOR SEQ ID NO:1394:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

| | |
|--|-----|
| TTTATGCTGA AGTATTATCG ACGAATGCAA TTATCATTGA AAAAAACAT AATATATAAG | 60 |
| TNATTATCTC TAAAATCATT GATGATTTC A GAGTGTAAGG TTTCAATGAA TGANGTTTAA | 120 |
| AGGATGTTAG CATGTTTTAC CTTTATAATG ATGATAACTT TTCCAAAAC T GCTTGACTGT | 180 |
| NGAGGTTAAT TAAATTTNCT CTTGGAGCCC TACATACCAT CTGGATTCTT CCCATACCCA | 240 |
| CCAATTAANT CCCGGATCGG TTGGTCCATA AAACCGTGGA TATTGGGTCT NTCCAGTGGC | 300 |
| CGCCGTTAAA ATGGGNTTAA CCCCCTATNN CACCGGACAC T | 341 |

(2) INFORMATION FOR SEQ ID NO:1395:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

| | |
|---|-----|
| AGCCACATGC NCTACGNTTA NNANGCCTAC GCATACCTNC AATATATTGA NTCTGCAGGA | 60 |
| CTTTGTAGNC CGGNTAAGGN GTTAACGCCG ATACAGGCAT TAACAAAGCG NATTTGTCAG | 120 |
| CAATCTAAGT AACGTCGCAA TCANTTTTCT TNAATCCCAC ATCATTTGCA NTTCCATTAN | 180 |
| TTCTCAAACA TCCATGCCCA ACG | 203 |

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 429 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

| | |
|--|-----|
| TAGTNAGGGT CAGGTGCAGA TGGCGATGAN CGGCGGCATC TANAATGAAA GCAATGCCCC | 60 |
| GCTCGGTTTG TACATNGAAA ACGGTCAGCA GAAGGTGGCG TTAAATCTCG CTTTCAGGTGA | 120 |

| | |
|--|-----|
| AGGGAAATTN NTTTATCCGT CCTGGCGGCG TGTTTTAATG TCGCGGGAGA ATAAAGTCGG | 180 |
| CATCGTTCGT CTGGTATGCC TTCAAAACCA GTNAAAGNGA TTCATTTTGC GGTGCAGTCC | 240 |
| AGGGCCAATN TTGATGGAAA ACGGTGTAAT TAATCCGCGT NTTTCATCCCA ACGTCGCCTN | 300 |
| AAGCAAATTT CGTGAACGGT GTTGGGGTTA ATAAAACCTG GGGAACGCCN TGTTTTTTTT | 360 |
| TGNGCCCGCA GGCANCAAAT TTTTAATGGA TTTTGTCCCN GTTATGNCCC AGGGGAAACT | 420 |
| TAACCTTTG | 429 |

(2) INFORMATION FOR SEQ ID NO:1397:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

| | |
|---|-----|
| NAGCTTTTNG TATTTTAAAT ATNAGGTACA TAAGAGTTN AATTTGTTCC TTTTTTAAAA | 60 |
| TAACCTTNAA AATTATTATA TGGTAACCTT CTTTATTATG AATACTTGNA AAATGTAGGC | 120 |
| ACACAAATAA CCTTTTTGAA TTTATATCCT GTAATGTATA TTTCCCCAGT CTTTNNACTT | 180 |
| TACTCCAGTC CACTAGGAAA TCAGTGGTTG GTTGTTTACC TCTCTTGAAA TGTCTTTTTG | 240 |
| TATTGTGGTC TCCACCGTGC CATTTCNATA ATGGCATATT TNTNTTTGNG CCTAGCCATG | 300 |
| TTTAGNGGTG TTTG | 314 |

(2) INFORMATION FOR SEQ ID NO:1398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

| | |
|---|-----|
| TCCATCATAG TCAACTGCTT GGGANGAGAA AGCCAAANGA NTGCAATGTT GTGAAAGATT | 60 |
| CCANTTNATG CCAGTAAACC TAATCCAAAT GAATGTGGAG TTTGAATAAA TCTGTATTTG | 120 |
| GATATGATTG GAATCATCCA TCCCTGTACT CATCCTGAGG ACAAACCAGC ACCAAAAANT | 180 |
| GNGGNTGNNA ATGAATGGTT GCAATTTT | 208 |

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

| | |
|---|-----|
| TGANTATTCA NCGTGNGAAA GAAGANTTGG AACAAAGGGA AGCTGAACTC CAGAAAGTCC | 60 |
| GGAAGGCTGA GGAAGAGAAG GCTGCCCCAG GNAAGCAAAG GNGAGAGAGA AGGAGCGTAT | 120 |
| CTTACAGGAA CATGANCAAT TCAAAAAGAA AACTNTCCGA GAANCNTTTG GNGCAGATCA | 180 |
| AGAAAACAGA ACTGGGTGCC AAANCTTTCA AAGGTATTGA ATATTGAAGA CCTTNAGGNA | 240 |
| TTGGTTTCCA GTTTTTTCCT GGGTTAANCA GGTTGANCAC TGGGGAAAG | 289 |

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

| | |
|---|-----|
| GGCACGAGCA TGGCTTTTAA TGAAGAAGGA CAGGCAACAG AAACAGACAC AAAANTCAGA | 60 |
| GTGTGCACCC GGGCCTACCA TCTGCTTGTN AAAAACTGG GCTTTAATNC AAATGACATN | 120 |
| ATTTTTNACC CTAATATCCT AACCATTGGG ACTGGAATGG AGGAACACAA CTTGTATGCC | 180 |
| ATTAATTTTA TCCATGCAAC AAAAGTCATT AAAGAAACAT TACCTGGGNG CCAGANTAAG | 240 |
| GTGGAGGGTN TTTCCAACCT GTCCTTCTCC TTTNCCGGGG ATTGGAAGGC CTTCNGGGAA | 300 |
| GGCATTGCTT GGGGTTTTCC CTTTACCCTT GCATTCAAGT NTTGGCTTGG CCTTGGGGGT | 360 |
| TNTTNATTNC TGGGAAACCC CCCCCTGGNA TTGGGG | 396 |

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

| | |
|---|----|
| GGCACAGGNT TTTTTTTTTT TTTTTTTTTT TTTTTTTTNG GGNTTTTTTT TTTT | 56 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

| | |
|---|-----|
| CAAAGGCGGA GGACCCGTGG CCCACGAAGC TCATCTTTNA ACTNTCCCCG CNTTCTCCCG | 60 |
| CCTTGAANTT GTGAACCCTA GGCCCTTTGG GCGGACCTNT NAACCCAGCT AGCCAGATCC | 120 |
| CGGACCCAAA CCATGTTCCC TGTGAAAGGT GAAAAGTGA GGAATCAGA GCTGGAGATG | 180 |
| GCCAAAGCCC GGTAACCAAC TGGTTGCTGT TTTGCAGTNT CTGCTTGGAG GANGAGTCAC | 240 |
| ATGGNACAGG GAGCGTNTGG TTGAGGGAAG CTGGGGAAAA CACCCTCAGG ACACCCACAA | 300 |
| TAAGGNACTG TTTCCATCGC AGGCCACTGG GNAAAAGGG CCATCTTNCC CGTTTTTCCC | 360 |
| CCACCAAGGG GAGGGAAGAA GAAGNGGGG NGATTGGTTG | 400 |

(2) INFORMATION FOR SEQ ID NO:1403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

| | |
|---|-----|
| TATATTGTAG CTCATCANGG GNAATNGGNA CTGTTCAAAA NGGATTGCCC CACAAGTGTT | 60 |
| ACCATGGGCA AACTGGAAG AGTCTACAAT GTTACCCAGC ATGCTGTTGG NCNNGGTTGT | 120 |
| TATNCAAACA NGTTTANGGG GCAAGATTCT TTCCAAGAGT NTTTAATGTG CGTATTTTAG | 180 |
| CACATTTGGC ACTCNAAGTG TCCGCGATAG CTTTCNGAAA AGTGTTNAAG GGNAATGAA | 240 |
| TTCAG | 245 |

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

| | |
|---|----|
| GGCAGAGTGG TCATCGAGTT CTCCAGCCGC CCCGGCCAGC ACGAGCTGAT GGAGCCCGAG | 60 |
|---|----|

| | |
|--|-----|
| GTGAAGCTCN TCGGCAACAT TCATGGCAAC GAGGTGGCGG GCCGGGAGAT GCTCATCTAC | 120 |
| CTAGCCCAGT ACCTGTGCCT CTNAGTACCT GCTTGGTAAC CCCC GCATCC AGCGCCTGCT | 180 |
| CCAACACCAC CCGCATCCAC CTGNTGCCCT CCATGAACCC TGACGGCTAT GAAGGTGGNC | 240 |
| AGCTGCCGAG GGTGCGCGG TTACAACGGG TGGGACGGAG CGGGAAGGTN AGTAACGTG | 300 |
| CAAAACCTGG GTNTCTNGAA CCGAAATTTT CCCGGGACNT | 340 |

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

| | |
|--|-----|
| AATCGCAGAG CTTGTNACAT TTTGGAATGC TGTAATGGGC TGGCCCAGGA ATGTNATCGG | 60 |
| CTCCATCGGA CAAGCCTTTA AGCTCCGGTT TAAGCAATAT TTACAGTGTC CTACCAAGAT | 120 |
| TCCCGCTCTC CATGAATCGA NTGCAGAGTC TGGATGAGCC ATGGNACGGT AAGAGGAGGG | 180 |
| AGATGGCTCA GAACCACCCA TTA CTTACAA CAGCATCCCA AGCAAGATGC CTCCTCCCAG | 240 |
| GGGGCTTTTC TTGGATACTT AGGACTGAAA CCCAGACCCC ATGGTTCCTG AACACAGCCC | 300 |
| AGTTTTGCAG GGAAAAGAGG CAGATTTTTT ACCAGGGAAG ACATTTGGGG GACATTTTGG | 360 |
| CGANANTGGG CAGCAAACAN CTTTAAGGGC AAGGTNCCCG GANAT | 405 |

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

| | |
|--|-----|
| GGCAGAGCCC AATTCTTCGA AGGTCTGGAA TGTATACTGT AGCCATTGCT TTTTGTGGCT | 60 |
| CTNGTAACAA CAAAGCAATT CGAGGACTGN TAGATGTTGC TGTAAGTAAT GTTAATGATG | 120 |
| ATGTCAGGAG GGCAGCAGTA GAATCACTTG GGTTCATTCT ATTCAGAACC CCTGAACAGT | 180 |
| GCCCAAGTGT TGTCTCTTTG TTGTCAGAGA GTTACAACCC TCATNTGCGC TATGGAGCTG | 240 |
| CAATGGCCTT NGGGATATGC TGTGCTGGTA CAGNAAACAA GGAAGCCATT AATTTGCTAG | 300 |
| AACCANTGNA CAAACGACCC CGTGGAAC TA CGTGAAGGTC AAGGGGCACT TCTTAGGCTT | 360 |

NCAGTNCCTTC ATCCATGTTT CCAGGCAGAC TNGNAATCCA CTTGTTCCAA AGGTNGAT

418

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

| | |
|--|-----|
| GGCAGAGGAA GATTGACGTG GGGGAAGCTG AACCACGGAC TGTGTGATNC GGCCTGGTAC | 60 |
| ATTCGTGCCC AAGGAGGAAC TGCAGGACAG GCTGGTAGTG GTGCTGTGCA ACCTGAAACC | 120 |
| CCAGAAGATG AGAGGAGTCG AGTCCCAAGG CATGCTTCTG TGTGCTTCTA TAGAAGGGNT | 180 |
| AAACCGCCAG TGANACCTCT GGACCCTCCG GCAGGCTTCT GCTTCCTGGT GGAGCACGTG | 240 |
| TTTNTGAAAG GGCTATGNAA AAGGGCCAAC CAGATGGAGG GAGCTCAAGC CCAAGAAGAA | 300 |
| AGTCTTTTCGA GGAAGTTTGC CAGGCTGGAC TTTCAAATTT TCTGAAGGGA GTTGCATCGC | 360 |
| CCAGTTGGGN AGGCAAACCA ATTTCATGGA CCAGTTGGGT TNCCNTTNCC GTAAATCGTT | 420 |
| GAAAGGGGGG NACATTAGTT TGCCAGCCCG CNTTTTCCCC TTTTTCAC CTNGGGTCAT | 480 |
| NTGTGTNTTT TCNTTTGTTC | 500 |

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

| | |
|--|-----|
| TACTATCCCG AACTGGCTGC GCTGAATGTN GNAANCTTTA AAACCGACAA ACCACAGCCG | 60 |
| GTTAACGCGC TGCTGAAGAN CCGAAAAACG CAACCTGTCTG CTGTTACAGG CACGCTTGAG | 120 |
| CCCAGGNCCT GNGCGGCGAG NAAN | 144 |

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

| | |
|---|-----|
| GGCACGAGGC GGGGCTACAA CTACGCCACC TGCCTGGAAG GAGCCCTGAA AATTAAAGAG | 60 |
| ATAACCTACA TGCACTCAGA AGGCATCCTG GCTGGGGAGC TGAAGCACGG GNCCCTGGCA | 120 |
| CTGATTGACA AGCAGATGCC CGTCATCATG GTCATTATGA AGGATCCTTG CTTCGCCAAA | 180 |
| TGCCAGAACG CCCTGCAGCA AGTCACGGCC CGCCAGGNTC GCCCCATTAT ACTGTGCTCC | 240 |
| AAGGACGATA CTGAAAGTTC CAAGTTTTGC GTATAAAGGN CAATCGGAGC TGCCCCACAC | 300 |
| TGTGGGACTT GCCTTCCAGG GGNATTCCTT GAGGCGTGGA TTCCGTTGGC AGTTGCTGTT | 360 |
| CCTTNCACCT GGGCTGTTCT TCCGAGGGAT ATGACGTTGA CTTTCCCCAG AAATTTGGCC | 420 |
| AATTTTAA ANTN TGGGAT TAGGNTNAGA CCGTNAAAAG GCCATTAACC ACTTT | 475 |

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

| | |
|---|-----|
| ATGGGAGTGG ACATCCGCCA TAACAAGGAC CGAAAGTTCG GCCGCAAGGN GCCCAAGAGC | 60 |
| CAGGNTATCT ACCTGAAGGC TGTTGGTCAA GTTATACAGG TTTNTGGCCA GAAGTAACCA | 120 |
| ACTCCACATT CAACCAGGTT GTNTTGAAGA GGTGTGTTAT GAAGTGGCAC CAACCGGCCG | 180 |
| CCTCTTTCCC TTTCCCGGAT GAATACGGNA AGNATGGAAG CTTTCCTGGG CCGGGGAAAA | 240 |
| CAAAGACGGG CCGTGGGTTN TGGGGGGACC ATAAACTGAA TGATTTGCGG GGTTCAGGA | 300 |
| AGGGTTACCC AACTTTAAG TTATGTGNCA CTGNCGTNA ACCCAACGGG GNCCC | 355 |

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

| | |
|---|-----|
| ATGATAATAG TGTTGATACA GCCACGCAA ACCGCGACCA GACAGATAAT TTAAATGCA | 60 |
| GCCATGCTGA CCACAGCCGC AGCGNCGTGA ACGGGAAAAT CCAACCCCAT CATGGTTAAC | 120 |
| GCATCAACCG GCAGACGCAT ATGGNCAAAC TCGCCGGTAA ATGTAGCTTT TACCGGTAAT | 180 |

| | |
|--|-----|
| CGGTTTGCCG TTGAAAAATC AGCCCGCCGC CAACACCGGT GCCGAGANTC AACCCCATCA | 240 |
| CCAGTGGGAT ATTGGAGTAA AATTTTCATCA TCCCAGGNTT CTGNAAGGGG CAAAACAGTT | 300 |
| GGCATCGTTT ATTCAAGGCG TACATCGGGG TTCAAGAACG TCGGTTTCAGT TCGGCAGGNN | 360 |
| GCGGTTTTTAC NTTGTCNAGG GGGGGAACCA TGGGNGGCTT ACAGGGTTAC CCTCTTTTGG | 420 |
| TTT | 423 |

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

| | |
|--|-----|
| GGCAGAGCNA GNCCGGAGTG TCAGNGNATG ATGCGGTTNA TGCTATTATT CAGCCGGCAG | 60 |
| GGGAAAACCTG CGGCTGCAAA AATGGTACCT GGCCACTTCG GACAAGGGAA CGGAAGAAGA | 120 |
| TGGTNCGCGG NCTCCATGCA GGTGTCTCTG GCTCGAAAGC CCAAGAATGT GCAGCTTCCT | 180 |
| GGAGTGGAGG GNACCTCAAA GTTGTCTATT AAGAGATATG CCAGCCTCTA ACTTNTGCTG | 240 |
| CGCCATTCGA GGGCCAAGAC AATGNAGCTT CATCACACTG GAGCTGTATT CCACCGATAC | 300 |
| GTGGAGCTCT TTAGGACAAA TACTTTGGGC AGTNTGTGCC GAAGCTGGAC ATCATCTTTC | 360 |
| AACTTTNNAG GAAGNCTNA TTTTCATCCG GGATGAGTTT TTTGATTGGG GGGGGGNTTT | 420 |
| CCAGGACAAC TTCCAGAAGA GTGTGCTGAA GCCATTCGAG CAAGGTGANC NACTTGNANA | 480 |
| GGG | 483 |

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

| | |
|---|-----|
| AGCCCCCTAG ACAGGTTAAA ANGTTATCTN TGGCAATCAA NGGCAGTTTG GATGAAGCCA | 60 |
| AGGNTCTTTN CAAACCTCCA AAGGACTCCC AAGAATGACG AGAGTNAACT CAAATGCCGN | 120 |
| GGAGGAGCAG ACTACGANGC GCCCGGAGAA CCCACACTGG GGGTTTCAATTT GGNCGNCAAA | 180 |
| CG | 182 |

(2) INFORMATION FOR SEQ ID NO:1414:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

| | |
|---|-----|
| GGCANAGGGN TCAACTACCT CACTGTAATT GGCTACCCAA ATGCTGAGTT CAAATCTTGG | 60 |
| TGGCCGGCCA CTGCTCATAT CATAGGTAAG GACATTCTCA AATTCCATGC CATCTATTGG | 120 |
| CCTGGCCTTC CTGTTAGGGG NCCGGTCATN AGCCCGNGCA CAGCNCATCT NTNGGCCATT | 180 |
| ACCCACTGGA CAGTCTGTGG CCAAAGTTG TTCCAAGAGC TTGGAGCAAC GTGGTNGNNT | 240 |
| GCCGAGGACT TNGCCTTTAA CCGCTATACC GTGGTATGGG NTT | 283 |

(2) INFORMATION FOR SEQ ID NO:1415:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

| | |
|--|-----|
| GGCAGAGTNT CGATGCCACT NTCAACAAGG CCCTGGCAGA AAGATTCCAC ATCTCAAAGT | 60 |
| TTCCTACGTT GAAGTATTTT AAGAATGGAG AGAAATACGC ATGCCTGTGC CTCAGGTACA | 120 |
| AAGAAGAAGT TTCTCGAGTG GATGCAAAAC CCTGAGGCCC CCCC GCCCCC AGAGCCCACG | 180 |
| TGGGTAAGAG CAGCAGNACA AGCGTGTTGC ACCTGGTGGG GGACAACTTC CGGGGGGACC | 240 |
| CTNGAAGAAG AAGGAAACAC ACTTGTTTCA TGTTCTTACG NCCTTGGTGC CCACACTGTA | 300 |
| AGAAGGTTCA TTNCCGATT TTA CTGTTAN NGTTGATGCC TTTCAAAGAT GGACCGAAAG | 360 |
| NTTGNCTGTT GCCGTTGTTT GATTTTTTAA AGG | 393 |

(2) INFORMATION FOR SEQ ID NO:1416:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

| | |
|--|-----|
| TCCCNNTGGG ACAAACACTGT TGGTTCAATT AAGGGTTGTT TTTTCANGAG GNTCCTTGGT | 60 |
| TCTTTAAAAG GCAAGGTCCC GNNGGGGAAG GGTCCAAGGT TCAAGTTTGT NAAGGGG | 117 |

(2) INFORMATION FOR SEQ ID NO:1417:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 277 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

| | |
|---|-----|
| GGCANAGGGA AGAAGGAAAC CCAAGGTTGT GGTATGCTGC TTTACTGTCT TTCACAAGCG | 60 |
| CCTTTNATAT CCTGTCAATC ATCTGTGTCG GGCTGCTCTA TACATATTAC ACCAAACCAG | 120 |
| ATGGCTGCAC AGGAAAACAA GTTCTTCATC AGTATTGAAC CTGATCCTTT GCGTTGTGGC | 180 |
| TTCTATTATG ATCGATCCAC CCAAAAATTC CAGGGAACAC CAGCCTTCGN TTCCGGCCTC | 240 |
| TTGNCAGTTC CTTCCCTNCA ATNCAACCCC TNCTGAC | 277 |

(2) INFORMATION FOR SEQ ID NO:1418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

| | |
|--|-----|
| GGNACGAGCT GGTGGCTGGC AAGATCGTGG AGATGGAGGA TGTGGGTTTA CTCTTTGCNC | 60 |
| GCCTTGGAAG GTACATTCTG TGCTGCCTGC TGGGTCACGC CATCCATGGG CTCCTGGTAC | 120 |
| TGCNNGTCAT CTACTTCCTC TTCACCCGCA NAAACCCCTA CCGCTTCCTG TGGGGCATCG | 180 |
| TGGACGCCGC TGGCCACTGC CTTTGGGAAC CTCTTCCAGT TCCGCCACGC TGCCGCTGAT | 240 |
| GATGAAGTGC GTGGAGGAGA ATTAATGGCG TTGGCCAAGG CACATTCAGC CGTTTTTCATC | 300 |
| CTGGCNCATC GGNGGCCACC GTNCAACATG GGACGGTGGC CGACGGTTCT TTCCAGTGCG | 360 |
| TGGGCCGCAA TGTTTCATTG CACAGTTCAG CCAGCATTC TTGGANTTCG TNAAAGATCA | 420 |
| TCACCANCTG GTCAGGGCAC AGGTCCANGT TGGGGGCAAN GGGCATCCTG CTGGAGG | 477 |

(2) INFORMATION FOR SEQ ID NO:1419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

| | |
|---|-----|
| TCAGCAATCA GACTGTCGAC ATTCCAGAAA ATGTCGCATT GACTCTGAAG GGACGCACAG | 60 |
| TTATCGTGAA AGGGCCCCAG AGGAACCCTG CGGAGGGNAC TTCAATCACA TCAATGTAGN | 120 |
| AACTCAGCCT TCTTGGNAAA GGAAAAAAA GAGGCTCCGG GTTGACAAAT GGTGGGGTTA | 180 |
| ACAGNAAAGG GAACTGGNCT ACCGTTCCGG GACTTATTTG TGAGTNCATG TTACAGGAAC | 240 |
| ATGGATTCAA AGGGGGTGTT TNACCACTTG GGGGGCTTTT CCGGTTTAAC CAAAGGNNTT | 300 |
| GNAGGGGTNC TTGGTGGTTA TTGGGCTCCC AAATTTTTC CCCCCAAA | 349 |

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

| | |
|---|-----|
| CAAGNTCNNC GGCAAGNGT TTTCCANACC CTGGTTGCTT CAAGGACACA TTAGAACTCA | 60 |
| CACGGGGGAG AAGCCTTTTT TTTGCCCTCA CTGCAACAGC NGCATTTGAC AGACAGGTGA | 120 |
| ANTCTGAAGG NGTCATCTGA CAGACCCATT NTATTGTGAA NGAAATACCA | 170 |

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

| | |
|---|-----|
| GGCAGAGCGA GAGCATGCCC TTNTGGCTTA CACTGGGT GTNAAACAAC TGAATTGTCG | 60 |
| GTGTTAACAA AATGGATTCC ACTGAGCCAC CCTTTTTTTT TTNTTNGTNT GTT | 113 |

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

| | |
|---|----|
| GGCANAGCAG CCACGGATCT NCGGGTGGAG GCATNAATGC TAACATGAGG GGTGTATTTC | 60 |
| TACATGTTTT NGCAGATACA CTTGGCAGCA TTGGGN | 96 |

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

| | |
|---|-----|
| GGCAGGAGCC CAATTNTTCG AAGGTCTGGA ATGTATACTG TAGCCATTGC TTATTGTGGC | 60 |
| TCTGGTAACA ACAAAGCAAT TCGACGNCTG ATNANATGTT GCTGTANGTG AATGTTAATG | 120 |
| AATGATGTCA GGAGGGCAGC AGTAGNAATC ACTTGGGTTC ATTCTATTCA GAAACCCCTG | 180 |
| AACAGTGCCC AAGTGTTGTC TCTTTGTTGT CAGAGAGTTA CAACCCTCAT GTGGCGCTTA | 240 |
| GGGNGCTTGC AATGGCCTTT GGGGATATGC TGTGCTTGGT ACNGTAAACA AGGGAAGNCC | 300 |
| ATTGAATTTT GNTAAGAACC CCANT | 325 |

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

| | |
|---|----|
| AACAAGACGG AATTGGAACG GGGTTNTGNG CTACTATGGT NCCACTCCGN AGTGTGTGGG | 60 |
| GATGCTAGGA AACCCACCC | 79 |

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

| | |
|---|-----|
| CNCATGAANC GCTTCGAGGG GNTCACGGTG CTAAAGGNT GCGCCGTGGA NCCGGGACTG | 60 |
| GGAACGTGGG CAGTCAGGGT GCTAGCTGCT TCTGGAGGTG AGCGAGCGGG TCGGAAACCT | 120 |
| TGACCCGGCC TACTTNTNCC CGGAACGNCC CTGCTTCTTT CCTTNACCCA NCT | 173 |

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

| | |
|---|-----|
| GGCANAGCAA GANCTCACCT CAAAGAGAAG CCCTTTGACT GCAGTCAGTG TGGAAATGCA | 60 |
| TTCCGGACCC TCTCGGCCCT GAAAATCCAC ATGCGAGTNC AACTGGCGA GAGGCCTTAC | 120 |
| AAGTNTGATC AGTGCGGGAA GGCTTACGGC CGNNGCTGCC ACCTCATCGC ACACAAGAGA | 180 |
| ACGCACACCG GAGAGAGGCC CTACGAGTGT CACGACTGTG GGGAAAGCTT TCCAGCACCC | 240 |
| CTCCACCTC AAAGAGCACG TNAGGAATCA CACGNGGGGA GAAGNCCTTA CGNNT | 295 |

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

| | |
|---|-----|
| CCGATCGATC AGCTGGCGAC CGATTCTAAC TACCTGGAAG TTTGTNACAT CCTGCTGAAT | 60 |
| GGTGAAAAAC CGACTCAGGA ACAGTATGAC GAATTTAAAA CTACGGTGAC CCGTCATACC | 120 |
| ATGATCCACG AGCAGATTAC CCGTGTGTTC CCATGCTTTC CGTCGCGAAC TCGCATCCAA | 180 |
| TGGCAGTCAT GTGTGGTATT ACCGGCGCGC TGGCGGCGTT CTATCACGAC TCGCTGGATG | 240 |
| TTAACAATCC TCGTCACCGT GNAATTGCC GCGTTCCGCC TGCTGTCGAA AATGCCGACC | 300 |
| ATGGCCGCGA TGTGTTTACA AGTTATTNCC ATGGTTCAGC CATTTGGTTT NACCCGGGGN | 360 |
| AACGATCTTT TCNTANG | 377 |

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

| | |
|---|-----|
| GACCAGCCCC TNCCGGGNGT CCTCTTATCC NTGAATTGGT GGCCTGTTTC NTTCCAACCT | 60 |
| NTTGACCCAG GACAACGGCA TTTTACCATT TTCAAACCTG AGGCCCTGGA CCANTTNTTA | 120 |
| CTTCAAACCC ATGAATGCAA GGAGTTCCGG TTTGAAGCCA TCCTACACAG AATGAATNGA | 180 |
| GNTGCAN | 187 |

(2) INFORMATION FOR SEQ ID NO:1429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 438 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

| | |
|---|-----|
| GGCAGAGCTC GTCCANGANA GNATTNTNCC CCATGGGGAA GAACTNACAC TGCGTCCGGT | 60 |
| TTGTNCCCCA GGAGATGGGC GTGCACAGGT NCAGCGTCAA GTACCGTGGG CAGCANTTCA | 120 |
| CCGGNCAGCC CCTTCCAGTT CACCGTGGGG CCACTTGGTG AAAGGAGGCG CCCACAAGGT | 180 |
| GCGGGCAGGA GGCCTGGCCT GGNAGAGAGG AGAAGCGGGA GTCCCCAGCT GANTTCAGCA | 240 |
| TTTGGGACCC GGGGAAGCAG GCGCTGGAGG CCTCTCCATC GCTGTTGAGG GCCCCATTAA | 300 |
| GGCCGAGATT TACATTCGAT GACCNTAAAA ATGGGTTCGT GCGGTGTTAT CTTATATTGC | 360 |
| CCAAGAGNCT GGTAATTAGG AGTGTTCNC AATTTCATG TTGNGCACNT CCGGAAGCCT | 420 |
| ACNGGTGCNG TTNTGAAC | 438 |

(2) INFORMATION FOR SEQ ID NO:1430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

| | |
|---|-----|
| GGTACAGTAA TCATGGACTC CCGTCACCCG GATACCCTGC TGGCGGCACG TTCTGGTAGT | 60 |
| CCGCTGGTGA TTGCNTGGG GATGGGCGAA AACTTTATCG CTTCTAACCA GCTGGCGCTG | 120 |
| TTGCCGGTGA ACCCGTCGCT TTATCTTCCT TGNAAGAGGG TCGATATTGC GGAAATNACT | 180 |

| | |
|---|-----|
| CGCCGTTCCG TAAACATCTT CGATAAAACT GGC GCGGAAG TAAACGTNC AGGATATTCG | 240 |
| AATCCAATTC TGCAATTATG ACGCGGGGGA ATAANGGGCA TTTTACCGTC ACTACATGGC | 300 |
| AGGAAAGGGA TCTTACGAAA CANACCGAAC GGGANTCANA AAACNACCTT TACNCGGAN | 359 |

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

| | |
|--|-----|
| CCCCCGCCCG TGAATGCCGA AATGGTTGCC GATGTGCGCG TACTGGGGGC CATTNGCGTG | 60 |
| GTCGAAACCA CTNCATCCGG TGAATATGGC GGC GCTGCAA AAATTCTTTG TCGAACAGGG | 120 |
| TGTCTGGATC CGGCCTTTTG GCAAACGTAT TTACCTGAAT GCCGCCCTAT ATTATTCTCC | 180 |
| CGCAACAGTT GCAGCGTCTN ACCGCAGCGG TTAAACCGGC GTTACCAGGA TGAAACATTT | 240 |
| TTTTGCCAAT AAACGAGAAG TCCGCGTGAG GGTTCCTGGC TACACTTTCT GCAAACAAGA | 300 |
| AAGGAGGGTT CATGGAAANT CATCAGTAAA CGGTCTGCGC GTTGGGGNTT AAATTGCCCCG | 360 |
| CANTCGTCAT GTCTTTTAAC GGGCATGGGG TTACNGATGG GGGTTAATAT TTTCANCNGA | 420 |
| TTTGGGGTGG GGNTGATGTT CNCGNNGGGA CGAAAAGTT TTTTGTACAC CTGTTACGNC | 480 |
| CC | 482 |

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

| | |
|---|-----|
| CAACGGATGA AACCAAACCT GGTGTGCGGT CCGGTACAAA TNTGCTGGCA TAAATTCGCC | 60 |
| CGCNACTGGG AATGTGGAGC TCGTGAAAT CCCTATGNCG CCCCAGTCAG TTGTTTATGG | 120 |
| ACCCGAAACG CATGATTGAA AGCCTGTGAA CGAAAACACC ATCGGCGTGG TGCCGACTTT | 180 |
| NGGCGTGACC TACACCGGTA AACTTATGAA GTTCCCACAA CCGCTGCACG GATGCGCTGG | 240 |
| GATAAATTCC AGGCCGACAC CGGTATCGAC ATCGACATGC ACATCGACGN TGCCAGGTGG | 300 |
| GCTTTCCTGG GCACCGTTNG TTCGCCCCGG ATTATTCGTC TGGGAATTNC GNCTGCCGNG | 360 |

TGTGAAATCG NTCATGTTTC AGGCCTNAAT TCGGTTTGGT TCCTTGGGTT NGGTTGGGTT 420
ATTGGGGTAA GANAAGCGTT NCCAGAATNG TTGTTNACGT 460

(2) INFORMATION FOR SEQ ID NO:1433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

AGCAGGGAGC AGCACTTTAT CGGGNTCGGT GNTTTCACCG TCAATGAACA ATTTTTTNCG 60
GATTAAATAA GTTGATAGCA ATGGCGATGG TTTTACCCAG ATGACGACCG ACATACTCAA 120
TTACTTCCGA CGCCAAACTA TCGCCTTTNT TCGCGGCTTT GCAGATTAGT TTTGAATGGT 180
GCAGTCGTCC AGCGGCAGGA NCTGCTGGTA GCCCTGCTTT TAACAGGTTC AACACCCGTT 240
GTTCCAATGG CAGCGTTGGC AGCGATATTT TTCCAGGCAG CCAAGTTGCC GCAATGGCAG 300
CGTTTCACCC AGCGGTTTCG ACCTGAATTA TGGGCCATTT TCACCGACGT TGCCCTTGNG 360
GGCCAATAAA AATGCGCCCN TTAGGGGNT NATNCCGGGG CCCGGGTNNC CCATT 415

(2) INFORMATION FOR SEQ ID NO:1434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

TTCTGGGCAA AACCATGACC CGGAACAGAT TGATTTGATT GATTTACTAG TGCAGTTGTG 60
GCGTGGCNAG ATGACAATCA TCATTTCCGT CATTGTGGCT ATTGGCCTGG CTATTGGGAT 120
ATTTGGCAGT GGCGGAGGNG AAATGGGACG TCAACAGCAA TTATCACTCA GCCCCGACGTG 180
GGGCAAATTG CTGGGCTATA ACAATGCCAT GAATGTTAAT CTATGGTCAG GCTGCACCGA 240
NAAGTTATCG GNTTTTCCAG GANGTCGTTN AATTGGTCGG TTTTCAGTTC TGCCNNNCTC 300
TGGCATTNAG CAGAAAACGC TTGGGATAAT TCAGGGNAGG GANCGNGGAA AANNTTTACC 360
CNTGGGAAAC CTTGCTGTTT TAGGAANCCA GGCAATTTTA CCCTTGGATC TTGTTTTCTT 420
AATGNTNNGG GGCAAACTN TCAGAGGGGG GGGCACAATT TGATAGTTT 469

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

| | |
|---|-----|
| GTGAAGGGCT GAAAAATCGC TACGGCGCGC TGATGGNNGC CATTTNCGGC GTGCACTACA | 60 |
| NTTCTCTCTT GCCAATGGCA TNACTGGCAA GCAAGTGCGG TGNTATCTCG GNCGCTGATG | 120 |
| CCAAANAGAA AATTTCTGCG GGCTATTTCC GCGTTATCCG CAATNACTAT CGTTTCGGTT | 180 |
| GGGN | 184 |

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

| | |
|---|-----|
| TAACCCGTCT NACCTTGAGA TTGTAAGCCC GGTAGTTATC GGTTCNTTTC GTGCCCGTTT | 60 |
| GGACAGACTT GAATGAGCCG AGCAGCAACA AAGTGCTGCC CAATCACCAT CCACGGTGAC | 120 |
| GCCGCAGTGA ACCGGGCAGG GCGTGTTCA GGAAACCCTG AACATGTCGA AAGCGCGTGG | 180 |
| TTATGAAAGT TGGCGGTANG TAGTATTCGT NNATCAACAA CCAGGTGGT TTTCACCACC | 240 |
| TCTAAATCCG CTGGATGCCC GTTCTACGCC GTACTGTACT GATNTTCGGT AAAGATGGTT | 300 |
| TCAGGCCCCG ATTTTCCAC GTTTAACGCG GACGATNCGG AAGCCGTTNG CCTTTNTGAA | 360 |
| CCCGTTTGGG GGTTCGTTTT NCGTAACAAC TTTTAAAGGN GA | 402 |

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

| | |
|---|-----|
| GGCGGGCGTA TTAAGACCAC GNTCAAGGCC AGCTGTNAAG GCATCGGCAG AGTTTTCCTG | 60 |
| CGGCGGCAAA CCTGNGNCAT TCAATGAGTG ATTTAACAGT AAATAATGTA ATTCACCGGT | 120 |

| | |
|---|-----|
| CATCACGGTG CGNAAAATCG TTGAATTTGC TGGCTNTCGG NCTGCACCCA TTTGCAATGG | 180 |
| GTTCCGGGCA TGNCATAAAG AGAGGAAGGA GCCAGNGCTC GCGCGCCGNT TCAATTGTGT | 240 |
| TTCTTCCGNC GGGNGTTCAC ATTGTGGTTT ATCGTCATGA GAGACACATT AATCCGGGGA | 300 |
| TTAATCCCAG ATTATTGTNC GCCAANTNGA CGNTTAATTT GTTTCGGCCA TTAGGACGGG | 360 |
| NAAAACAGGG CCAGG | 375 |

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

| | |
|---|-----|
| TCAGAGGCAA GTTCAGACCG TGTTGTTTTT TTTTCACGGA TCCNGCCCTN NCTTCCCGNA | 60 |
| AAGAAGACAG CTTGGGTCG CGATTGTGGG GCTTNGAAGA GTCCAGCAGT GGGCAATTTT | 120 |
| TAGGAATTTG GGAATCGAGT GCATTTNCTG ACATTTGAGT ACAGTACCCA GGGGTTCTTG | 180 |
| GAGAAGAACC TGGTTCCCAG AGGAGCTTGA CTGACCATAA AAATGAGTAC TGCAGATGCA | 240 |
| CTTGATGATG GNAAACACAT TTAAAATATT AGTTGGCAAC CAGGTNATTN CATCTTGGNT | 300 |
| TTTATGGGGG GAAAGGTTGC AGTCAGNGGG | 330 |

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

| | |
|---|-----|
| GCATGANGAA TGTNCAGCTC GTCGATTCN TGGGGTTCCG CGCGGCCAG ACTCCAGCTC | 60 |
| AACGCTTTCT CTTTNATCTC TTCATAGAGC GCCANACGGC GTTTTTCGCT CAGCTTTTTG | 120 |
| GGAATCATTC AGCCCGGCAA TCGGGCGCGC CCGGGTCAAG GATCACCGCA GCGGTGACGA | 180 |
| ACCGGCCCAA CTGAACGGAC CCGCNTCCGA TTTCATCCAC ACCCGGCAAC CAGCTGNGTG | 240 |
| TGCGGGATNA AACAAATTCG GTGCATTGTG NTNAATNCCA GNAACGGTTT GTGCCACCTG | 300 |
| GTNCATCGGA CATTGACAGC GGNTTTGCTA GATGGNAGTT NCACGGNAAG GTTTTCGTNN | 360 |
| CANCGCGTGG TTGGTTTNC CNGTTAGGNC AACAGTGTTT AACAGTGACC GCAGCCAGTT | 420 |

TTTtagggTT CACATTTTtn CTGGCANTAA TTATTtGGGA TTAA

464

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

| | |
|---|-----|
| ATACGTCCGG TGGAGAAGGA GATATGGCAC AGCACTAAAG AGGCCACCAT CACCACCATT | 60 |
| TCTGGCGCAC CAAGTGCAAA CTGCAATTCG TTACCCGTCA TAAAGGCAAT TAGCGTGACG | 120 |
| ACAGGTNACG GTGAAGCGAA AATGGTTGCT AACACTGGAA CCAAAGAACA GATTCATCGC | 180 |
| GCGCTGAAAC CTGGTTGTTC AACACTGCTT TTNAATGCAC CTGAAACCTT CCGGCGACAG | 240 |
| ATTCAACAGT GCCACCAGGN AAGCCAGTTA AAGGCGACCA GGGGTCATTT CATGCTGTTC | 300 |
| GAGGCAATGT CTTCCCAGCG AGCTTGGCGT TNCATTTTTG GTTCACCGNA ATTAACGGGN | 360 |
| AATTCAGNTG GGNTAATTCA AACC | 384 |

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

| | |
|---|-----|
| GANTACCAAT GGTACCGACC AGCATAGAAG CCATAAAGGT TGACCACTCA ATATTCAACC | 60 |
| CGCTGGTCAT CAAGATCATT CGGGAACCAT GACCTATCGA GCCAAGCAGC GCACACCAGC | 120 |
| NTTAATTTCC GCTCTGTAAA ACGTTCATCA TGCCTTTGAA TTTGCCCCTG ACAACGCGCT | 180 |
| NAAGGCTNCA TACTGGTATT GCAGGCTGTT ATCGGCAAAC TGGGTGCGTT CGCGAATACC | 240 |
| ATAATACGGA CGGTATTNAC CGTCCAAGNC GAAAGGCTGG TNCCGGAAT NACGGTNTTT | 300 |
| GNCAGTTCCT GCGGGTTAGG NAGGGCGTTC ANGCCCTGAC GCCCGGNAA TGTGTTTGA | 360 |
| CGTTTGGAGG GTNCATCGTN CAGTGNAAC CCACCATTGG TTTGNATACC CCGTCCCAC | 420 |
| GTTTGNCATG NACNTTTTTT TNAAGTTTCA CTGGGGCAAA ATCGGTTATT CGNGGGGCCT | 480 |
| GN | 482 |

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

| | |
|---|-----|
| AACTCCGTGC NTGGCGACCG CAGCCCGGTT GTAGATATCA NCTTCCCGGA AATCGAGAAG | 60 |
| TTTGACCGTN TACCGGAACC GCGCGCCGAA GGCCGGACCG CTTTTTTTTC CATCATGGAA | 120 |
| GGCTGCAATA AATATTGCAC CTACTGCNTG GTGCCTTACA CCCGTGGTGA AGAGGTAAGC | 180 |
| CGTCCGTCCG ACGGATATTC TGTTTGAGAA TTGCCAGCT TGC GGCTNCA GGGCGTGCNT | 240 |
| GAAAGTCCAA CCTGCTCGGT CAGAACGTGA AACNCCTGGN GTGGGTGGAA AATAACGACG | 300 |
| GGCACCACCG GTTNCGTTTT G | 321 |

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

| | |
|---|-----|
| TTTCTGCATC CCCTGCGGGA AGCCTGCTGC CATGACAGCC TGAGCGTGAA TGCGCGGNTA | 60 |
| TCAATGCCGA CAATTCACGN CCGTATCACC CCAACAAGCG CAGATGTTTA AATATCATCA | 120 |
| GCTCGCGGTG GACAACAATT GGCCTCCCG TAGACTGNCC CTCATTGCCA TCAATCCGGC | 180 |
| TATCAGGGGC GCATGGCGAT CCACGNAAAT GGATGGTGGT GACGCCGNA ATTAACGGGN | 240 |
| CCGCTAATTG CATGAAAAAT GTGGATGNAA CAAGCACTGG GAGGCGAACT TAGTACCGGN | 300 |
| CAACAACACA AGGNCCTTCA ATCAAAAATG GGCCTGCAAA AAGTGATNAG CGGTGTACAC | 360 |
| N | 361 |

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

| | |
|--|-----|
| TTATAACGGC GCGCTGGTAC AGAAGGCCGC TGATGGTAGC ACCGTGGCGC AAACGTCTCT | 60 |
| CAGCTATGAC GACTATCGTT TCCTGGAAAA ACTCTCTCGC GAGTCGGTTC TCATTTTCNAC | 120 |
| GCCCTGGACC GCACCACGCT GTACACCGCC AACCGTGAAT ATCAGCTACT ACACGGTGCA | 180 |
| TGAATCCTTC GTTGCCACCA TTCCGCTGGT GTTCTGCGAG GGAGNAAAAT GGACCCCAAT | 240 |
| ACCCAGTTCC TGAAAGTGAA TGATGATTGA TGAACCCGCC ATCCTCGGAC CAGGCTTATT | 300 |
| CGCGCGTTAT TTCCGCAGAA GTTGNAAGA GGAAATATTA CCGTGCTTGN AAAAGTGGCG | 360 |
| NCNGTAATTT CCTCGGAATT CCTCGGTTAA ACGGGGTTAA ACAAAGGTTA CGGGGGGTNG | 420 |
| AAAATCATTG GGCCNACGTN TTAAGTTTTT NAAACCGGAG GGAATTCATG GGGGNTTGG | 480 |
| | 480 |

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

| | |
|---|-----|
| GGCACGAGTA ACTCTNTCTT TTCCTGATAA CATGGCCAGC AAGAAAGTAA TTACAGTGTT | 60 |
| TGGAGCAACA GGGGAAGCTG GTGGCAGACT CCGCCAAGCA CCTGGGTCTG AAGCACGTGG | 120 |
| TGTACAGCGG CCTGGAGAAC GTCAAGCGAA CTGACGGATG GCAAGCTGGA GGTGCCGCAC | 180 |
| TTTGAACAGC AAGGGCGAGG TGGAGGAGTA CTTCTGGTCC ATTGGCATCC CCATGAACCA | 240 |
| GTGTCCGCNT GGCGGCCTNA CTTTGAAAAA CTTTTCTCGN GGNGTGGCGG CCCGTGAAAA | 300 |
| GCCTCTGAAT GGNG | 314 |

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

| | |
|---|-----|
| TAATGCNCAC GGAAGTGGAA GGGAATTTTA AATGATTCCA CCCTGCTGGC GGATCTCAAT | 60 |
| AGCCCATTGC CAGAAGGCTC CGTGCGTAAC TGGAATCCTG CCGGTCGTCG CGGNNTAGTG | 120 |
| AATTCTGGTC ACTAAAGAAG CGCATTGCCT TGGCGATTG TTGATGAAAG CCAATTAACG | 180 |

| | |
|---|-----|
| GCGGCCTGGA TGTGAAAATC GCGGCAGTTA ATTGGTTAAC CACGATAATT TACGTTCTCT | 240 |
| GTTTGAGCGT TTTGAATAAT TCCGTTTGAG CCTGGTAAGC NCATGNAAGG GTTTAACCCG | 300 |
| NAAAGGNGCA CGNTTCAAAA GATGGGGGG | 329 |

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

| | |
|---|-----|
| ACTAATGGCA CCTGCAGATG ACCGTGGGCT GGATTTTCAG TAAGTCTCTG GGGGTTGATG | 60 |
| AATCCACCGT GGCAATCGTT GTTATGGCAA CCATGCTGCT GCTGGGTATC GTTACCTGGG | 120 |
| AAGACGTGGT TAGAAATAAA GGCGGCTGGG AATACCTTAA TCTGGTACGG CGGTATTATC | 180 |
| GGCTTAAGCT CTTATTATC GAAAGTTAAA ATTNCTTCGA ATGGGTTAGC TGAAGTCTTT | 240 |
| AAAAATAAAC CTGGGCATTT TGTGGGTCCA CGGGTAACGT TGNGTGTCTT CGTTAATTAT | 300 |
| TTTNCCTCAG GATTGTTTCGT GGCCTTAATT TCCTTNGNT TTCCCGTTAG GTG | 353 |

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

| | |
|---|-----|
| GGCANGAGGG NAGACAGAAA ACAGGTCTTG NTTCCCAAN TGGCATTGGA CTTTCTGAT | 60 |
| ATTACTGCCA ACTCTTTTAC TGTGCACTGN GATTGCTNCT CGAGCCACCA TCANT | 115 |

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

| | |
|--|----|
| GGCAGAGGN AGAATGGAGA GGGGGCTGCC GCTCCTCTCC CCCGTGCTCG CCCTCGTCCT | 60 |
|--|----|

| | |
|--|-----|
| CGCCCCGGCC GGCNCTTTTC GCAACGATAA ATGTGGCGAT ACTATAAAAA TTGAAAGCCC | 120 |
| CGGGTACTTN ACATCTCCTG GTTATCCTCA TTCTTATCAC CCAAGTGAAA AATGCGGATG | 180 |
| GGCTGATTTTC AGGGTTCCGG ACCCCATACC AGNGNATTAT GATCAAANTT NAAACCTTCA | 240 |
| ATTTGGATTT TGGAGGGACA AANGAC | 266 |

(2) INFORMATION FOR SEQ ID NO:1450:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

| | |
|---|-----|
| GGCANAGGCA AAGATCCCTG AGGATGTGTC TGGTCTCGTT TCTCTTGAGG TTCTTATCTT | 60 |
| ATCAAACAAT CTTCTAAAGA AGCTTCCCCA TGGTCTTGGA AACCTTAGGA AGTTAAGAGN | 120 |
| AGTTGGGATC TAGAAGAGAA CAAATTGGGA ATCCTTGNCC AAATGNAAAT TGNCATATCT | 180 |
| TAAGGNTTTA CAGAAATTAG TCTTGACAAA CAACCAGTTG ACCACTCTTC CCAGAGGCAT | 240 |
| TGGTCACCTT ACTAATCTGC ACACATCTGG GGCCTTGAG AGAACCTGAC TTGACTGCAC | 300 |
| CTTTCCTGNA GGAAATTGGT AACTGAGGAG GAACCTTGGA GGNACTGTAT TTGNANTGAC | 360 |
| AAACCCCAAC CGGCATAGGC NTTCCCTTTT | 390 |

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

| | |
|--|-----|
| GCGAAGCTGC CTGCAACCTG GAACCGGGNA GCGGCACAGG AGACGGTGCG GCTGCTGGGC | 60 |
| GGGCCAGNGA AGCAAGGNGG GGCCGCCCCG AGGGAAACCA TGCTGCCTTC CAGGCTGACG | 120 |
| TNTCTAAGGC CAGGGCCGCC CAGTGCCTGC TGGAAACAAG TNCCAGGCCT GCTTTTTTTCG | 180 |
| CCCACCATCT GTGCGTTGTN TCCTGTGCGG GGCATCACCC AGGATGAGTT TTCTGCTGCA | 240 |
| ATTTGTTTGA GGATGACTGG GANCAANTCA TNAGCTGTNN AACCTCAAGG GGCACCTTTC | 300 |
| CTAGTCACTC AGG | 313 |

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

| | |
|---|-----|
| GTCGTCGCCT TTAATCAGAC GGGTATTAAA ATCATCGGCA AAGCAGCTAT TAAAAATTTC | 60 |
| AATCAACTGC TCGTANTGGT GTGTACTGTT CATTAGTTCA TCCCCAACCA NTGGGGGNTC | 120 |
| TCCTGTCCGT GGTGTGCGTA ANTTAATTTG GCACTGCATC ACCGTNCGAG ACGNTTAACA | 180 |
| | 180 |

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

| | |
|---|-----|
| AACCTGGCCT CANTTTGATT CACCCGCTTC AGGTGTTCGA GGTGAACAG CAGGATAATG | 60 |
| AAATGNTGGT CTATGCTGCC CCCCCTGAAT GTGCGTGAAA CGTACCTGGG CAGCTTGATA | 120 |
| CGCCTTTATT TACGTTGCGC TTTTCTCCC CACAGGTAAG GTATTGTCGG TGTGCGGATT | 180 |
| GAGCATTTTC AGGGGGCGCT GAATAACGGT CCTCATTATC CGCTCAATAT TTTGCAGGAC | 240 |
| GTGTAAGGTC ACAATCGAAA ACACAGAACG TTATGCTGAG TTAAAAAGT GGGCAACTTA | 300 |
| AAGCGNCGCG TNTTCAGCAA AAGGTGGAGT TTCTGGGTCA CTGGGATTTT TCTGAGGCAA | 360 |
| CGGNGNGNCG TTATTAACCG GTTAGTTCAG TGGAAAATTA ATTGGGTAC GTGCAGGACA | 420 |
| NGANTAATTC ACGCAATTAT ATGTTNAGG CGGTTGATCT TGGGGTTGGG GAACAGTTTA | 480 |
| GGGTCNNGG | 489 |

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

| | |
|---|-----|
| TATCAATGCC GAGAATATCC AGCCACTGCT GCACCANTTT TTGCTGGCGA ATCCGAAACG | 60 |
| GCCTGATAAA TGGCCAATCG GAATCAAAAT GAGNCCAGTA AAGGAATGCA CATTNACGGN | 120 |
| ACGGTAAGNT NGNAGCCCGG TNAATGCCAG ATGGCAAAC TAACTTGCTGN ACGTGAACCG | 180 |
| NATNATGNCT TTTTGAATAT CCCAGAATGG GTTTNCGCCC GCTGCCGNGA ACGTTCGTTC | 240 |
| CGAAAAAGGC GGTGCAAATC GTTTGCTGTT AACCTTGCGG GATGGATNGT CATTAACCAG | 300 |
| GGTTNATTA AGTGNGTTTT NCCGG | 325 |

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

| | |
|--|-----|
| AACCATTTTCG ATATCTCTCT GCGGATGTTT ACCCATGTGG GCGCGGCGGC ACCGGGTAAT | 60 |
| CCTACCGCTA TCGATACCCA CTGGATTTGG CAGGAGGGTG ATTGTGCCTT GACCCAAAAT | 120 |
| CCGCTGGAGA TTA AAAACGG AAAAATTGCC GTTCCTGATG CGCCCGGTNC TGGGGTGGNA | 180 |
| GCTGGNACTG GGGAACAGGT NNCAAAAGGC ACATGAGGCC TATAAACGT CTGCCTGG | 238 |

(2) INFORMATION FOR SEQ ID NO:1456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

| | |
|---|-----|
| GGCACGAGCC TTCATTGCCT CATGTAAGAC AACCTCACCA AATACAAGAA AACAGTGTCC | 60 |
| AGCCACCTT TGACACAGTT TTTNCTTGAT TGTGGAGGAC TAGCTCGAAC AGATAAGAAA | 120 |
| CCTGCCATTT GTAAAAGTTA TCTCAAATA ATGACAGANC TGTGGCATAA AAGCAGGCCA | 180 |
| GGATCTGTTG TGCTACTAC TCTGTTTCAA GGAATTAAAA CTGTAAATCC AACATTTCCG | 240 |
| GGTATTCTC AGCAGGATGC TCAAGAATC CTTCGGTGTT TAATGGATTT GCTTCATGAA | 300 |
| GGATTTGAAA GAGCAAGTCA TGGAAGTAGG AGGAAGGTCC GGNAAACCAT AACCCCTTNT | 360 |
| GGGGGGCCAT TGGGAGGGNG GGNCAAGGGC NATCCGGTTT TTGGGTTTTT CAGG | 414 |

(2) INFORMATION FOR SEQ ID NO:1457:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

| | |
|---|-----|
| GGCACGAGGA CATATTGATC CCTCTCTNAG ACTCATCTGG GATTTGGCTT TCCTTGGAAG | 60 |
| CTCTTACGTG ATGTGGGAAA TNACAACACA GGTGTCACAC TACTACTTGG CACAGCTCAC | 120 |
| TAGTGTGAGG CAGTGAAAAA CTAATGATGA TACAATTGAT TTTAATTATA CTGTTCTACT | 180 |
| TCATGAATTA TCAACACAGG AAATAATTCC CTGTCGCATT CACTTGGTCT GGTACCCTGG | 240 |
| CAAACCTCTT AAAGTGAAGT ACCACTGTCA AGAGCTACAG ACACCAGAAG AAGCCTNCGG | 300 |
| GAAACTTGAA GGAAGGATCT NCNTGTAGTT ACCCAACAGA GCTTTAGTAA TTTTTTAAAA | 360 |
| AGGAAAAANT GATNCTTTTT TCCG | 384 |

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

| | |
|--|-----|
| CTGCTGCCCC TNAGGGGCCA AGCCAACANA GGCTGCTACG GGATCCCAGG GATGNCCGGC | 60 |
| CTGCCCCGGG CACCAGGGAA GGATGGGTAC GACGGACTGC CGGGGCCCAA GGGGGAGCCA | 120 |
| GGAATCCCAG CCATTCCCGG GATCCGAGGA CCCAAAGGGC AGAAGGGAGA ACCCGGCTTA | 180 |
| CCCGGCCATC CTGGGAAAAA TGGCCCCATG GGNACCCCTT GGNTNTTTAA GGGGTGCCCCG | 240 |
| GCCCCATGGG CATCCTTGGA GAGCCAGGTN AGGAGGGCAG NTACAAAGCN GAANTTTCCA | 300 |
| GTAAAGTTTT TCACGGGTCA NTNGGCAGAC CCCAACCAGC CCCTTGNAAC CNAAAAGCTT | 360 |
| NTTANNTTTA AAGGGGGGTT CTTAACAAAC CCGAAGGGGT TTTTNNACA AGGGCAATTG | 420 |
| GNAATTTTAA CTTGAAAANT NCCCGGTTTT AATATTTTTT TTTTACCA | 468 |

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

| | |
|---|-----|
| GGCANAGCCA GCATCAGGCT TCCAGAGTTT GCAATTCCGA CTATTAGAAA ACAAGATAGG | 60 |
| TGTTCTTCAG AACATGAGAG TCCCTTATAA CAGAAGACAT TATCGTGAAT AACTTCAAAG | 120 |
| GAGAAGAAAA TGAAGTCTA CTAAATCTG AGCCAGGAAA AGACACTTCT GGAAATTAGT | 180 |
| GGAGGCATGG CTGGAAAGAA CTCCAGGTTT AGAGCCACAT GGATTTAAGT TCTGGGGAAA | 240 |
| GCTTGAAAAA AATATCACCA GAGGCCTGGA AAGAGGAATT CCNTAAGGTT TCAGGCTAAA | 300 |
| GAAGAGTCTG ANGAAAAGGG GGAACAGTGG CTGAATTTCG GANGCAAAG AGGTGCTATG | 360 |
| TCCNTATTTG TTGAGAAACG TCCTGAACCA TTCCCTTNGT NAAGGTTAAA NACGG | 415 |

(2) INFORMATION FOR SEQ ID NO:1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

| | |
|---|-----|
| GGCAGGAGCT CGGCTACATT CACCTGCTAT GCTTGTNACT CCACCCTGCT CTAATGCCGC | 60 |
| TTTCTCTGCA GGCTCTTCTT GGTCCCCAA GCTAAGTGGC TCTTGCCCTT GTGTACCTGC | 120 |
| ATTGCAGTTT TATGATACTT CTCATGTCGT GTCTGTGCTT TCCTACCATG CATTATTATT | 180 |
| CACGTGCTTG TCTCATCTCT TCTGCCAAAT TCTAAGCATC TGGATGGCTG GGTTTAAGTT | 240 |
| GCATCTCTGT GTCCTTCAGA CCATATGCCA TAGTGCCTTG TGCCTCACGG TGACTTGTAT | 300 |
| TTTGCAGAAG CTTAACAGAT ATTAAGTGG ATATCCAATT ATAAAAGAGT CATNAAATAG | 360 |
| ATGGTATTTT ATGGTTAACA ATATTTAAAT GTAGGAAGTT TATTCAGTTC CTGCGNAAAA | 420 |
| TCAACTCTCA AATTCCAGTT TTGTTTTTCT TTGAAAGTGT CTGAAAACT NG | 472 |

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

| | |
|---|----|
| GGCAGGAGGT TTCTTATATG CACACAGCAT GCCTCTGCAA TGCCATCATT GCTTTGCTGA | 60 |
|---|----|

| | |
|---|-----|
| AAGTTCCCCT TTCTTTCCAG AGATATTTTT TCCAGAACT ACAGTCTACC AGCATCAAGC | 120 |
| TTGCTCTGTC ACCATCGCCC CGGAATCCTG CAGAGCCCAT TGCTGTCCAG AATAACCAGC | 180 |
| AGCTGGCGCT AAAGGTAGAG GGAGTGGTTC AGCACGGGAT CTAAACCAGG ACTCTTCCGC | 240 |
| AAAATTCAGT CTGTCTGTCT TGAATGTTTT CTTCCACACT GCAGAGTAAA ATCTGGGACA | 300 |
| AGACTTACAA GGTTACCCCA TTTGACAAAC ATGGACCCAA TGNGGTTGGA GCAAAGGGTT | 360 |
| TGAACNCCN AATGGTTATT TTCAGTACTC NATTTCTGTT GGAACCTTTG GTTATCCTTG | 420 |
| GGACCACACA CCTTTCAGTG GGATNTTTTT TTGAAAGATG NCCATGGTTT GGTTTTGGAG | 480 |
| GCTTGAG | 487 |

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

| | |
|---|-----|
| GTTCGGCGTT TTGCGTCGCT GTGNCCTTCC ACCATCGNAA TCATCCGATC CAGAAATNTC | 60 |
| TCGCCGGGGT TAACGCTACA CTCAATCACC AGCCAGTNAG AAAGNAATAC GCGTGCCTTC | 120 |
| GGTGAACGGA GGCAAANATN CGCCGCCGGG ATTCACGGAT CACCGGTGAC CNATNTCCCC | 180 |
| GGTGATGGTC GNTTTCGATA CGACCGANGC ACCCCCTTCA ATAAACTTNA CCATCGCAGG | 240 |
| GGG | 243 |

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

| | |
|---|-----|
| GGCANAGCCG CAGGACCCCA TCCTGTTCTC GGGGACCCTG CGGATGAAAC CTGGACCCCT | 60 |
| TCGGCAGCTA CTCAAAGGAG GACATTTGGT GGGCTTTGGA AGCTGTCCCA CCTGGCACAC | 120 |
| GTTTGTANGG TCCCAGCCGG CAGCCTGGGA CTTCCAGTGC TCAAAGGGCG GGGAGAATCT | 180 |
| NAGCGTGGGN CANAGGCAGC TCGTNTGCCT GGGCCCGAGC CCTGCTCCGC AAGACCCGCA | 240 |
| TCCTGGTTTT AAAACGAGGC CACAGCTGCC ATCGAACCTG GGNGACTGAN AACCTTCATT | 300 |

| | |
|--|-----|
| CCAGGGTTAC CATCCGGNAC CCAATTTGAA TACCTGNANT GTTCCTGACC NTGGAAAACG | 360 |
| GNTTTAACAT TTTCNNGGATT ACANCAGGTN CTGGTTCCTG GACAAGGAGT AGTAGTTGAT | 420 |
| TTAATTNTCC AGCCAACTTC NTGCAGTAGN GGCATTTTTT AGGGATGGCC AAAATNTTGG | 480 |
| ATTTGTC | 487 |

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

| | |
|---|-----|
| CCTGTGTACA NAGGATTGCT NCCNCTACGC TATGTGGGAC ATTGNCCATC CCATGCAACA | 60 |
| ACAAGGGAAG CTCNATCAGT GGGTTTGAAT GTGGTGGCAT GCTGGGCTCG GGAAAGTTCT | 120 |
| GCGCATGCGG TGGGCACCAT TTTTCCCCGT TGAGACACCN CATGGGAAGG GTTNATGTCC | 180 |
| TNGTCCTCGT NACTTCNGAC AAGAG | 205 |

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

| | |
|--|-----|
| GGCAGAGGAT TTGAGTGGCA TATAACCAAA GGCGGAAATA TTGGGGCTAA GTGGACTATT | 60 |
| GACCTGAAAA GTGGTTCTGG AAAAGTGTAC CAAGGCCCTG CAAAAGGTGC TGCTGATACA | 120 |
| ACAATCATAC TTTCAGATGG AAGATTTTCAT GGAGGTGGTC CTGGGGCAAG CTTGACCCTC | 180 |
| AGAAGGCATT CTTTAGTGGC AGGCTGAAGG CAGTAGGGGA ACATCATGCT GAGCCGAAAA | 240 |
| CTTCAGATGA TTCTTTAAAG ACTTACGGNC AAGCTTCTGG AAGGGGCACA CTNACACTTT | 300 |
| TTANTGAAAA ATGGGANTCC TTAAATAAC TCTCTTTCAC CCCAANTANG GTTTGGNTTA | 360 |
| TTCTGGCAAA AGTGATTTAG GANCTTAGGT TGCAGGGGAA ATTGGTTTTA ACTTTTTNCA | 420 |
| GTTTTTC | 426 |

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

| | |
|--|-----|
| GGCAGAGCTT TTTCCANAAT TTAAAATTGT AATAGAAACA GAAGATGAGA TTATGCCTGA | 60 |
| GGTTGTGGAA AAGGAAGATT ACTCAAAGAT TATAGGGAGC ATGGGGATAT AATGGGAAAG | 120 |
| CAACACTCCA GTGGTGCAGA TGCTCACAGT CTTATGGAGG AGCCCAAATG AATATCTGGG | 180 |
| GAAGTTAAAG TCCATATGAA TGNACTGATA AAGAGTACAA TACAGGTGCC ATGGGGANCA | 240 |
| CGTGNGCATT CACTGGAAGA CTGCCTGGNA GGGGGCCGCG CGTGTTTTCCT ATGGCCTATT | 300 |
| ACGGTTAANC CTGGTNACAT AATGGAAAAT GCTTATNCTT TAGGTGGAAA GGNGAGCCTN | 360 |
| GAGTTTAGCC GGTTCAGGG T | 381 |

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

| | |
|---|-----|
| GGAACGACCT TAATNAAAGC NATTNAGGCT TATGGAATGA NGCCACATNA AATATTCAAG | 60 |
| GCAAATAACC TTTTANGAA TTGGAAAACA TGNNCCAGGT TCAAACACT CTGGTGGCTC | 120 |
| TGGACAGGTC TGGCTNAAAN CAAAAGGTTT CCATACANCC ATTGACATTG GGGTTAAGTT | 180 |
| TGCGGANAAC CAANCAAGAG GTTTTGATG | 209 |

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

| | |
|---|----|
| GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTAN NCCCCCN | 57 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

| | |
|---|-----|
| AGATGCAACT ACCATCACAG AATGTNTTCA TACCTNNNGT AAAAGCTGCA TCGTAAGACA | 60 |
| TTTTTACTAC AGCAACAGAT GTCCAAAATG CAATATAGTA GTACATCAGA CACAACCTCT | 120 |
| TTATAACATA AGGTTGGACC GACAGTTACA AGACATAGTG TACAAATTAG TGATCAATCT | 180 |
| AGAGGAAAGA GAAAAAAGC AAATGGCATG GATTTCTATA AAGGNAAGAG GTCTAGNNGT | 240 |
| ACCTNAAACC TGCTGTTCCA CACNC | 265 |

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

| | |
|---|-----|
| AAAGGNTTGA ACCGTGCCTC ANAGGCAGTA NAAGCCCCAT GGTGGTGGTG CTGNGTGGNA | 60 |
| GTATGGAGCC GGCCTTTGAA AAGAGGTGAA CCTCCTGTTC CCTAAAAAAT TTCCGGGAAA | 120 |
| GNCCCAATNA AAGATGGTGA AATAGTTGTT TTTAAAAGTT GANGGGNCGG GN | 172 |

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

| | |
|---|-----|
| NATGTTTAAAG ANCACTCGTN AACTGCNTT CAGGCCATCA AGGGTATGCA TATAGAGAAA | 60 |
| GCCACGAGTA TTCTGANAGA TGTGCACTTT ACGGAAACAG TGTGTACCNT TCCGACGTTA | 120 |
| CATGGTGGNG TTGGCNGTGT GCGNGGTCAG G | 151 |

(2) INFORMATION FOR SEQ ID NO:1472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

| | |
|---|-----|
| GGCANAGGNC AAAANATACT AGAATTNATA GTGGAGAGAA ACCTTACAAG TGTAATGNGT | 60 |
| GCAGCAAGNC CTTCCGTCTA AGGTCATACC TTGCAAGCNA TCGCAGNGTT CATAGTGGTG | 120 |
| AGAAAACCTT ACAAGNGTAA TGAGTGCAGC AAGGNCCTT | 159 |

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

| | |
|--|-----|
| GGCANAGGGG ANGCCAACCTT CANTNTATCC TCAATNCATG GAGACATNCC CANAAAGNGC | 60 |
| GGGNGTCCAT CATGAAGGAG NTCCGGTTCG GGCGCCACCN GGTGCCTTAT TTCTGACAGA | 120 |
| TNNTCTGGGC CAGGGGGTTG GATGNCCCTC AGGTGTCCCT CATCATTA | 168 |

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

| | |
|--|-----|
| GGCAGAGACG GNCACGAGAA GACTTAAAGG TAAAGCGTAT TACCCCTCGT AACTTGGCAA | 60 |
| CTTGCTATTC GTGGAGATGA AGAATTGGAT TCTCTCATCA AGGGCTACAA TTGCCTGGTG | 120 |
| GTGGTGTCAT TCCACACATC CACAAATCTC TGAATTGGGA AAGGAAAGGA CAACAGGAAG | 180 |
| ACTGTCTGAA AGGGTGCCTG GNATTCCCTT GTTAATCTCN AGGNACTGTT AAATNACTCT | 240 |
| GAGCAGNTGG TCCCAGTGTT GGTGATTCCC AGTGGA CTGT GATGNTCTGT GAAAAAAACC | 300 |
| ACAATTTTTG CCCTTTTTTG GGTAAATTGC TGTTTTNAGG CCAAGTTTGG GGAAGNTTTA | 360 |
| AATTAGNNTT TTCC | 374 |

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

| | |
|---|-----|
| TGCCAGTATT TGANCATTAC CATGAAGGAA CTAGCAGTTA TGAAGTACT GGTTTAGCCA | 60 |
| GAGGTGGGGA ACAGTTGGCT AAATTAAAGA GGAATTATGC CAAAGCAGTG GAACTNACTG | 120 |
| GTGGNAACTN AGCTTCTCTG CCAGACTTCT TTTGTTACTT TGGATGAAGC TATTAAGATG | 180 |
| AACCAACAGG CGTGTGAAAT GCCATTGNAN CATGTGCATC ATCCCCGGG ATTGANCGTA | 240 |
| CTCTTGCTTA TATCATCCAC AGTAGCTGGG ATGGAGGAGA GAGNN | 285 |

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

| | |
|---|-----|
| GGCAGAGATG GGCAGTGGTG CTGGATTAA NGTTGATGCC ACTAAAGATC CTTGGGAAAA | 60 |
| CCAACTACAG AATGTNCTCT TAATGTNACA AAGGAGCTTC CCCAACTNAT AAATGCCCCA | 120 |
| TTTNCCAGTG GGATCCCCAA AGGAATGTCT ATTTTGGCC ACTCCATGGG AGGTCATGGA | 180 |
| GCTCTNAATC TGTGCCTTTG AAAAAATCCT GGGAAAATTA CAAATCTGTG TNAGCATTTN | 240 |
| NTCCCAATTT GGNAACCCTG GTAATTCTGT CCCTGGGGCA AAAAAGNCTT TGGTGGAT | 298 |

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

| | |
|---|-----|
| GGCAGAGNCA CCAGCCTCTN ACGGAGGCAT CTTAATGTNA ACCTACCTAC CATTGCCCTG | 60 |
| TGTACACAGA TTCTCCTCTG CGCCTATGTG GACATTGCCA TCCCATGCAA CAACAAGGGA | 120 |
| AGCTCACTCA GTGGGTTTGA ATGTGGTGGA TGCTGGCTCG GGAAAGTTCT GCGCATGNTT | 180 |
| GGGCACCATT TCCCGTGAAA CACCCATGGG AAGGTCATGC CTGGATCCTG TACTTCTACA | 240 |

GAGNATCCTG AAGAGGATTG AAAAAGGAAG AGGCAGGCTG CTGCTGNAGG AAGGCAGTGA 300
CCCAAGGAGG GAATTTTTC A GGGGTGAATG GACTGCTTCC CGTTTCCTGA GTTTCAATGG 360
TTAATTTAGG CTTGNGTTNN CANATTTGGT TTN 393

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GGCANAGCTA TGGGTCGTGG AACAAAAGTT AATCCTACAC CTAAANANG ACCAAACTAA 60
GTACTTGGAG GAACGAGNNA TAAAGGTG 88

(2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GGAAGAGTNT CTACTGTGGG CAAGTNTTTA AGANGTCCCC CATGCGGTAA AAGANCTTNG 60
GAATCTGGCT GC 72

(2) INFORMATION FOR SEQ ID NO:1480:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

CTCCGTGNCA CTTTATGAGC GCATGAATCA GTCTCTCTCC CTGCTCTACA ACGTGCCTNN 60
CAGTGGCCGA GGAGATTCAG GATGAAGTTG AATGAGGTNC TTCAAAAAGA GGCAAACTG 120
ATTNCAAATG ACGTCTTGGC CAACATGATT AGTGAACCAA GGAATCAGTT ACGGAAACGA 180
TGCTCTGCAT GCCATTCTTT NAACCGAAAC GAAAACCACC GTGGGNGGNT TCCTTTCCCG 240
TNGNAATGG 249

(2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

| | |
|---|-----|
| GGCAGAGGNT GAATCTCCTA TAATGATGGA AGAAGAGGTT CTCTTGTCTT AGATAGATNA | 60 |
| GAGCCTTCTC CAAGAGCAAT GTCAAAACTT GGGCTGTCAT CTTTGAGCTG TTTACCAAAA | 120 |
| TACAGACCAT TATTGAAGAA AAACAAATTA TCTATTTTGT TTTCCCCCAT CTAATATGAT | 180 |
| AGTGCCCCCA ACCAGGTTGT AGCATTGCCT TTTAAAAGAG ACTCACTCAC TCTTAGTTTT | 240 |
| TAAGGAACTG GGAAATTTCC CATCCTCAGA TCCCTTAAAG GATGAAGAGT TGGCTGTACA | 300 |
| CTTAGCGGAC TTGCCTCNTG GTATGCAAGG GANTACTGGT TTGAAGGTCN GTTTTGNNCG | 360 |
| TGTC | 364 |

(2) INFORMATION FOR SEQ ID NO:1482:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

| | |
|---|-----|
| GGCANAGGGA CAGACCAAAG TATCCTGGAA TCAAATTTGA AGAACTCTTT CCAGATTGGA | 60 |
| TATTGGCATC ANAATCTAAG CGAGACAAAA TAAAAACAAG TCAAGCCAGA GAATCTGTTA | 120 |
| TCAAAAATGT TAGTGAATTG NATCCTGNAC AAGCGGATCT CTGTAGACGA ANGCTCTGCG | 180 |
| TGCACCCATA CATCACTGTT TGGTATGACC CCGCCGAAGC AGAAGCCCCA CCACCTTCAA | 240 |
| ATTTATGAAT GCCCAGTTGG GAAGAAAGAG AACATGGCAA TTGAAGATTG GGAAAGAGCT | 300 |
| AATTTTACAA NGAAGTCCTG GGT TTGGGAA GGAAAGGAAG CAAGGANTGG TGTTTGTA | 360 |
| AGGATCNAGC CTTCCGATTG CCAGCAGTNA GTTGNC | 398 |

(2) INFORMATION FOR SEQ ID NO:1483:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 259 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

| | |
|---|-----|
| GGCANAGTNA GGAATGGAGA AGCCAGAGAT TATTGATGAG CTGCTGAATA TAGAGAAAAA | 60 |
| TCCCCAAAAG CCTCAATATA GTATGGCTGT AGAATTCCT CTAGTCTTAT ATGAACTGTG | 120 |
| ANTTTGAAAA TGTGCAAGTG GATCTATGAA CCAGGAGGCT CAGGAGTTCA ATATTACCCA | 180 |
| CCTACAACAA CTGTGGGTCT TAATCATGCT GTNCAAAACT GCACATGGTT TGTATTAGG | 240 |
| TATNNGTAAC NTGAGTTNT | 259 |

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

| | |
|--|----|
| GGCAGAGGAG TTTTTTTTTT TTTTTTTTTT TTTTTNNAT TNTNAAANTT TT | 52 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

| | |
|--|-----|
| ATCCTAACTC CAACCCACCA TGTNACAAGA CAATGGATGA GGATATTGTG AATTCAGCAG | 60 |
| GACGATGAGA TCCGCTTAAA GATTGTGGGG ACCCGTGTGG ACAAGAATGA NNATTTTTGC | 120 |
| TAATTGGCTC CCTGAATGGA CGATTACTTG GGGCTTGTA GCTGAGCCTG GTGGCCTCCT | 180 |
| ACCNTTGGTC CTA CTCTAGG AAGTGTGATT GTAACNCTTA TCATGTTGTC CAGAGGTCCA | 240 |
| GTTTGGCTGC TGTGTGGAG GCAAGGNAGG CAACTCATNC CAGAAGGCAT CTGGGTGCTT | 300 |
| CTGTAGCTT AA ACTAATTG CCTCCTCATN TTTCAAGTAT GTGGTCTTA AGTATTAAAA | 360 |
| AGTNCCTNGG TTTCTCCAAA AAAAAANAAA AN | 392 |

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

| | |
|---|-----|
| GGCANAGGGA GACCCAGGTT GCTAGGACTC TTTCTTGGC TTGATGAAGC AAGAGGCCAT | 60 |
| GTCAGGGATC CATGAGGCCA GGAAGGAGGG CAGCCCACAG GAACCTCTGC AATAACCTAG | 120 |
| GTGAGCTTGG NAAGCAGCTC CTTCCCCAGC CTCACGTTCA GATGAGCTCT CCTCCCTGAG | 180 |
| TGATACCTCG ATCAGATCAC AATTCTCAGC AGACTCAGCA AAGCCATGTC CAGCCTCCTG | 240 |
| GCCCACAGAA ACCACAAGAT AATAACTGTA TGTGTGTTAG GACCTTAAAG CTCNTAGTCA | 300 |
| TCCATTCCAC AGCAATAGAT ANTACTGGAT AAAAGGAGGT TAGGAAAGAA ATTTNTTTAG | 360 |
| GTTAGGTTAG AGTGAAAGAG TCCCTCAGCC AGAGTTTCCC TTTTAAACAC AAAGCAGNCC | 420 |
| CNGGNAAAAC ATTTCTNGTT TTAACAAGGG GC | 452 |

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

| | |
|--|-----|
| GGCAGGAGAG ATCAATGACT TTTGCCGTTT TCAGTGCCCT CCAATTAAGT TTATCAGTGC | 60 |
| AGATGTACAT GGAATTTGGT CAAGGTTATT TTGTGATTTC GGTGATGAAT TTGAAGTTTT | 120 |
| AGATACAACA GGAGAAGAAC CAAAAGAAAT TTTCATTTCA AACATAACGC AAGCAAATCC | 180 |
| TGGCATTGTT ACTTGCNTTG AAAATCATCC TCACAACTG GAGACAGGAC AATTCCTAAC | 240 |
| ATTTTCGAGAA TTAATGGGAT GACAGGTTTA AATGGATCTT TGACAACAAT TAACGGTGAT | 300 |
| NTCGCCATTT TNCTTTTAGT ATTGGTGGAC ACCACAGAAN TGGNAACCTN TTTGACNGGN | 360 |
| GGCCTAGGNG TGCCAGTTNA GGANTCCTAA AACANTTTTT TTGGATTCAN GGNGGGGNGC | 420 |
| TTTAAACNT CCAAGTGCCC TTTGTGGGT TTTNGNCAAC NGGCGGGCA CCTTGGGGGT | 480 |
| TTACACAGT TTGTTTGNCC TG | 502 |

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

| | |
|--|-----|
| GGCANAGGAA AGATGGTGTT ACTGCAAGNA TGCTACTCGT GAGGTGNAAT TCGTGAAC TG | 60 |
| ATACCAGTTC TGTCATTGAT GCACAATGTT CAATCCTTGT GGGTATTCTGA TGAATGGATG | 120 |
| AAATCGGATG GAACTTATTG GACTATTCAA CATCACTNCA GACCAGANTT TCTTATGTTA | 180 |
| GNTTGGACAA CTTAGTCAGC CTCTATGATG NCNGTCAGAA GT | 222 |

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

| | |
|---|-----|
| GGCACGAGGT NTCCCTGTTG CCCTTGGTCT CGGGGNCGCT GTCGGCGCTG AGGCTGCAGC | 60 |
| TATCATGGTG AACTTACTTC ANATTNTGCG GGACCACTGG GTTCANGTTC TTGTCCCTAT | 120 |
| GGGNTTTGTC ATTGGATGTT ATTTAGACAG AAAGAGTGTA TGAACGGGCT AACTGCCTTC | 180 |
| CGGAACAAGT AGTATGTTCA TNTAAAAGGG AATTGCAACC CAGTGAAGAA GTTGATCTGG | 240 |
| TAAGTTAAAG ACTAGCTNAG NATTATCGAA TGTTACATT TNNAAGTTC TGTGGAGAAN | 300 |
| GAAAAACATG AAG | 313 |

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

| | |
|--|-----|
| GTTGTANGNA ANGTAATCA AAAANTTGA AGCTGTACAC AGCAAGACGT TAAGTTACAT | 60 |
| GTTCCAAAAG ATTTATGTNA TCAGTTTGGC TGACCCCGT CTCCCCCTGC GNCTGGNTGA | 120 |
| TGCTGTNCGG CCTGAGGCAG AGGGAGANG | 149 |

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

| | |
|--|-----|
| AGTAACATGA TAGANAGTTG GTCGATTACA TTGCNATACT GCTTAGTTTN AACTGGTTTA | 60 |
| TTTTAATTGT AGCAGAAATG ANCNGAAAAA AAATATGGGT TTAANANTCA CACACATGAA | 120 |
| AGTNCCATTT TGTAACCTCAN CNAAAGNTAA ANCATTCTTN ATCAAAAGGC TTCTNGCTTG | 180 |
| GTGTCAGGTT GTCACATGTG ACCNCTGTGN CAATGCGAAG CATNACTTCT TCAGTGCCAC | 240 |
| AANGTCATGT TTAACCTTGG GAAAGNGGN TGCTACAGTG GTTTCCAAAG TTCCGTGTTG | 300 |
| TGGGCCNNGG AATTTTCCCT TAGTCTTGCT TG | 332 |

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

| | |
|--|-----|
| AACAGTGCCT CCNAATNAAA TCTAACGANA GCTTCCCAA TCGTTTAAAC GTGGATATCG | 60 |
| GCANANGGTT TTCCTAGACT GTGGAGCCAT GGCTGAGCCA AANCTGAAA ATTNACTGGG | 120 |
| TCACTCCCAT TGGGAAATAA GNTAACTNTG GAAACCCTTT NAAATAATTN CAAGCTAAGT | 180 |
| NGCGAGGGTA CCTTGGGAAA TATCTAAGCA TACAATTTGA NGA CTCAGGA AGGTACACAT | 240 |
| GTNTTGCCCA GANTGTCCAG GGCAGNCAT CGGGGTGGCC ACCATTNAGG TTTACGGG | 298 |

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

| | |
|---|-----|
| TNATTATCCA AATGTNAACC ATGCCAAGGT GAAATTCCAA GGNAAAGGAA GTTGGTGTTT | 60 |
| ATAANGCTCT GAAGATGACA GCTGGCTCAA GGGANGATTT TTTNACGACT GACCAGCGCG | 120 |
| TGGCGCTCNT | 130 |

(2) INFORMATION FOR SEQ ID NO:1494:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 236 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

| | |
|---|-----|
| CTTCAAAAAA TAACTGATTT NCAGAACCAA CTCAAGCAAC AGGAGGAAGA CTTTAGAAAA | 60 |
| CAGCTGGTAA GATGAAGAAG GAAGAAAAGC TGAAAAAGAA AATACAACAG CAGAATTAAC | 120 |
| TGNNAGAAAT TTAACAAGTG GCGTCTCCTC TATGAAAGAN CTATATAATA AANCAAAACC | 180 |
| TTTTTCAGCTA CAACTAGATG CTTTGTNAAG TAGNAAANCA GGCATTGTT GGAATG | 236 |

(2) INFORMATION FOR SEQ ID NO:1495:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

| | |
|---|-----|
| GGCANAGCGG CACGAGGTG GACCGACAGT TACAAGACAT AGTGTAACAA TTAGTGATCA | 60 |
| ATCTAGAGGA AAGAGAAAAA AAGCAAATGC ATGATTTCTA TAAAGAAAGA GGTCTAGAAG | 120 |
| TACCTAAACC TGCTGTTCCA CAGNCAGTGC CCTTCAAGCA AAGGNAAGAT CTAAAAAAGT | 180 |
| CCTAGAAATC AGTGTTTCGT ATTCCACCTG AACTTGATA TGTCTTTATT ACTGGGAGTT | 240 |
| CCATTGGTGC TAAATGAAAG GCACGGGNAC ATTTTAAAGC CATTGGGAAA AGAAAGTTTG | 300 |
| TTCCGAGTTT TCAGGAGGAA GCAACTATTG GGACCATGTT GGAAAATTC CTCAGANGAA | 360 |
| AATGGGGTCT TGATCCCNCT TGTNCCAGTA GGTTTAATCC GTGGTGATCA CTGTTGGGGC | 420 |
| CGTNTCAACT CTTAGGGNAT TC | 442 |

(2) INFORMATION FOR SEQ ID NO:1496:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

| | |
|---|----|
| GGCANGAGAA GGTACTGCAA CATTTNAATG GGACGGCAAT AGCAAATGCA GTTGNTAAAG | 60 |
|---|----|

| | |
|--|-----|
| ANCTTGCTGA GACTATAAAA TGTCGTACAT TATTTNCAAC TCACTACCAT TCATTAGTAG | 120 |
| AAGATTATTC TCAAAATGTT GNTGTGCGCC TAGGAACATA TGGCATGCAT GGTAGAAAAT | 180 |
| GAAATGTGAA AGACCCCAGC CAGGAGACTA TTACGTTCTT CTATGAAATT CATTAAGGGA | 240 |
| GCTTGTCCTA AAAGCTATGG CTTTAATGCA GCAAGGCTTG CTAATCTCCC AGAGGAAAGTT | 300 |
| ATTCCAAAAG GGNCATAGAA AGCAAGGNAT TTGNGGNAGT TGANTCCGTC CCTC | 354 |

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

| | |
|---|-----|
| TNATGTNCTT TCTGCATGGT TATATACTAC TAGTNNTTTT ATCAAAACTN CTAAAATTTA | 60 |
| AATTACGTGG TAAAAGATCT GTAAAAGGCT GCATAAATGT TAAGTTGGCA CATAAAGACA | 120 |
| ATTGTAGAAG TTGAAAAAAT GATTGCAATA TTTCAATGNT TATNCCCACT CAACATACTG | 180 |
| NCTTCTAAAG CTTCCCTTTT TTTGTTCCAA AGGCATGNTC CTTGAAAGGT NATGTTTAAG | 240 |
| TTAATGGNTG TAATGCCAGG GTTCCCTACA CTGTGATTNN GGGCGCATGT GCNGTGGGCC | 300 |
| CTCTGTGCCC CTAGANTATA TGCCACACAG GGGGNCAAGT TNAAAAGCT | 349 |

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

| | |
|---|-----|
| GGCACGAGCT GTCTGGAATT TAGCCAAGTN AACAATCCCC TCATATCCAG GCTTTATNAT | 60 |
| CTATATAGCT TCCAGGTCAT CCCTGNCCTG GGAGAGGTCA TCGCTGGAGA CTGNAAGTCC | 120 |
| TATCAGTACC TTGTAGAGAG TATCCGAAGG TTTCCGTCTC AGGAAGNAGT TCAAGGACAT | 180 |
| GATAGAAGAT GCAGGCTTTC ACAAGGTGAC TTACGAAAGT NTAACATCAG GCATTGTGGC | 240 |
| CATTCATTCT GGCTTCAAAC TTTAATTCCT TTCCTATCAT GGAGCATGAN CCAGTCATAT | 300 |
| CCTGTTTGAA AGCCTGGAAC TTNAAGGNTA ATCTGGGCAA TGAAGACAGC AGCAGAGCAT | 360 |
| CTCCCTCTTT AAGGATACGT GGCCTTGGNA CTCATGTTTG AATCGGACAG TCTCAAAGTG | 420 |

GGGAGGACAA TTCTTGTCAC TTTTACAG GTTCTTTT GGGTTGTTT CAGTCCCATT 480
TCCCAAG 487

(2) INFORMATION FOR SEQ ID NO:1499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

TCNNCAANNT NGAACGATGC AGGGTCCAGC TGGGCGGATC TGATCAACTA GGCAACATCA 60
TGTTCCGGAT ATGAGTTCAT CAACAAGTTG ACTGGAGAAG ATGTATTTGN GAATCACCGT 120
TCCTCTAATT ACAAGTACAA CTGGNGCAAA GNTGGGGAAA GTCTGCTGGC AACGCTGTTT 180
GGCTAAACAG AGATAAGACA TCTCCATTG AATTGTATCA ATTCTTTGTC ANGCAACCGG 240
ACGTTTCANT GGNAAGGTAC CTGANGNTGT TCATTT 276

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GGNGGCGTTC AGCTGCTTCA AGATGANGGT GAACATNTCT TTCCCAGCCA CTGGTTGCCA 60
GAAACTCNTT GA 72

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

AAAATNTCCC AACTNATGAT ATCCACATGA NGCAAGTTGA TCTGGAGANT GTATGGCTTC 60
ATTTTATCCG GGAGTTCATT GCACCANTTA CACTGAAGGT NTTTGCAGGC TATTATACGA 120
NGGGNTTTGC ACTACTGAAT TTTGTAGTAA AATACTCCCC TNANCGACAG CNTTCTCTTN 180

GTCTCATCA TGATGCTTCT ACATTTTACC ATAAACATTG GCACTTAATA ACGTGGGGAN 240
AAGACTTTCC AGGGGAGNTG GTTGCAAATT TNNAAGGGNT CCAATTTGCC C 291

(2) INFORMATION FOR SEQ ID NO:1502:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

TGGAAATACT TGTTATTGC ATGATCCAAT GGCTTACTGG CCATCTTCCT TGGGAGGATA 60
ATTTGAAAGA TCCTAAATAT GTTAGAGATT CCAAATTAG ATACAGAGAA AATATTGCAA 120
GTTTGATGGA CAAATGTTTT CCTGAGAAAA ACAACCAGG TGAAATTGCC AAATACATGG 180
AAACAGTGAA ATTACTAGAC TACTGTGAAA AACCTCTTTA TGAAAATTTA CGTGACATTC 240
TTTTGCAAGG ACTAAAAGCT ATAGGAAGTA AGGATGATGG CCANTTGGAC CTCAGTGTG 300
TGGAGAATGG AGGTTTGAAA GCAAAAACAT TANCAAGGAN GCGNAAGTAA GNATTGNTGA 360
AAGCAAGGAN CNCGTGTTTG AAGTTACGGN TTGTCCAACN CACCGTCCGN GGTGGGCCCTT 420
CCGACCCNTT TCAGGACCCG AAGGGGTCCC GAGTATTCGG TGCTGTGACC CGTTTCC 477

(2) INFORMATION FOR SEQ ID NO:1503:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

GGCAGGAGCA AAGGCGAGGA GTCCAACAGC TCAGCCANCA AGTGTCTGCT GAAGGTGGCT 60
GGTTACGCTG NGCTNCTNGA GCAGTATCAG AAGGCCATTG ACATNTACGA NCAGGTGGGG 120
NCCANTGCCA TGGNACAGCC CCCTTCCTCA AGTACAGCGC CAAAGACTAC TTTCTTTCAA 180
GGCGGCCCTC TGCCACTTCT GGCATCGNCA TGGCTCAGCG TGCAAGNTGG CTGGTCCAAA 240
AGNATNNAGG 250

(2) INFORMATION FOR SEQ ID NO:1504:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

| | |
|---|-----|
| GGCACAGAGA AGATTCCTTC ATGAGTGTAG AAGTTGGACT GATTTCTAAA GTNCCTTTCT | 60 |
| ATTTTAAGAN TCTNTTCTGC ACAGTTATGA GCTACACATA ATGCACTGAA TCTGTCCCT | 120 |
| TGNATAGTTT CTGCATAGGC TTTGGTTGTG CCACAAGTGT GCCTGGCAGT GAAATGAACC | 180 |
| TGGTCTAAAC TCTGGCATTG GTCCTAGGGN CTGNAACTGT TNCAGGAATN TGNGCTAATC | 240 |
| CTNGNGGG | 248 |

(2) INFORMATION FOR SEQ ID NO:1505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

| | |
|---|-----|
| ANACAGCCAC ACCCGTNACG GTGCATTAGG GACAATGGCA GTCGGTGAGG GCGGCGGTGA | 60 |
| GTTGGTAAAA CAGCTGCTTA ATGACACCTG GGATATCGAC TATCCGGGCG TGGTTGCGGT | 120 |
| GCATCTAACC GGAAAACCTG CGCCGTATGT GGGGCCACAG GATGTNGCGC TGGCTATCAT | 180 |
| TGGCGCGGTG TTCAAAAACG GTTACGTCAA AAACAAAGTC ATGGAGTTCG TTGGACCGGG | 240 |
| CGTTAGGGCG CTTCTCTTAC CGATTTCCGT AACAGCNTTG ACGTGATGAC CACTTGAAAC | 300 |
| GGACCTGTTT AAGTTCTGTT TGGCAAACCG TTGAAGNAGT NCCATAACTG GTTGGGGGTT | 360 |
| TNAACGTTNG GGG | 373 |

(2) INFORMATION FOR SEQ ID NO:1506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

| | |
|---|-----|
| GGCANAGTCC AGAAGCTACG CTTTGAAAT CTATGACATA GACAACAAGA CGCCAGACCT | 60 |
| GAGGGATGAT GACTTCCTAG GGGGTGCTGA GTGTTCCCTA GGACAGATTG TTTCCAGCCA | 120 |
| GGTACTGACT CTCCCCTTGA ATGCTGAAGC CTGGGAAAAC CTGCTGGGCG GGGGACCATC | 180 |

| | |
|---|-----|
| ACGGTCTCAG CTCAGGGAAT TAAAGGACAA TCGTGTAGTA ACCATGGAGG TAGAGGCCAG | 240 |
| AAACCTAGAT AAGAAAGGAC TTCCTGGGNA AAATCAGATC CATTTTNTGG AGTTCTTTCC | 300 |
| GCCATGGTGA TGGGGNAATG GGCACNGGGT GTTACAGTTC TAAGGGTNCA NTCAAGGACC | 360 |
| AACCTGGAAC CCTTACATGG GAAGTTTTTT TTNAA | 395 |

(2) INFORMATION FOR SEQ ID NO:1507:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

| | |
|---|-----|
| CAAACAGCCC AACAATTTCA CCACTGCGAA CCGCCAGACT TATTGGCGTA CGCACGTCTG | 60 |
| TGTGCTTTCA CAGCATCAAG ACGTAGGGCN TGCCTCGCCA TGAACACGC GGTGCCAGC | 120 |
| CGTAGTATNA TCGTCCAATG ATCGTCGACC CGTACCNATN CGNCTCTTGG TGTGGGGTGT | 180 |
| GT | 182 |

(2) INFORMATION FOR SEQ ID NO:1508:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

| | |
|--|-----|
| GGCAGAGTNT TGGGGCATTG CCGGCGGGCC CACCCGGA CT CACGCAGCCC ACTCTGTGTC | 60 |
| CCCCGGCAGT ACCCTGGCTA AAGCCGGGNC CGGAGCCTNC TGCCCCCTCTC ATGCCCGCAG | 120 |
| CCAGCCTGGG CTGTGCAACA TGTTACAAGG ACTCACACCA CCCGGNCAAG AACTGCTCAC | 180 |
| TACGGCTCCC TGCCCCAGAA GTTCACACGG NCCGGACCCA AGATGAAAAC CCCGTAGTCC | 240 |
| CACTTTCTTT CAAGAACATT GTGAACGCCT NGCACACCAC CCCC GTTCGC AGGGGAAAGG | 300 |
| GNGAGAGGGA CTGTTCCNTG AGCAGATTTT AGCTNNGGGG GCCGAGCAGA GNAACCCAGG | 360 |
| NTTTTGGGTT ACGGAGGCAG AGCGTTCGA TTTTAAATCG GTTCACAAGG GGTTC AAGG | 420 |
| GATTCGTTGC CCAGGGAAGT TTTCCAAATT TTTTAAGTTG GGAGNAGAGN TAGTTGGTTT | 480 |
| TGGT | 484 |

(2) INFORMATION FOR SEQ ID NO:1509:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

| | |
|---|-----|
| GGCANAGNCT GCATCCTACA GAGCCATGGA TGGNGGCAAG TGTTTGCAAT GGGAAGTGTG | 60 |
| TGTGTTTGGA NTCATGAAAC ACAGACACTG GTGGAAGACA TTTGAAGTGT GTGATCTTCC | 120 |
| TGTTTCGTAG CTNCAAAGTT TGGTTGNCAA AGGGAAGNAT TTTTTNGTGT TG | 172 |

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

| | |
|---|-----|
| GGCANAGGCA TCAATGTTAT AGCGTGTGTC AGTCCTTCAT GACTTTCTGT GGATGAATAA | 60 |
| TATTCCATTG CATGGATATA CAGCAGTTCG TTTANCCATT CAGCAATTGA TGGATATTTG | 120 |
| GGCCTGTTTT CACATTTTGG CTATTATGAA ATCCANTTTT TTAAAGAGAA GATAGNAAAC | 180 |
| CTGGATTTTT GAAATCTAGT GTTTAAATGT TGGCTGTGNA ATTTTAAAAA TTNAAGAATA | 240 |
| TGTTTGAGC TAATTAAAAA GCTATCTGGG GATGGGCACA GGNNGCTTGG TTGACTGCCC | 300 |
| ATTGGTCCAT CTCTTTGCCA CTTGGGGNCA GCCTGGGGAC CCTTTNTNGG TT | 352 |

(2) INFORMATION FOR SEQ ID NO:1511:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

| | |
|---|-----|
| GGCANAGNCA AGACTGGTCA CCCTCGGTTC TTCAACCAGC TCTTNTCTGG GTTGGATCCC | 60 |
| CATGCTCTGG NCGGGNGCAT TATCACTGAG AAGCCTCAAC ACCAGCCAGT ACACATATGN | 120 |
| AAATCGCCCC CGTGTGTTGTG CTCATGGAAG AGGAGGTGCT GAGGAACTG CGGGCCCTGG | 180 |
| TGGGCTGGNA GCTCTNGGGA CGGAATCTTC TGCCCTGGTG GCTCCATCTC CAACATGTAT | 240 |

| | |
|---|-----|
| GCTGTNAAAT CTGGCCCGCT ATCAGGCTTA CCNGGGATTG CAAGCAGAGG GGNCTCCGNA | 300 |
| CAATGCCGCC CCTGGCCCTT ATTTACATC GAAGGAGGTT GGGAAGAGGC ACAGGNCCAA | 360 |
| CCCTGGGTTC NTGATTTTAA TTTCCAGCCN GTTAAGTAGA GACCTTCCAG TTTTGTTCCT | 420 |
| GGCCTTNNTA ACATTC | 436 |

(2) INFORMATION FOR SEQ ID NO:1512:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

| | |
|--|-----|
| GGCANATNGG GACTTCCCGT GCNCTCTGGC TGAGGGGTGT TGCTGCCTTT GGTAAGCTGGC | 60 |
| CCTGGTGTTT CAAGTACCAC CCTTAGGGTG GAAGTGGTAG CTTTTTTAAA GANTGTNNCC | 120 |
| CAAAACTACA GTTNCCTGTGC ACTCACTTAC ACAGTATT | 158 |

(2) INFORMATION FOR SEQ ID NO:1513:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

| | |
|--|-----|
| GGCAGCAGCT TCACTAAGGT GGGATGGATA GCAGGTCTN AGGCACAACC AGTAATGGAG | 60 |
| AGACAAANCC AGTGATATCCA GTCATGGAAA AGAAGGAGGA AGATGGCACC CTGGAAGCGG | 120 |
| GGGCACTGGT ANCANCAAGN TGGAGTTTNT CCTGTNAGTG GCTGGGGAGA TCATTGGCTT | 180 |
| AGGCAACGTC TGGNGGTTTC CCNATCTTTG CTAACAAAAN TGGGGGAGGT GAGTTGAGAG | 240 |
| CCCTTTTGCC CACCCNACCC ACTCCTGGAA GGGGNTTACT TCCATCTCCC TGCATTTACG | 300 |
| NNCCCTTT | 308 |

(2) INFORMATION FOR SEQ ID NO:1514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

| | |
|---|-----|
| GGNAGAGGGG ACACAAAGGT CGGNAGGCAG CACACAGAGG GACCTACGGG CCAGCTGTNC | 60 |
| CTTCCCCCAA NTCAAGAATC CCCGGAAGNC CCGGNGGCTG NCAGCAGGAG AGANCCATGA | 120 |
| AAGTAAGCTG AATGGTGGTG CCTGNGTCTG AATTGCCTGC AGCCTGGGCC AGAGGAGCAG | 180 |
| AATGAANTTG GTGCATGGCG GACCCTGNGA NCAAGACATC TTNACCCCTN ACCAAGCTGC | 240 |
| CCTCTNACAC CTGGGGCCAC TTGCTCTGTG GTGGGGTCCT TATTCCATCC ACTGTGGGTC | 300 |
| CTNANAGNTG CCCACTGCAA AAAACCGTTT TTCCAGGTCT TCCTGGGGGA GGGNTTAACC | 360 |
| TTGGNGCAAA GG | 372 |

(2) INFORMATION FOR SEQ ID NO:1515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

| | |
|--|-----|
| TGCTGAAATT AAAGAAATNT NGCAATGATT TTA AAAACGG AGNTGTGACA GTAAGGAGGC | 60 |
| CTGACCCCAT TAACTGGTCA TTGAAGTATA AAACCTCTGN ATTTTANGNC TNCGGGTTTT | 120 |
| ATGACAGTGG CAATG | 135 |

(2) INFORMATION FOR SEQ ID NO:1516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 159 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

| | |
|--|-----|
| AATTCCGGCAN AGGNNAGCCA TGNCTGGCGA TGGTGGCAGC GGCTGTNACC TTGGAGGTTG | 60 |
| CTGCAGGCCC GTGGCTTTCC ACAAATTTT GCACCCAGCC TGGGCCTANG AGCGAGGACT | 120 |
| TGTTCCCAGG GCGACTGCTC GTNATTCNCG CANGNCTGT | 159 |

(2) INFORMATION FOR SEQ ID NO:1517:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

| | |
|--|----|
| AGCCCCGCAT CTTCCACCT CGNCGCCGCC GNAGCTCCCC GCGCTCGTGC CACCGNCGCC | 60 |
| GGT | 63 |

(2) INFORMATION FOR SEQ ID NO:1518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

| | |
|---|-----|
| TATTATGGAA AACTGTTGCG GGGCATATGG AAAACTGTTG CGGGGCATGT GGTAGAGACC | 60 |
| ACCCAGATGA GGCCCTCCAA GACCTTGTTG TCTAGGGTGA TTTATTCCCT TTATTTAGAG | 120 |
| ACCCAGGCAA TTGAATTCAT TTCTTTTTGT GNATGATAGG CTTTTGGCTG TTAGACCAGA | 180 |
| CCAGACGCTG TGTTACTCTA TGAGATGAAT AATAGTGGAG AACTATATAA CTTAACTATT | 240 |
| TTGACTTTTT ACCTTGCTT CCAGGAAGCA TAGAGTGCAA TCTCGNTTAC TGCAATTTNC | 300 |
| AATGAATTGA CACATAGCCT AGGTTTTTGG TACAACCACC TTTG | 344 |

(2) INFORMATION FOR SEQ ID NO:1519:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

| | |
|--|-----|
| GGCAGGAGCA TGTTTCCTGT TTTGTGTGTG TAGTCTGTGG AATGNCCATT CGGATGAATG | 60 |
| TTTTTCACTT GGAGGATGGT GAACCCTACT GTGAGACTGA TTATTATGCC CTCTTTGGTA | 120 |
| CTATATGCCA TGGNTGTGNA ATTTCCCATATA GAAGCTGGTG ACATGTTCCCT GGAAGCTCTG | 180 |
| GGCTACACCT GGGCATGTGA CTTGCTTTGT ATGCTCCAGT GTGTTGTGAA AGTTTGGNAA | 240 |
| GGTCAGACCT TTTTCTCCAA GAAGGACAAG CCCCTGTGTT ANGAAACATG CT | 292 |

(2) INFORMATION FOR SEQ ID NO:1520:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 188 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

| | |
|---|-----|
| GGCAGAGGG NGCACCCNGG TAGGGGGNCG GCTGAGCCGG CAGTGCGGTA CCCTCGCGGG | 60 |
| GAAGTGCGCC GCCGACACCA TGTCTCAGGA AGGTGTGGAG CTGGAGAAGA GCGTCCGGCG | 120 |
| CCTCCGGGAG AAGTTTCATG GGAAGGTATC CTCCAAGAAG GCGGGGGCTC TGATGNGGAA | 180 |
| ATTGNGCT | 188 |

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

| | |
|---|-----|
| GGCAGAGCTC ATGATGACGT TTGCTTTTCC TCCCGACTCA AAATTTACCT TTTGGGGTCT | 60 |
| TACCCTGGTT GTAGNGCTG GNTTTTCCTG GGGATTAAGG CCTAANTCTT CCTACNCNTC | 120 |
| GCACTGCCTT GCACTGCCCC CCATATGTTC CCAGGGTAGC TCTCCAGCTG GANCCTTGCT | 180 |
| GATGCCATGT CCCAGAAACA CCTCCAGATC AACCAGACGT TTGAGGAGCT GCGAACTGGT | 240 |
| CACGCAGACA CAGAGNAATG AGTTTAAAAA AGCTGCAGCA GACTTCAGGA GTTACTTTCA | 300 |
| TGCATCCAGT TACCAGGNAG AGCCTNGAGG GATTCCAAGC TCAGTTTTGG GCCCGTTGG | 359 |

(2) INFORMATION FOR SEQ ID NO:1522:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

| | |
|--|-----|
| GGNANAGGCA ACCCCTTGTTN TCGTGTGGAT GGGGCGCTNG CCGGCGCTGT GAACCTNAAC | 60 |
| CTGCAGNCCG ACTGCAAGNN TGCCCTGGAA GTCCTGGCAC GACATCCGCC GAGACAACCTG | 120 |
| CTCTGGCCAG AAGCCTCTGC TTCTGCTGGG AGCACANCCA GCTCCNAGCA CAACCTGTNT | 180 |
| GNCCTTCCTN GAGGTTCA | 198 |

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

| | |
|---|-----|
| TTGCCATCGC GAATGGGGCC CAGTGGCCTA ACGCCCCGGC GGCGCTTNGG TAAAACCGAC | 60 |
| ACCACGGCAC TCTGTCGGCC AGGTTGCAGG TTCCCATTTT TCCGTGGAAG CAGTGGCGAG | 120 |
| AATTGCCGTT TTTNAGGTTG GTCATCAGCT TGTCGAAGAA ATACACACCA GAGAAAAAGC | 180 |
| GTAAATTCTG TTCCGACCGT GCAGTTNACC GTAGAGCGAA AATTTTGCG CCATATAAGC | 240 |
| CGAGAATGCT GGCGCGCTTT ACCGGNAACT TNTCTTTCCA GATCCATCCC CAGCACCAGC | 300 |
| GCCTGGTCCG GAAAGTTCGG CACCAGCAAA CCGTACATNC ANTTTAAAGG TGGTCGATTT | 360 |
| TNACCCGGGC CTTTGGGGCC CCAGNAAACC AAAAATTTTC CCCAAGTTTN AAGGGCAAAT | 420 |
| TTGACGTGAT CCGTTGGGNG GCAAAATNCC CCAATTTTTT TGGTCAATTT TTNGGTTTGG | 480 |
| GTT | 483 |

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

| | |
|---|-----|
| AAAACAATCC CTTCTATCAA TTATATCGGC TATCTTGAAG CCAATGAGTT GTTAACTGGC | 60 |
| AAGACAGATG TGCTGGTTTG TNACGGCTTT ACAGGAAATN TCACATTAAA GACGATGGAA | 120 |
| GGTGTTGTCA GGTATGTTCC TTTCTCTGCC TGAAATCTCA GNGTGAAGGG AAAAAACGGT | 180 |
| CGTGGTGGCT ACTGTTATTA AAGCGTTGGC TACAAAAGAG CCTGACGAGG CGATTNCAGT | 240 |
| CACCTCAACC CCGACCAAGT ATAACGGCGC CTGTNTGTTT AGGGTTNCGC GGCACGGTGA | 300 |
| TTAAAAAGTT CATGGGTGTC AGCCAATTCA GCGAGNTTTT TGCGGTTCGC GATTNGAACA | 360 |
| GGCATGNCAG GCGGTGCAGC GACCAAGTTN CNTCAGCGG | 399 |

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

CACCNCCTAA AAAACTCGCT GGATCTNNAT CTGGAAATGT NCCCGGCCCA GGTGNCAGCT 60
TCCTCCNCCT CCAAGCNAGG NTTNANTTCC ACCTGGGAAA TCTGGCCANA GAAAGGTGCT 120
TGAAAATCCT TCCNGCACAT GCCAAACCCT AGAACCCGGG GANAGCACGG GGGNGGTGGG 180
ATTACCTGGT GCAGCANACT 200

(2) INFORMATION FOR SEQ ID NO:1526:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

GGCAGAGTGA ACAGCCCCCG NCGGCGCANA CGAGCCCGGA CCACACCCGG TNCCGGAGGT 60
TCCCACAGCA AAGACAGGCA CCGGAAGGAG ACGGACCGGG AAGCGTAGGG GCAGCGNCAG 120
CAGGTAAGGN ACAGCCGNCA CCGNCG 146

(2) INFORMATION FOR SEQ ID NO:1527:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

GGCAGAGNCA ACGCCACTCC TTCTAAGTCT TCATCGATCA ATGACATTTN ATCCATGTCC 60
ACTGAGCAGA CGCTGGCCTC AAACACAGAC AGCAGTCTTA ATGCCTCGAA CGGGNACCCC 120
TTGAAAGGCT GTCGAATGGA TAGGTTAGGA AATAGCAAAC CTGTNNAGCA TTGAAGGGAA 180
CTCTGNACCT GCCGTGGGGC CTGAAATGCT TGGGAGTTGA TGGGAACCAA ATAGAAAAAC 240
TCCATGTTCC TGGCATGTAA AGAAACACAA TGNCTTGGNC CTNTTTCAAA CCGGTGGGGT 300
TTGCNCTGCT TTAGATGGTT AAAAAATGGGG GGCAGGANTA TGTTTTG 347

(2) INFORMATION FOR SEQ ID NO:1528:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

| | |
|---|-----|
| GGCAGNGCAG CTATGCTAAT TTGCAAACAG GTTCTGGAGT NCTTAAAGAT AGTTTNTCTG | 60 |
| GTGGAATGCA GTTGCTTCCA GATCCTNTAT ATTCTCTTCC TACNNATAAT ACTTACCTTT | 120 |
| TAACAATAAC TTNCACTGAT AATGGGCAGA ATTTTCTTGG CTGGNAAAGG ATGGCTGTTT | 180 |
| ATATGAAAGT AGCCTACCAG GCTGTAAGCA GGGTGGTTTA GCCAAAGATG TAGGGAAAAT | 240 |
| AAACCACTCA AAGAGCTTCA CTTTCTTTNC CTTGGTNCCT TCCTTGGCTA CCAATTTAC | 300 |
| GTTTCTTCAG AAGGATGNAT NCCNTATTTT TT | 332 |

(2) INFORMATION FOR SEQ ID NO:1529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

| | |
|---|-----|
| GGCACGAGGG AAAATCGCAA TACTATATTA TGTTTGGNCC CGATATTTGT GGATTTNATA | 60 |
| TCAAGAAAGT NCATGTTATT TTACATTTCA AGAATAAGTA TCACGAAAAC AAGAACTGN | 120 |
| ATCAGGTGTA AGGTTGGATG GCTTCACACA CCTGTACAC TCTAATTTTN AAGACCAGAT | 180 |
| CTTTCTTATG ATGTGNAAAA TTGATGGTCA GTGCAATTGG AATCCGGCAG CATAGAGTTA | 240 |
| CGGACTGGGA ACTTAAACAT CACTCCAAGA GGGAAACGTC CCCCAGNCAG ATTCGAAGGA | 300 |
| TTGGGCAACA GGAAGTAAAG GNNCAACAAA GCCCCAGGGA CTTGGGGC | 348 |

(2) INFORMATION FOR SEQ ID NO:1530:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

| | |
|---|-----|
| GGCACGAGCT CGTNCGNTGC AAAACCACTC CCACCAAGTG AACGCTTGGA ACAGGAACTC | 60 |
| TTTTCTGGAG GCAACACTGG GATTAATTTT NAGAAATACG ATGACATTCC AGTTGAGGCA | 120 |

| | |
|---|-----|
| ACAGGCAACA ACTGTNCCTC CACATATTGA AAGTTTCAGT GATGTTGAGA TGGGAGAAAT | 180 |
| TATCATGGGA AACATTGAGC TTACTCGTTA TACTCGCCCA ACTCCAGTGC CAAAAGCATG | 240 |
| CTNATTGCCT ATTATNCAAA GAGAAAAGAG ACTTGATGGC TTGTGCCCCA AACAGGGTTC | 300 |
| TGGTAAAAAC TGCCAGGNAT TTTTNTTGCC CNTCTTGAGT NCAGATTTAT NCAGATGGTC | 360 |
| CAGGCG | 366 |

(2) INFORMATION FOR SEQ ID NO:1531:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

| | |
|---|-----|
| GGCACGAGGC TTGGCGGGGT GGATAATATC CTGGTCAAAA TNACTGACCC ACATCANTAA | 60 |
| TGTCGTTTCT CCAAAGATGC CGTGGGTCAA ATATCTGTNC ATGTGGACAT CACTGCCACC | 120 |
| CCAGGAACGG GAGATCATAA AAGTCACTGT AAAAAGTGAA TTGCTATTAA TGACCTAAAC | 180 |
| TGGCAGACCA CAGCAATGTT CCGCCCCTTT NTGGAAGTTT GTATACTGGG ACCCAACCTT | 240 |
| GGAGACAAGA AGAGAAAACA AGGCACAAAA ACAAAAAGCA ACACATGGTC ACCAAAGTTA | 300 |
| CAATGNAACT TTGCAGTTCC TTTTGCGGAA AGGAAATTCG GCCAGGGTTT ATGAAATTGC | 360 |
| TCTGTCCGTT AAGGGTTATG TTTTGCCANG NAGTTCGNTT NTNGGATG | 408 |

(2) INFORMATION FOR SEQ ID NO:1532:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

| | |
|---|----|
| GGCACGAGGT TTTTTTTTTT TTTTTTTTNG GAAAAAANAA NCTTTNAAAA NT | 52 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1533:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

| | |
|---|-----|
| GGCACGAGCC CGACCGTNAA TGTGTGTNTN CTCTTCCCCA GTNCTGGCCA TTCAGGCCCG | 60 |
| AAAGCGGAGG CCGAAAAGAG AGAAACATCC GAAAAGCCG GAGCCTCAAC AGAAAGCTCC | 120 |
| TTTAGTTCCT CCTCCTCCAC CGCCACCACC ACCACCACCG CCACCTTTGC CAGACCCCAC | 180 |
| ACCCCCGGNG CCAGAGGNGG AGATCCTGGG GTCAGATGNT GAGGAGCAAG AGGACCCTGC | 240 |
| GGACTACTNG CAAGGNATTT ACAAGTTTTG TNACTATTTA TTGGAGNAAT TATTTTtagc | 300 |
| T | 301 |

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

| | |
|--|-----|
| GGCACGAGGT TGGATGGTGC AGTGGCTGTA TTTNATGCCT CTCCTGGTGT AGAGGCCCCAG | 60 |
| ANTCTCACAG TATGGAGGCA AGCTGATAAA CACAATATAC CTCGAATCTG TTTTAAAC | 120 |
| AAGATGGACA AAAGTGGAGC AAGCTTTAAG TATGCAGTTG AAAGCATCAG AGAGAAGTTA | 180 |
| AAGGCAAAGC CTTTGCTTTT ACAGTTACCA ATTGGTGAAG CAAAACCTT CAAAGGAGTG | 240 |
| GTGGATGTAG TAATTGAAAG AAAAATTCT TTTGGGAATT TGCCAATTCC AAATGGATGG | 300 |
| AAAAGACTTT GAGGAGAAGN CCCCTCTTTG GGAATGNATN GTTCCNGGAT TTGCTGAAGG | 360 |
| GGAACCACCT NAGGCAAGGG | 380 |

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

| | |
|--|-----|
| GGCACGAGGT GAAGTTCAAA GATGTGGCTG GCTGTNAGGA GGCCAAGCTA GAGATCATGG | 60 |
| AATTTNTGAA TTTCTTGAAA AACCCAAAGC AGTATCAAGA CCTAGGAGCA AAAATCCCAA | 120 |
| AGGGTGCCAT TCTCACTGGT CCTCCAGGCA CTGGGNAAGA CGCTGCTAGC TAAGGCCACA | 180 |
| GCCGGAGAAG CCAATGTCCC CTTTCATCACC GTTAGTGGAT CTNAGTTTTT GGAGATGTTC | 240 |

GTTGGTGTGG GCCCTGCTTA GAGTCCGAGA CTTATTTGCC CTTGCTCGGA AGGAATGCCC 300
CTTTGCATCC TCTTTCATCG GTGGAATTCG TCGGGTGGNG AAGGGAAGAG AGGAAGAGGC 360
AANTTTTTGG AGGGGCAAGA NTTTNGNCAG GGGGG 395

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

TGTTTTNAGT TTCTTTTTTT NCGTTTNATT TTTTNNAAT TGCATTTTAC AGTAGAAATG 60
CAGACCACTT TGGATAGCTA TGGCTCGATA CTTCTGGGTG CCCTCCTCCT AAGANATCCT 120
CTTCTTACAT TCCACTGANC AGAAAACCAT CCCTTCTACT GGCATGAACT TCTGCCCAAT 180
GAGGCATTTG CTGCAGCAAG AGCACAGAAA GCACTCTGTG GNATGCATGC CAGCTGAAAT 240
TGTTATAGGT CACCCGNTGC ACTTNCTGGG TCGATGGGCA TTGTGGGCNT CCTTGACACA 300
CCACAGGGTG ATTTNTTNCA AATAGC 326

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

GGCAGGAGAA GCTTTCCCAC ACACATCACA CTCATAGGGC TTCTCTCTAC CGTGGATTCTG 60
CTGGTGTCCA ACAAGAGCTG AACTGTATCT GAAGGCCTTT CCACGCTTGT CACATTCATA 120
TAGTTTCTTT CCACTGTGGA TTTTCTGGTG ACAGAAGAGG CCCAAGCACT AGCTAAAGCT 180
TTTCCCTCAC TCACTACACT GCTATGGCTT CTNTTCAGTA TGAACCTCTGA TGTGTCTCA 240
GATATGAACT CAGAGAGGAT TTCCCACAAT CATTACACTG GTATGGTTTC TTTTCCGTGT 300
GGAGTTTCTC TGGTGTCCAA ATAACATCTG AGGTNGTGGA TGGAAAGGAC TTTCCCACAC 360
TCACTTACAT TGGGAAAGGG TTTCTTCCTG TNGTGGGGTC CTTCAAATGN TGNNTAAGGT 420
TATGNACTGT AATAAAAGG 439

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

| | |
|---|-----|
| GGCAGAGCAA AGAGGCATTT GGGCAGTCCT TCTCCATCCA CCGGAAGGTT GCTGAAGATG | 60 |
| GAGAGACTCG GGAGGAAACG CTTCTCCAGG AGTCAGCATC GAAGGAGGCT TACTATCTGG | 120 |
| GGAAGATCTT GGAGATGCAG AACGAGCTGA AACAGAGCCG GGCTGTGGTC ACTAATGTAC | 180 |
| AGGCAGAAAA CGAGAGGCTC ACCGCAGTCG TGCAGGATCT GAAGGAGAAC AATGAGATGG | 240 |
| TGGAGCTACA GAGAATACGG ATGAAGGATG AAATNCGCGG ANTATAAGTT CCGGGAGGCA | 300 |
| CGGCTCCTTT CAGGACTATT ACTTGAATTT GGGAGGANGA AATTTTCACC TTGCAGAAAC | 360 |
| TAGTGTTCCN CGTTTGNAGG CAGANCCAGT TGATTACGNG GGTTTAAAGC CTGGGTTTAG | 420 |
| CGCTTTT | 427 |

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

| | |
|---|-----|
| TTTTCNAGTT TCTTTTTTTN CGNTTAATTT TTTCNAAATT GCATTTNACA GTAGAAATGC | 60 |
| AGACCACTTT GGATAGCTAT GGCTCGATAC TTCTGGGTGC CTCCTCCTAA GACATCCTCT | 120 |
| TCTTACATTC CACTGAACAG AAAACCATCC CTTCTACTGG CATGAACTTC TGCCCAATGA | 180 |
| GGATTTNNTG CAGAAAGAGC ACAGAAAGCA CTCTGTGGAT GCATGCCAGN TGAAATTGTT | 240 |
| ATAGGTCACC CGCTGCACTT CTGGGTCGAT GGCATTGTGG CATCCTTGAC ACACCACAGC | 300 |
| GTGATTCTTC ACATAGCAGG GCTTGACAC GGGCTTGTTA TTGACCATCA CGTATATTCT | 360 |
| CCCCAGNTAG ANTGNTNTCA CAGTCAAAGC AGCAGAAGTG TTTCAGGTGC CATTCTGGTT | 420 |
| TTCTGCCTGG GTATACTCAT TGTNGATATC AGTTCGTCAC AGCCAGCACN CGGGGTTTTT | 480 |
| GGTGTCACA | 489 |

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

| | |
|--|-----|
| GGCANAGGNT TTCCTTGCCC GATTCCTTCA TGCTATATCT CATGAACCTC TGTAATCTTG | 60 |
| GGGGAGAGAC TATATTTAAT GATGACAAAC CTGTCACCAG TGTAGCAACA ACAGTGTGAG | 120 |
| GACAAAAGCA AATAAAAATT AAGNAAGCGT TCAAATTTAT ATTCAACAAG GAAGTCATTT | 180 |
| CAATCAACAA CTTCTGCTGC ATTATTTTTTC CAAGATGAAC CGATACACAA CCATGAGACA | 240 |
| GTTGGGGGAC GGCANTATGG GAGTGTGCTT ATGGGCAAGA GTAATGAATC CGGGGNGCTG | 300 |
| GTGGCCATCA AAAGGNTGAA GAGAAAGTTC TATTCTTGGG GTGATGGCAT GAACTTNNGG | 360 |
| GGAGTTTAAG TTTCTGNAGG AACTTTATTC NGGCCATGTT ATTTAAATNG AAAGANGTTT | 420 |
| TTCNNGGGAA ATGACCCTCT TTATTTTATA TTGGATTTTT GG | 462 |

(2) INFORMATION FOR SEQ ID NO:1541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

| | |
|--|-----|
| GGCACGAGCC GGACTCTTTT CCCTCTACTG AGATTCATCT GTGTGAAATA TGAGTTGGCG | 60 |
| AGGAAGATCG ACCTATCGGC CTAGACCAAG ACGCTACGTA GAGCCTCCTG AAATNATTGG | 120 |
| NCCTATGCGG CCCGAGCAGT TCAGTGATGA AGTGGAACCA GCAACACCTG AAGAAGGGGA | 180 |
| ACCAGCAACT CAACGTCAGG ATCCTGCAGC TGCTCAGGAG GGAGAGGATG AGGGAGCATC | 240 |
| TNCAGGTCAA GGGCCGAAGC CTGAAGCTGA TAGCCAGGAA CAGGGTCACC CACAGACTGG | 300 |
| GTGTNAGTNT NAAGATGGTC CTGATGGGCA GGAGATGGAC CCGCCAAATC CAGAGGAGGT | 360 |
| GAAAACGNCT GAAGAAGGTG AAAAGCATTC ACAGTTTTAA AAGAAGNCAC GTTGNAATGA | 420 |
| TGCAGGTTGT TCTATGTTGG GAATTTGTTC CTTTNAATTT NTCCCATTAAG AGGTTTTACA | 480 |
| GCCTTTNTGC AAAG | 494 |

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

| | |
|---|-----|
| GGCAGAGGNG ACTTGAGAG ACACCCTACC CCCCATTGC CGTTTGTTGA CGTGGCAACA | 60 |
| GGGTCCCTAG GTCAGGGATT AGGTACTGCA TGTGGAATGG CTTATACTGG CAAGTACCTT | 120 |
| GATANGGCCA GCTACCGGGT GTTCTGCCTT ATGGGNGATG GCGAATCCTC AGAAGGNTCT | 180 |
| GTNTGGGAGG CTTTGTCTTT TGCCTCCAC TACAATTGG ACAATCTCGT GGCGGTCTTC | 240 |
| GACGTGAACC GNTTGGGGAC AAAGTGGCCC TGCACCCCTT GTGGCATGGC GCAGACATCT | 300 |
| TACCAGAATT GCTGTGAAGC CTTTGGGTT GGAATAATTN ANTTANTGGA TGNCCATGA | 360 |
| NTGTTGGAGG CCTT | 374 |

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

| | |
|--|-----|
| GGACGAGGTT TGCGGGACAG GCTCTACCA TCCTGGGAAG TACTGGACCA GTGCTTGTTT | 60 |
| TTGAAAAGAT TTTNTTCAA TTCTGCAAAG ACTATGCTCT TTCATACCTC TCCCTGCGAG | 120 |
| CTTGTATTGG ACTGTGGACC GCTTTCCTGT GTATTGTCCT TGTGGCAACT GATGCCAGTT | 180 |
| CCCTTGCTCTG CTACATTACC CGTTTCACTG AAGAAGCATT TGCCTCCCTA ATTTGCATTA | 240 |
| TTTTCATCTA TGAAGCAATA GAAAACTGA TTCACCTGGC AGAGACCTAC CCCATCCACA | 300 |
| TGCACAGCCA GCTGGACCAC CTTAGCCTCT ATTACTGCAG GTGTACTCTG CCAGAGAATC | 360 |
| CAAACANTCA CACCCTCCAG TACTGGAAGG ACCACAACAT CGTGACAGCA GAAGTCCACT | 420 |
| GGGTTAACNT GANTGTTTCTAT GTAAGTTTGG GNGTTGCCAG TTGTCNTAGG CNTGT | 475 |

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

| | |
|---|-----|
| CTACCTGCCA ACTTTNCCCA TGGGCCTTCA ATTAGTACAT TGAATAGGA GTNCGGATGC | 60 |
| TGGGGCAAGG NAAAGAGAGC TANGAAGGGT CCTNCTGAGG TTTTCTCAA CAATGATGAA | 120 |
| GGCCTTATTA ACAAAAAGTT ACCCAAAGAA CTTCTGTAA GAATATTTNC CTTCTTGGAT | 180 |
| ATAGTAACTT TNTNCCGATG TGCACAGATT TCCAAGGCTT GGAACATCTT AGCCCTGGAT | 240 |
| GGAAGCAACT GGCAAAGAAT AGATCTTTTT AACTTTCAA CAGATGTAGA GGGTCGAGTG | 300 |
| GTGGAAAATA TCTCGTAGCT GATGCGGTGG ATTNCTGAG GTAGCTCAGN TTTNCTAAGG | 360 |
| CTTGCAATTGN NTGTTGGG | 378 |

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

| | |
|--|-----|
| GGCACAGGTG GATGGGCATC TNAGTGGTTG TCGTCTTTTT CTCTTCCTTT CACCTCTTTT | 60 |
| NAGGTTTTAT TGTGACTACT GCGATACATA CCTCACCCAT GGACTCTCCA TCTGTGAAGA | 120 |
| AAGACACACT GCAGGGGAAG GGAAACACAA AGAGGAATGT GCAAAGACTA TTNATNCAGA | 180 |
| AATGGGATGG GAAGAGCAGG CTTAGAGCC TGATTGGACA AAACAACGGC TGGCATTTC | 240 |
| ACAAGGGAAA GGTNACCTCC TGACTIONCAT TCTNCTGGTN CCTTCCTCCT GGCAAGGGGC | 300 |
| GGATGGTTAC CACCTTNC | 318 |

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

| | |
|--|-----|
| AGGTGGAAAT GGCCCTAGAA GAATCATGGG AGCACAGTAA AGAAGTAAGT NAAGCCGAGC | 60 |
| CTNGGGGTGG TTCCTCGGGA GATTCAGGGC CCCCAGAAGA AAGTGGCCAG GAAATGATGG | 120 |
| TGGA AAAAGA GGAAATAAGA AAATCCAAAT CTGTGATCGN ACCCTCAGGT GCACCTAAGA | 180 |
| AAGAACACGT AAATGTAGTA TTCATTGGCC ATGTAGACGC TGGCANGTCA ACCATCGGAG | 240 |
| GNACAGATGA TGTTTTTGAA CTGGGAATGG TTGACANAAG GATCACTNNG | 290 |

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

| | |
|---|-----|
| GGCAGGAGAG GAAGGCTCAC TCTGCTCCGT CTCCATCGAG AAGGCACTGC CTGAGNGACA | 60 |
| GAGGCTTATA CAAGTTTGTA GCCAAGATTG ACGCTGGCCA GCGGAGTGC TCCTGCCAAG | 120 |
| TCACTGTGGA TGAATGCTCC AGCCAGTGAA GGAACACCAA GGCCCCAGAG ATGAAATCCC | 180 |
| GGAGNCCCAA GAGCTCTCTT CCTCCCGTGC TAGGAACTGA GAAGTGATGC GACTGTGAAA | 240 |
| AAAGAAACCT GCCCCCAAGA CACCTCCGAA GCAGCAATGC CCCCTTCAGA TCATCCAGTT | 300 |
| CCCTGAGGAC CAGAAGGTTA CGCGNCAGNG NAGTCAGTGG AGTTTTTTNG GCAAAGTGGA | 360 |
| CAGGGCATTG AGNCCATT | 378 |

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

| | |
|---|-----|
| GGCANGAGGG AATCAACTCC TGAGCTTTCT GCAGAACCCA CACCAAAGC TCTNGNAAAC | 60 |
| AGTCCCAAGG AACCTGGTGT ACCTACANCT AAGNCTCCTG CAGCGACTAA ACCTGAAATG | 120 |
| AACTACANCA GCTAAAGACA AGACAACAGN ANGAGGACTT ACGTACTACA CCTGAANCTA | 180 |
| CAACTGCTGG CACCTAAGGT GNCAAAAGCG G | 211 |

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

| | |
|---|----|
| GGCAGGAGCA AGCCCTCCTT ACCATAGTAT GATGGGTGAT GATGAAGATG CGTGTAGGGA | 60 |
|---|----|

| | |
|--|-----|
| CACCGAGACC ACTGAAGCCA TGGCGCCAGA CATCCTAGCC AAGAAATTAG CTGCTGCTGA | 120 |
| AGGCTTGGAG CCAAAGTACC GGATTCAGGG AACAAAGAAAG CAGTGGGAGA GGAGGATAGT | 180 |
| GAACCTCTCA CCTGAAGAAC GAGAAAAAAA GCGACAATTT GAAATGAGGA AGGAAGCTTC | 240 |
| ACTACAATGA AGGACTTCAA TATTCAAACT TAGCCAGACA ATTAATTTTC AAAAGACCTA | 300 |
| CATGNTGGTG GTTGAAGTTG NAGAAATGTT TAGAGANTGC AGATGGNGGA AAGCCTTGAA | 360 |
| TTACGGGAGG NTTCAATTCC AGGTCT | 387 |

(2) INFORMATION FOR SEQ ID NO:1550:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

| | |
|---|-----|
| GGCAGAGCT ACCCCAGCAG CACCAATGTG GAGACCGTCA ACGATGGTGN TGAGTCGGCC | 60 |
| ATGTTCAAGC AGCTGTTCCA GAAGTGGTCA GTAAAGGACC AGACCATGGG CCTGGGGAAA | 120 |
| ACGTTGAGCA TTGGTAAAAT TGCTAAAGTT TTCCAGGATA AATTTGNATG TGAATCTGCT | 180 |
| ACACACCAAG CCAGAGGTAG CTGCCCAGGG AAAGAATGGT CGATGGATGG CAACGGGAAA | 240 |
| AGTTGAGGTC TGGGAGGAAT TNGAGGAACC TGGGNGCTGG GTCCCTGTGG GAGTTATTCA | 300 |
| ATGGTNTGGG CTTTCTTTTN ATGGGNGGGA G | 331 |

(2) INFORMATION FOR SEQ ID NO:1551:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

| | |
|--|-----|
| GGCAGAGCAA CCCGGTGCCT AAACCTCTACA GATCTGTAAT TGAAGATGTA ATTGAAGGAG | 60 |
| TTCGGAATCT ATTTGCTGAA GAAGGTATAG AGGAACAAGT TTTAAAAGAC TTGAAGCAGC | 120 |
| TCTGGGAAAC CAAGGTTTTG CAGTCTAAAG CAACAGAAGA CTTCTTNAGA AATAGCATCC | 180 |
| AATCACCTCT GTTTACTCTT CAGTTGCCGC ACAGCTTGCA CCAAACATTG CAATCGTCAA | 240 |
| CAGCATCATT AGTTATTCCT GCTGGTAGGA ACTCTTCCCA AGTTTTACCA CGGNGGAACT | 300 |
| GGGGCATTTC AAATTCCATG GCAAATTTAC NTTTTNCCCG GTTNTNCCCT TCCNGTACCC | 360 |

| | |
|---|-----|
| GCAGGTNTTG NCCTTTCCGG CTGTTTTTGG GTCACTTTTT NAAGGGCAAT NTCCCATTTT | 420 |
| GGGTGCCAGG GTTTTTGGGG GGGGCCGGGT TTTTTTNGGG TNCCATTGG GGNAG | 475 |

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

| | |
|---|-----|
| GGCANAGGGA ATGCTTTTNA TCCAGTTGCC AAAGATTCCA GTTTATGTGG GCCGTTAAAG | 60 |
| TACTTCTATA GAGGCCTTGT ACCTAATAGC AACTAATGGA ACCCCAGAAC TTCAGAATCC | 120 |
| AGAGAACTT TCCCCAATGA TTTCGGGGAT TTCTTAAATC GATGTTTGGG AAATGGATGT | 180 |
| GGAAAAAAGG GGTTCAGCCA AAGGAATTAT TACAGCATCC TTTCTGAAA CTGGCCAAAC | 240 |
| CGTTATCTAG CTTGACACCA CTNNTNCATG GGCAGCTTAA AGNAAGCAAT GGAAGAGTTA | 300 |
| ACCGTTNAAC ATCCACTG | 318 |

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

| | |
|---|-----|
| GGCAGGAGCN CGGTGGTACG CTCNAGGNCG CGAGCCNACC GAGCGGACGC CAGTGGATGA | 60 |
| CCCGCGGCGG GGGAGGAGGN GATANCATCA GCAAAATGCC AGACGTCAAG GAGAGTNTNC | 120 |
| CCCCGAAATA TCCTGGCGAC TCAAAGGGCA GGTCTGTAA GCCCGAAACC TCAGGACCCC | 180 |
| CCCAGGAAGA CAAGAGCGGC TCCGAGGACC CCCCTCCCTT TTTTCTGTC ACAGGTCTGA | 240 |
| CAGAAACCGT TAATGAAGTT TCCAAGCTGA GCAACAAGAT TGGGATGAAT TGTGATTACT | 300 |
| ACATGGGAAG AGAAGGTTTT ACCTCCAAGC AGTCTGGGAA GGCAAGGTTT AAGGAGACAG | 360 |
| TGCACAATGC CTTTTTGGGG ACCATNTTAA AGGGCAANTN TCAGCAAATT CCCCTTGANT | 420 |
| TCAGNTGTGC TCTTTGAACT TTTTGAAAGG AATTTTAAGG GGTTTTT | 467 |

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

| | |
|---|-----|
| TCCTGAAACA CCACGGGNGC AGTTCAACCA AGGTCATTGA CTTTGGGTCC AGCTGTTTCG | 60 |
| AGTACCAGAA GCTCTACACA TATATCCAGT CTCGGTTCTA CAGAGCTCCA GAAATCATCT | 120 |
| TAGGAAGCCG CTACAGCACA CCAATTGACA TATGGNGTTT TGGCTGCATC CTTGCAGAAC | 180 |
| TTTTAACAGG ACAGCCTCTC TTCCCTGGAG AGGATGAAGG AGACCAGTTG GCCTGCATGA | 240 |
| TGGAGCTTCT AGGGATGCCA CCACCAAAAC TTCTGGAGCA ATCCAAACGT GCCAAGTACT | 300 |
| TTATTNAATT CCAAGGGCAT ACCCCGGTTA CTGGTCCTGT GNACTACCCA GGCAGNTAGG | 360 |
| GAGGGTTGTG NTTGTGGGGG GTCGNTCACG TAGGGGTAA AAAGCGGGGT NCCCCAGGCA | 420 |
| GCAAAGATTG GGGACAGCAT TGNAAGGGTG TGGTGGCTAT TTGTTTATAG GGTTTTTTGA | 480 |
| AAGGT | 485 |

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

| | |
|---|-----|
| AGCGGCACGA GGNCTCCTNT TGGCAGANTT GGCCAGTNTT CCCCAGTGAC AGCCTGGNTC | 60 |
| TTTGGATTCA AGCTGCCTGG TCAGACTGCA NGTTCATCTG TACAAAGAAG GAAGCAACAG | 120 |
| TGCCAGGTTT CAGCGTGCCT TCCAAGTTCC ACATTCTGTG TGGCAGACTC CCAACGCCAG | 180 |
| AGCAAAGGCA GGCCCTGGC AGGGGGACTC TGNAGGAAAG TGGAACNCC AGGAGACACT | 240 |
| GCCTGNAAAT TGTTCCTAAA GTTCAAAGGG AGCCAAACGG TGTNACGAGC TTCCCTCTTT | 300 |
| NGCCGTNCCC CTNTTNAAGA AGCCAGCCAT GGCCCTGAGT GATTGT | 346 |

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

| | |
|---|-----|
| GAGTCACTGG CATTACGAA CTCAGCTTAT GCAAAATNTC AGTCACAGGT AGTCCAGGTA | 60 |
| TGCAGAGAAG NNGAAGAAAA ATCTTAGATA CGTCATGGGC ATATGTCCGG GGAGAAGAGA | 120 |
| ACTTAGCNGG ACTGGCGGCC CCGTGGGAGN ACAGCCTTCA TCCTTNAGCA CCANTGGGGA | 180 |
| GCTGGNGG | 188 |

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

| | |
|---|-----|
| GGCAGAGCTC ACCTCCAGTT CACATGTTAA AGTCCTCACC CCCAGCAAGA CAGTNTTGGA | 60 |
| GGTGGGGCCT TTGGGAAGGG GAGCAGGTTT AGAGAAGATC CTGGGGGACC CTCACGAATG | 120 |
| AGATGAGTGC CCTGATGGGN AAGAGACACC GGGAGCCTCC TCTCCAGGTA GTCACACACG | 180 |
| GGGACNGTGC ACATGAGCAA GAGGCTGCTG TGCCGTAAAG CTTGGGGGGT GGTCTTCCA | 240 |
| ACNGGTA ACT GGGNTGCTGT GGTACCTGG GAGGCTGTGT TTTCCCACT GNNCAGTAGC | 300 |
| TTGGGNGGA | 309 |

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

| | |
|---|-----|
| GGCACGAGCA ACAGACTCAA TAGAAAGACT CCCAGTGTAT AACAAAGCTG CCTGGAAGCA | 60 |
| TTACAACACC AACCACGAGG CTGACGACTG GTGCGTCCCC AGCAGAGAAC CCAAAGACAT | 120 |
| GACGACGTTT CGCAGTGCCT AGNACACACT TGGGAACATC GGNAAAATCC AAATGTGGCT | 180 |
| TTTGTATTAA ATTTGGAAGG CTTAACCTCT NCAAGCTCTT GAAGGTTATN AAGAGGGATT | 240 |
| GATTAGTGCC ATGGATTCCA GGTCTTGNAG ATTTAAAGGG CACGGAACGT NCCCTTCCCA | 300 |
| AGGTTACTGG CATTTTTTAA CAAGTTGGAA GNTTTGTGGG CAATTCTTNC ATTGNG | 356 |

(2) INFORMATION FOR SEQ ID NO:1559:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

| | |
|--|-----|
| GGCACGAGGG AAAGCACCCCT GAGAAGACAG GAAAGAAAGA ATGCAGCACT GGTTACCAGG | 60 |
| ATGAAAGCCC AGAGGCCAGA GGAATGCTTA AAACACATCA TTGTAGTGCT GGATCCAGTG | 120 |
| CTCTTACAGA TGGNAAGGTG GGGGCCAGCT CCTAGGAGCA CTGNAGACCA TGGAGTGCCG | 180 |
| CTGTGTGATT GAGGCGCAGC TGTGCCTTGC AGTGTCACTT GGAGGAGAAG GGCTGGGCCG | 240 |
| TCTGAGGACA GNGAGGACTG GGTGGAGGAG CCAACAGTAC TGGTGTGCT CCGGGCAGAG | 300 |
| GCATTTGTNT CCATGATCGA CAATGGAAAG CAAGGAAGNC TNGACAGCAT TATGAAAGGG | 360 |
| AAGGAAACGN TTCAGGGTTT TTAAGTGN CN TCACAGCAA GNCAGCAAGG AAAGTTTTTT | 420 |
| CACTGGTGAT TNTGGTTCAG GGNAATGTTT CATTGTTTCAG ATTCTCCCCA GAAGGGGNAA | 480 |
| CAGGGGCAAT TAACCAGCCC AG | 502 |

(2) INFORMATION FOR SEQ ID NO:1560:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

| | |
|--|-----|
| GGCACGGCTC ACACCGGCCT GTCCTGAGCA AGGGTTTGCT GCTGCTCCTC TGGCTCTCCT | 60 |
| TTGCTGAGAC CTGNAGTCAC CGGTTGCGCT TTGATGTNCT CACTCGTCTT GGTGTGTTT | 120 |
| TCATAGCCCT TGGCAACTTG CTTCTGGGAT ATTCAGTTTC AGGGTGTTTA GGNGTTACGT | 180 |
| TATTGAAGAT AAGAGTTTCT TTTTCTGTAA CTTGTTCTAA TTTGGGTGGG TAATAAGAAC | 240 |
| AGAGGCCTTC AGAGAAGTAT TTAAGTCTGAC GTCTTTAAAG CTTTTTAAGG CCCACGGCCA | 300 |
| GATTTCTTTA ATACACTTTG GGCATCCTCT GTCTGTAAAA TTAGGGAATT GTATAATGTC | 360 |
| CTCGCTAACA TACTTTCAGG TTAACCTGTT TATGGTCTG ATGTATTAC ATGAAATTTG | 420 |
| GGTAACACTA AATATAGTGA ATGTTTCTT ACAGACAGAA CCTCCACTCA ATACACCAGA | 480 |
| AAGCAGAGAG TATCTTGCAG NANT | 504 |

(2) INFORMATION FOR SEQ ID NO:1561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

```
GGCANAGNAA AAAAAATTCA AGACCAAGAC CAAGAGCTGG CCACTGTGCT GTTGCAATCG      60
GCANTCGATT GTATTTTGG AGTGAAGAG ATGGCTACAA AAAAGCATGA ATAGTCAAGT      120
TTGCTGCANG NTCTTTGGTA TCTTGNTACT GNGANACCAC CGGNACCATC TCAAGTACAG      180
CTGATCAAAG CCACTACCAA CTCCTTTGAT GTCAAGTGGG ATGAAGTGTC TACAGTTGNG      240
GGCTATCTTT TGCAGTTGAG TACAGACTTG NCATACCAAG CTGGCATCAT CNAGATTTTT      300
TCAGCAGCAC CAATTNTGCA AGGAGTTCAG GNTGGGACCN                               340
```

(2) INFORMATION FOR SEQ ID NO:1562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

```
AAGAGAAAGG AGGCTCTCAG TAAATGACC CAAATCATCC ATGAGACAGA CCTGTTAATG      60
AACACCATGC TCATAGAAGA GCTGCANGAC TGGGAGCGGC GGCACAAATC GCCTGCATCG      120
GGGGTCCACT CCACAATGGG CTCGACCAGC TTCAGAACTG CTTTACACTA TTGGCAGAAA      180
GTCTTTTCCA ACTGAGAAGG CAATTGGAGA AACTAGAGGA GCAATCTTAC CAAAATGNAC      240
ATATGGAAGG TGATCCCATT CCAATGCAA GAACTCACAT NGTTAGNAAG AGTCACCTTC      300
TTGNTTN                               307
```

(2) INFORMATION FOR SEQ ID NO:1563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

```
GGCANANCTG CTTCGGGGCA TAGACAGCTT ATTCTNTGCC CCNATGGACT TCCGGGGNCT      60
```

| | |
|---|-----|
| CCCTGGGAAA CTACCACAAA GAGGAGAACC AGGAGCACCA GCTGGGGNAA CAACACCCTC | 120 |
| TCCAGCCACC TCCAGATCGA CAAGATGACC GACAACAAGA CAGGAGAGGT GCTGATCTCC | 180 |
| GAGAAATGTG GTGGCATCCA TTGCAACCAG CGGAGGGGGA GCTTCGAGGG TGATTTGAAA | 240 |
| GGTACCCAGG ATGGAGGAGA AGGAGGCCCT TGGTACCCAT TNCAGAAGGN CCACGGGACA | 300 |
| GTTTTCCACA AAGAANTTCC NNCCCCGGTT TGG | 333 |

(2) INFORMATION FOR SEQ ID NO:1564:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

| | |
|---|-----|
| GGCAGAGGNA CCAGCGCGCC CCATTACCT TGGCTGTNGT NGTTNCACAT GACCCAGGCT | 60 |
| GGCCAGTNGT CAGGTTGCAC CGCCCTTTGG TTCCCAGCA TGCTGTTTTN TTTNAGCCTT | 120 |
| CTNTCCAACC TTAACCAAAT CGGCAGCAGC CACCTNGAAC CGNCCACACA TTCCTGGCCA | 180 |
| ATNAGCTCAG CTGTTTATTT ACCAAATGTT TTCACAACAA CTACAGCAGC AGCTTTCGGT | 240 |
| TAACAAAAAA GCAGGAAAAA TCCACAACAC CNNGTTGGGC AACCAANTAA ATCCAAGGGA | 300 |
| ACATNTGGNA AAACCTTTT | 319 |

(2) INFORMATION FOR SEQ ID NO:1565:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

| | |
|---|-----|
| ACGGAAACAA TCTGAAGGTG AAGAGAAGAC ATTAACAGGG GNCGTGTAAA ACCAGTCCTN | 60 |
| CCACGTAANT NNACC AAAGA AACAGCTGCC TTCTATTCCC AAAAATGCTT TGCCCA | 116 |

(2) INFORMATION FOR SEQ ID NO:1566:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

| | |
|---|-----|
| GCCCTGGAAG ACGATCCCNA GTTCAACGCA GGTGTGGGT CTNTNTTGAA CACAAATGGT | 60 |
| GAGGTTNAAA TGGATGCTAG TATCATGGAT GGAAANACC TGTCTGCAGT AGCAGTGTCC | 120 |
| GCAGTCCAGT GTATAGCAAA TCCCATTAAT CTTGCTCGGC TTGTNATGGA AAAGACACCT | 180 |
| CATTGCTTTC TGNACTGACC AAGGCGCAGC AGTTTTGCAG CAGCTAATGG GGGTTCCAGA | 240 |
| GATTCCTGGA GAAAACTGG TGACAGAGNA GAAACAAAAA GCGCCTGGAA AAAAGAGGAG | 300 |
| GCATGAAAAA GGTGCTTCAG AAAACAGGTT TGTTCANAA AACTTTGGGG AACCNATGGG | 360 |
| TGNTTGTNG TCTTGGGAN | 379 |

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

| | |
|---|-----|
| GGCAGGAGAG CCTCCTCAAC TGGAGGCGAG TTTNTTCCTT CACGGGGNCG GTTCCCCGCG | 60 |
| NCCCCGNACG NNCACCGAGC GGGGGCCATC CGGGAAGCTG ATGATCATCT TTGGAGGGGG | 120 |
| AAATAAGGGC ATCGCGGATG AAGCTGGCAC GTNTACAACA CGGCTACGAA TCANTGGTNT | 180 |
| CTGCCAGCTG TTAGAGGAGA TATCCCTCCA GGCTGTGNTG CCCATGGATT TGTCTGTGAA | 240 |
| TGGTACCAGG AATATTAGTA TTTGGGGGAA TGGTTGAATA TGGGAGNTTA CAGCAATGGA | 300 |
| GTTTATATGA AGTTACCAAG CAAGTGCCTT GGTTATTGGG AAAAAAGTG AAACCCCAT | 360 |
| NCCCCCTNCN TTNTGGTTTT AACNCCCTTG TCC | 393 |

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

| | |
|---|-----|
| GGCAGGAGG AAGAAGCACA GTAATGANTT TAANATGACG TCATTCCTGT TAATCCAACA | 60 |
| CCTGCNACCT TTTTACTGT NTGANGCGGT ACAGCGGGGA TGAAGGGCTT CATGAACTCA | 120 |
| AAATACAGCA AAGCACAACG GAACACTGCC TTAAGANCTT TAACCTCACC GAATACCGTC | 180 |

| | |
|---|-----|
| AGTACTGAGC CGAACCTTTC CATTCAAATC TACCAGCAGC TCTTGAAAAT TGCCGAGGGT | 240 |
| GCGTTACAGC CGNTGATAGT TTNTTCCCAT GTTGGGAAAT NNGGGGCTTT CCNGG | 295 |

(2) INFORMATION FOR SEQ ID NO:1569:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

| | |
|---|-----|
| GGNACAGGTC GGCATTATTT AAATGAAATT GGACAGTATG ACAAGGATAT GGNTTTTNGG | 60 |
| GGAAGAGAAA ATTTGGAAC TTNACTAAGG ATCTGGATGT TTGGAGGCCA ACTTTTATA | 120 |
| ATCCCCTGCN CTCGAGTAGG ACATATCAGT AGGAANCAAA CTGGGAAANC CTTCTACAAT | 180 |
| CATCAGTGCC TATGAACACA TNAAGTGNCC TAAGATCTGG TGGCACGTTT GGTGGATGG | 240 |
| ATTATNAGGG GAGCCAGTTT TTTNTTTCGG AAAGTCTGGT CTGGAAATAT GTNACCTNCG | 300 |
| GGAAANTT | 308 |

(2) INFORMATION FOR SEQ ID NO:1570:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

| | |
|---|-----|
| GGCAGACCGG CACGAGGNN AACTGGGTGC TGGAAATGGA AACCTGCAGT NCCTNGACAC | 60 |
| ATGCAGAAAG CCAGAGTGGA AACTAGCAGA GTTCTTCACA TCATGGNTTT NNAANGAGGG | 120 |
| CAAAACTTC TAAATNCCAG TTATTACAGC TGGTAG | 156 |

(2) INFORMATION FOR SEQ ID NO:1571:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

| | |
|--|----|
| CGCCAGACGG CCATGTCCGA AACCTACGAT TTTTNTTTA ATTCCTTGGT TATTGGAAAT | 60 |
|--|----|

| | |
|---|-----|
| GCAGGANCTG GNCAAATTTN GCTTACTTCA TCANTTTATT GAAAAAAAT TCAAAGATGA | 120 |
| CTCAAATCAT ACAATAGGAG TGGGAATTTG GTTCAAAGAT AATNAAATGT NGGTGGTAAA | 180 |
| TATGTAAAGT TACAAATATG GGATACAGCA GGNCAAGACC GATTCAGGTC CGTGNNGGAG | 240 |
| NAAGTTATTA CCGAGGCGCG GCCG | 264 |

(2) INFORMATION FOR SEQ ID NO:1572:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

| | |
|---|-----|
| TATTTGGTCA AGATACTCAC TTGTAATTAT NCCAAAAANT TGGAGTCTGT TTCCNGTTAA | 60 |
| TTCNTTTTTG GGGGCAGCAG GAGCCTCTCA CCTTTTNGGT ATTTGGAGAT ATAACCAAGA | 120 |
| NCTAAAAGCT AAAGCACACA AATGAAAAGA NTTCTGATC ACCTGANCAA TCTAGATGTG | 180 |
| GACAAAACCA TTGGGGACCT AGTTTATTAT TTGGTTATTG ATAAAGCAAA GCTAACTGTN | 240 |
| TGTTTAGAAA GGCAGTGTNA ACTGGTAGCT AGTTCCTTGG ATTCCAATAG AAAAATGNCA | 300 |
| GCAAACTTT TAATAACAG TTCTCTNTAN CATGG | 335 |

(2) INFORMATION FOR SEQ ID NO:1573:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

| | |
|---|-----|
| TTTTTANCTT CGGGCTCTNA ATTTTNGCGA GTAAAANTGG CTAAGTGAAT ATGGTGGAAA | 60 |
| TGGTTTCGGA AGGACGTNTT AGAATGATGT TGAAACTAT NACCCATG | 108 |

(2) INFORMATION FOR SEQ ID NO:1574:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

| | |
|--|-----|
| GGNAGGAGGT GTCGACTCCC TCAAAGCCAT GACCAGGCGA ANCAATACGG ANAAGTTNCT | 60 |
| AATCTCCTTN AGGGTGTAAT GAATGTCCTG GAAGCACTTC CACAAGTATA TGGGGATTCC | 120 |
| CCAGATCCGG CAGCTTTCCG AAAGNNTGAA GGCTGCACAG ACTGANTTAG GACAGCAAAT | 180 |
| CCTGGCAGAT TTTGAAAGAA GCGTTTCCTT CCCAGGGGCA CCAAGNGNCC AGGTGGACCC | 240 |
| AGCAATGTTC TTACGAGATG CATGTTCTGG TTGCTAAATA TTCTGGATTCC CCAGGGTTCA | 300 |
| ANCNGGNATC CTTCAANAAG TTTNTTAAA | 329 |

(2) INFORMATION FOR SEQ ID NO:1575:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

| | |
|---|-----|
| AGCTGCCAAA AGGGCATCCT GGAAGCCCCA TGGAGGACGG AGTAANATGG ATCGGGAAAT | 60 |
| TTCCATTGTT GTNCTTAATT TTNAATGAAA ATANGTTTTG GTATTTGGAG GAAAATNTGG | 120 |
| CAACCCATGG NTCCCAGGAT CCAGGCAGTA TTAACCTACA GGATGAAACT TTCTTGGAGA | 180 |
| GCAATAAAAT GCATGCAATC AATGGGAAAA CTCTATGCCA ACCTTAGGGG TCTTACCATG | 240 |
| TACCAAGGTG AACGANTGGC CTGGTACATG CTGGCCATGG GCCAAGAATG TGGATCTACA | 300 |
| CACCNATCCAT TTTTCATGCAG AGAGTTTCCC TCTATCGGAA TGGCGGGGAA CTACCGGGGC | 360 |
| AGTTGTGGGT GGTTCNTTTC CCCNNGGANT TTNAAGG | 397 |

(2) INFORMATION FOR SEQ ID NO:1576:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

| | |
|--|-----|
| AGCCCAGGGN AGCCCAGCCA GACGCCTCCG GTAGTGTAATA TAAGGACAAT GCCTGCTGGC | 60 |
| CCACATGAAC GGGGGGATGT AGACGGCAGC GGCGCCAGTC GTNCCTGGCA CCATGGACGA | 120 |
| TGCCACANTC CTGAAGGAAG AAGGGTTACA TCGTAGGCAT CAATCTTGGC AAGGNTTCCT | 180 |
| ACGCAAAATT CAAATCTGCC TACTCTGAAG CGCCTCAAGT TCAATGTGGC TGTCAAGATC | 240 |
| ATCGACCGCA AGAAANCACC TACTGANTTT TTGGGAGAGA TTCCTTCCCT CGGGAGGATG | 300 |

GGNCATCCTG GGCAACTNTN CAAACCAA

328

(2) INFORMATION FOR SEQ ID NO:1577:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

| | |
|---|-----|
| AATAAAGATG CTTCANACTG CAAAGAATTT GTTGAAAGAG GAGAAATTGG TGCATAGCTA | 60 |
| TCCGTATGAC TGGAGGACCA AGAAACCTGT GGTATTTCGT GCCAGCAAGC AGTGGTTTAT | 120 |
| AAACATCACG GATATTAAGA CTGCAGCCAA GGAATTGTTA AAAAAGGTGA AATTTATTCC | 180 |
| TGGATCAGCA CTGAATGGCA TGGTTGAAAT NATGGACAGG CGGCCATATT GGTGTATATC | 240 |
| AAGGCAAAGA GTTTGGGGTG TTCCAATTCC TGTGTTTCAT CCATAAGACC AAGGATGGAA | 300 |
| TACTTTGATN CAACAGGTTG GTTGGNCCCT GATGCCTTGG GAATATGTGC CCAGGTCCAG | 360 |
| GTNATTTTGG GGACATCTGG GNTTTGNTAG GCGGGAACCT TCC | 403 |

(2) INFORMATION FOR SEQ ID NO:1578:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

| | |
|---|-----|
| CGGCNTNTNT NTGCTCCGTC GCAGGACGCA GGGTTCGGGC CTAGGGTAGG CTCTCCTGAA | 60 |
| TCGACAGGCG CCGGACCTCT NACAATGCAG ATCTTCGTGA AAGACTCTGA ACTGGTAAGA | 120 |
| ACCATCACCC TCGAGGTTGA AGCCCAGTGA ACACCATCGA GAATGTCAAG GCAAAGATCC | 180 |
| AAGATAAAGG AAGGCATCCC TCCTGACCAG CAGAGGCTGA TCTTTGCTGG NNAAACAGCT | 240 |
| NGGNAAGATN GG | 252 |

(2) INFORMATION FOR SEQ ID NO:1579:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

| | |
|--|-----|
| TNTNCCCATC TTCCACATCC CTGGNCGTAC CTTCCCTGTT GANATCCTCT TCAGCAAGAC | 60 |
| CCCACAGGAG GNTTACGTGG AGGCTGCAGT GAAAGCAGTC CTTGCAGGTG CCACCTNTGC | 120 |
| GGGGGCCCCCT GGGAGACATC CTTATCTTTC ATGCCTGGNC AAGAGGACAT TGAAGGTGAC | 180 |
| CTNAGACCAG ATTNTGGGAG CATCTGGNAG GGAAGTNGGA GAACGNGNCC TGCCCTNNGG | 240 |
| TGTGNTGGNC CATCTAATTT NNAGTTGNNT TTTGAANCTT CCAGGNCAAA ATTTTTCAG | 300 |
| AAGGGTTCCA ATTGGGGGTT CGGGAAGTTG CATGGTTGGC CAACNATATT GCCCCGNGAA | 360 |
| GGTTTTTTNA ATTGTTTGAN GGGATCAAGN T | 391 |

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

| | |
|---|-----|
| GGCACGAGTA AAGTTAACCA TTAATATGAA CCCAAGCTTA TTATAGATCT TTCCAATTGG | 60 |
| AAAGAACAAA GCAAAGAAAA ATCTGATAAG AAAGGCAAAT CAAAATGTGA AAGGTAATGG | 120 |
| NTTGGTTAAA GCCCAGATAG CGCTAGAGGG AAGCATCACA GCAACTGGCT GGNAAAAGNA | 180 |
| AAGGGAAAAG NAATCAGGGA TTTGAATTTT GAATTCCTTT ATTGCAGGAA CTATTNCAGC | 240 |
| TTAGTTTCCC AGNCATGAGC CTAATGATGT TGTGATAAA ATTNAAATGG ACTTGGAATA | 300 |
| GCTCAGTGTT CCCAACTNNG AATTTGAAAA GGTTTTGATA TCCAAGGTTT CGTAAGNCCA | 360 |
| GGGAAAAANCC GGG | 373 |

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

| | |
|---|-----|
| GATTNAACAA CGCNTTACTG CTCGCTGGGT TCATCCCGCC NATGGNCGTG TCTATAACAT | 60 |
| TGGAATTCAA CCCTCCCAA NCTGTGGGGC ATTGGTGACC TGGACTNNGG GNGCCTCTGC | 120 |
| ATTGCAGC | 128 |

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

| | |
|---|-----|
| GGCAGAGCTC GTCCTNTTNC CCAGGGACAA GTGAGGTCGA TGAAATCTTT AAAATTTNCC | 60 |
| AAGTTTTAGG GACTCCCAAA AAAAGTGA CTGAGGAGG ATACCAGCTG GGCATCCTCT | 120 |
| ATGAANCTTC CGTTTTCCCC AGTGTGTTCC TATAANCTTA AAAACTCTTA TTCCCAATGC | 180 |
| CATAATGAGG CTATTCAGCT CATGACCGAA ATGTTGAATT GGGGTCCAAA GAAACGGACC | 240 |
| GACAGCAAAG CCCAGGCATT GAAACACCCT NTTTNCCAAG TTGGTNCAGG TTTAGGCCCC | 300 |
| TTGGTTCAAT CCATCTGGGA TNCAAAACAT CTTTAATTAA GCAGTNGCAA CCCTTAGATT | 360 |
| CAAAGCCCTC TTTAGTTTNG GGTNGGNCT TAGG | 394 |

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

| | |
|--|-----|
| GGCACGAGTG GACTAGGACT GGCCCCGGCA AAAACAAGT NTTATAGCTG CCCAGTGTCC | 60 |
| TCTGAGTGGA TGCTGGTGAT TCTGGTATGG AGCCCAGATG TAAGGCAGCA GGTGGTCCAG | 120 |
| AAGGCACCAG AAGAGGTCTC CTGTCAAAGT CAGGGCCAGA GAAGAAGGCA CAGGGNNCCT | 180 |
| ACTGCACGAG AACTTTCACT TGCAACGAGC AACCCTATGAT GAGGAGGGAG GATTCCTGGG | 240 |
| GGCATTGAGT CCCCAGACA CAAGGACCCN GNACCTTCTT GCTTGGGAAA GTGGANTTCC | 300 |
| TTCAGAATTC CGAGATGATG CCATTTTNGG AGGAAGNTGA CATGAGGGAC CCAAAACTTT | 360 |
| NTTGCTTTGG AAAGTGNATT | 380 |

(2) INFORMATION FOR SEQ ID NO:1584:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

| | |
|---|-----|
| GAGCTCGTGC GGNTTNANTT AATTCTNCTG TTTCGTGAAC TGCGAGTGGA ACAGGAATCT | 60 |
| CTGTTGANAG CTTTNNGCTG TGGCCTGCAG TTTTNAGGCA ACATTNCCTC ACGGATTGAA | 120 |
| GATTCCCAGT CTATTGTTTG GGTGCATGCT TTCCCAGAAC TTTTTTTGTC TTGCTTAAAT | 180 |
| CATCCGGACA AAAAAATTNT TGCCTACTNT NCAATGATTT TGTTTACATC CCTTAATCAT | 240 |
| GAAAGATTGA AAGANCTNGT GGAGGAACCT NAATATTGCA ATTNATGTCA TAGATGCTTA | 300 |
| CCAAAAACAT CCNGAATCAG ATGGCCGTTT CTTGAT | 336 |

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

| | |
|--|-----|
| GGCACGAGCT TTGCACCNAG CCTGTGCTAA TGGACATACA GATGTTGTAC TTTTCCTAAT | 60 |
| TGAGCAACAA TGCAAAATAA ATGTCCGGGA TAGTGAAAAC AAATCCCCAT TGATTAAGGC | 120 |
| AGTACAGTGT CAAAATGAGG ATTGTGCTAC TATTCTTCTA AACTTTGGTG CAGACCCAGA | 180 |
| TCTGAGGGAT ATTCGTTATA ATACTGTNCT TCACTATGCT GTTTGTGGTC AAAGTTTGTC | 240 |
| ATTAGTTGAA AAAC TGCTTG AATACGGAAG CTGGATCTTG AAGCGGAAAA ATAAGGGATG | 300 |
| GGTATACTCC ACTATTAGTT GCCGTTTATT TAACATTATN CCAAATGGT AAAATTTCTT | 360 |
| CTNGNGGAAG GGGGNTGATG TGAATGCTTT CAGN | 394 |

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

| | |
|---|-----|
| GGCACGAGGG NCTCTTCAGC TCAGCCCTCC ACAAAGTGTG AGCCTGAAGG ACCACCCTGA | 60 |
| ATTGCCCTTG TAGGACCCAG AACAGCTACC AGCAGAATCA GATTCTNATG GACCAACTGG | 120 |
| TATTCAAAGA GACAATCTGG GAATGAATGC GTTCTGGCAG AACCCCTGGG AACCAGGGAG | 180 |

| | |
|---|-----|
| NCCTGGNCAG TGAATTATCT TATTCATCAC CGCTGTCCTG CTTCTGAATC TTATTTGCCA | 240 |
| TCGTGTTTGG TTTACTCACT TCCACAGAAA AACTTTCAGT GTGNAAGCGG GTNAAAGAGG | 300 |
| AGTNAACCTG GACTTNGCTG GGGGACTGAG AN | 332 |

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

| | |
|---|-----|
| GGCAGAGCGG CACGAGAGAA CCAGAAGGCT GGGCTGGGCC CTCGCTTCTN GCCCATCACC | 60 |
| CCTCTCCAAC AAGCTGCTCC CGGAGTGGGT CCCCCCTTCA GCCAGGNCC AGCTCCCCAA | 120 |
| CTACCCCCAG GACCCCCTGG CGCCCCAAG CCACCACCTG CTTCCCAGCC CAGTCTGGTC | 180 |
| TCCACTGTGG CCCCTGGCTC CGGCCTGGTT CCCACGGCAC AGCNCGGGGC ACCGTTCCAT | 240 |
| GGCAGGCACT TTGGNCCCAG GAGGGGTGAG CGGCCCTTTC CCAGNCCAGT TGGAAGNCCC | 300 |
| CAGTCCTTGG GTTGGGGAAG CAATTNAATT TTTCCAATAA AGTTTTTTTG GNCTTGGGAG | 360 |
| CGGGGGTTNC TTGGANTTGG GNAAAGGGAA AACCCAAAAT TTG | 403 |

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

| | |
|---|-----|
| GGCACGAGAA TGAGCTCGTC GGCTGAAAGG GAACATCCGA GTAATTGCTC GTGTCCGGNC | 60 |
| AGTNACCAAA GAGGATGGGG AAGGACCTGA GGCCACCAAT GCTGTAACTT TCGATGCCGA | 120 |
| CGACGACTCC ATCATCCACC TGCTGCACAA GGGNAAGCCT GTNTCCTTCG AGCTGGACAA | 180 |
| GGTCTTCTCC CCACAGGCCT CGCAGCAGGA CGTGTTCAG GAGGTGCAGG CCCTGGTCAC | 240 |
| CTCTTGCAAT GATGGCTTCA ATGTCTGCAT CTTTGCGTAC GGCCAGACGG GCGCCGGCAA | 300 |
| GACGTACANG ATGGAGGGGA CCNTGNMNA CCCAGGTTTT CAACCAGNGG GCCNTGCAGT | 360 |
| NGTNTTATTC CGAGGTGNCA GGAGAAGGCG TTTTATTTGG GAGTTACACC TTCACCTTCA | 420 |
| GGNTTGNGGN GNTTTTACAT TGAGGTCNT CAGGGACTTN TTAGGGGAAG AGCCNTCAGG | 480 |

GAAAAATGGA GTTCGGTTNT GC

502

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

| | |
|---|-----|
| GGCAGAGCC CCGGTGTTCA CTCAGGAGGA GAGATACAAG ATGGTGCAGG CCATCAAATG | 60 |
| GGTGGACGAG GTGGTGCCAG CGGCTCCCTA CGTCACTACA CTAGAGACCC TGGACAAATA | 120 |
| CAACTGTGAA CTTCTGTGTT CACGGCAATG ACATCACCCT GACTGTAGAT GGCCGGGACA | 180 |
| CCTATGAGGA AGTAAAGCAG GCTGGGAGGT ACAGAGAATG CAAGCGCACG CAAGGGGTGT | 240 |
| CCACCACAGA CCTCGTGGGC CGCATGCTGC TGGTNAACCA AAGCCNTCA CAGCAGCCAG | 300 |
| GAGATGTCCT CTGAGTACCG GGAGTTTGGC AGACATTTTG GCAAGTGCCT GGTGGGCGGT | 360 |
| AACCCTGGGA CCGGGGNTT CCCATTNCTG NCAGACTTTT CAGNAGTNC TTCCATTGN | 420 |
| TTNTGGGGAA GGAGCCCCAG CCAGGGAGAC ATTCNNTATG TNGTTGGTGN CTTTGGACCT | 480 |
| TTCCACNTG GGGCTGTGGA TTTC | 504 |

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

| | |
|--|-----|
| GGCAGACCTG CACNCCTGAT CCATAATGCT NACGCCAAA AAAGTCCTT GGTCTNANA | 60 |
| GGCCTCCAAA GCCTACTCCA AGGTTTCACC NNTNTTNCC TGAAGTNANC CTGCTTCGGN | 120 |
| AGNATAGACA GCTTATTCTN TGCCCCATG GACTTCCGGG GNTTCCNTGG GAAACTACCA | 180 |
| CAAAGAAGGA GAACCAGGAG CACCAGCTGG GGGAGCAACA CCTCTCCAG CCACCTCCAG | 240 |
| ATCGACAAGA TGACCGACAA CAAGACAGGN GAGGTGCTGA TTTCCNGAA ATGTGNGTGG | 300 |
| CATCCATTNC AACCAGCGGT GGGGAGCTT TCGAGGGGTG ATTTTGAAAG GTACCCAGN | 360 |
| TTGG | 364 |

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

| | |
|--|-----|
| GGCAGAGTGA ACTTCTTCCT GTTGGTNTCC CCCC GCCGCT GTGGGGCCGT CGAGACCCGN | 60 |
| CTGGNCGCTG AGATCCTGTG CCAGGGCAAG AAGTTCTACT TTGTGCGCAC CAAGGTGGAC | 120 |
| GAGGACCTGG CGGCCANGGC AACCNCAGNG GCCGTCGGGC TTCAAAAAGG CCGCTGTTCC | 180 |
| TGCAGGAAAT CCGAGACCAC TGTGCCGAGC GGCTGCGAGA AGGCCGGCGT GGCTGACCCT | 240 |
| CGCATCTTCC TGGTGTCCAA CCTCTTNGCC GGTTCGNTA ACGACTTTCC CACGCTGGTG | 300 |
| TCCAAGTGGG AAGCATGACC TGNCTCCNA ACGGTGGCCA AGNTGGTCTG GT | 352 |

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

| | |
|--|-----|
| GGCAGAGGNT GGTTCATACC GACGGGGAAA GGCGACCTGT GGTGATGTCG ACGTGCTCAT | 60 |
| CACTCACCCA GATGGCCGGT CCCACCGGGT NATCTTCAGC CGCCTCCTTG ACAGTTTTTCG | 120 |
| GCAGGNAAGG GTTCCTCACA GATGANTTGG TGAGCCANNA GGAGAATGGT CAGCAACAGA | 180 |
| AGTACTTGGG GGTNTGCCGG CTCCCAGGGC CAGGGCGGCG GCACCGGCGC CTGGTACATC | 240 |
| ATCGTGGTGC CCTATAGCGA ATTTGCCTGT GCGCCTGCTT CTACTTGCAC CGGCTCTGCA | 300 |
| CACTTNCAAC CGNTCCATGC NNAGCCCTGG CAAAACCAA GGCATGANTT CTGTTCAGAA | 360 |
| CATGCCCTTC AGCAATGNTT GGGTTCCGGA AACAACCATG GGTGNAAAGT TGGGGCCTGG | 420 |
| NCNA | 424 |

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

| | |
|---|-----|
| GGCAGAGAGA ACTTCTGANC GTTGGTAGTN TGGGGATCCT GGCTTTNTNC TTCTTCACCC | 60 |
| ACCGTATCAG GATCGTCCAG GATACAGCAC CACCCCTCAA TTATTACTGG GTTCCTATAC | 120 |
| TGACGGTGAA TCGTTGGCTC CTACTTGNAT TGCACACGGT TTCTTCAGCG TCTATGGCAT | 180 |
| GTNTGTGGAC AGCTGTTTCT CTGCTTCTTG GAGGACCTGG AGAGGAATGA CGGCTCGGCC | 240 |
| AGAAGCTTTN ACTTGCATGT CTTCCACCCT CAAGAACTN TTGAAACAAG ACCAACAAGA | 300 |
| AGGNAGGGAG TTCCTGAAGG CCCCCTGNTC CCCAACTTTT CAAGGAGTTT TCATGNCGCA | 360 |
| GGTTGNTTCA | 370 |

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

| | |
|--|-----|
| GGCAGAGTGC CTGATCGAAG GCAGCNCGGC CAAGCTCACT TGCCGCATTT NGGCTTTCCC | 60 |
| GGACCCATTC ATCCGCTGGA GTAAGGNCGG CAAGGAGCTA CGTAACGGTC CCAAGTANCG | 120 |
| CTACGTNTTC AAGGACCCTG AACGTGGTGG CACTGGTGGT GCGCGAACGG CAAGCTGGCA | 180 |
| GACCTGGGCC AGTACAGCAT CAACGTTTAC CAACCCCTTC GGCCAGTGCT TCCGACTTCG | 240 |
| GNCGCGGCAT CCTCGTGGA AGTCCCCGAC GGAGGATTTC AAAAGGGGAC CCGACAACAC | 300 |
| TAAGGCGCGC AAAGGCACCA CCGTNAACGN TTGATTCGGG AGATTCTCTGG GGAGAGNCTG | 360 |
| CGCCCCGACG TAGGNTNGGA CCAAGGACGG GGGAGGGACA TTGAGG | 406 |

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

| | |
|---|-----|
| GGCACGAGCT GGGGTGCCTN ATGCNATCAT GCTGTGTGTG CGCCAAATCT GCGCTGTNAT | 60 |
| CCTGGAGTCC CCACCCANAG GAAGCCACTA TCCCCTACCA TCCNAGCCTC TCCCTAGGTA | 120 |
| CTGTTCTTCT CTCTGCCAAC CAGGGCTTCT NTGTCCAGGG TCAGTATGGG GCTGTGAACC | 180 |

| | |
|---|-----|
| CCAGCTGAAG GTCACCAAGC TCCAGCAGCT CTGNAAGCNA TGCGGTTCCC CTTTGGGNAC | 240 |
| ACCCAGCGTG GTGCCAGGGA CTGNGATCCC GGCACACAGA CCAGCTTCAC AGGAGTTCCT | 300 |
| TGGGTTCCCA ACGATTGAA TTGGTTGTNT GGATTGCGGN CGGCCCAGGG NAGCAAAGNT | 360 |
| TCAANGGAG | 369 |

(2) INFORMATION FOR SEQ ID NO:1596:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

| | |
|---|-----|
| ACAGAACGGC CACGNTTCA CCTGCCCAGG CACCTGCCCC AAACCATTCA AAAGAAGGTC | 60 |
| GGGGAGCCTG TGAAACCTTC TNATCCCTTT CCAGGGCAAG CCCCAGCCTC AGGTGAACCT | 120 |
| GGNACCAAAG AGGGGCAGCC CCTGGNAGGT GAAGGTAGGT GNAGCATCCG CAACAGCCCC | 180 |
| ACAGANACCA TCCTGTTNCA TCCGGGTCG | 209 |

(2) INFORMATION FOR SEQ ID NO:1597:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

| | |
|---|-----|
| CCTTTGTCCG TNTGAATTAC CAGCACCGTA TGTCCCCTGA AATTGCCCGC CTTTGTACCC | 60 |
| CCCACATTTA CCAGGATCTG GAGAATCATC CATCTGTTCT TAAGTATGAG AAAGATTAAG | 120 |
| GCCAAGTNCA AATTCCTGCA GAGCTTTGGC AACTGGGAAT GAGAAGAAAG CATAAGAATT | 180 |
| TCAGGGNATG AATTTTNATC TTTTTTNAAA GCTTACGATT AAGAAAGTGC CACGTTTTC | 240 |
| AATTGCTCCC TNCTGGGGNT TCTTGGGACC ACTGNNCTTC CTTCCCCTTC TGCCAAGGAG | 300 |
| CCGNTTTGCT TGTGATTG | 318 |

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

| | |
|---|-----|
| CTAGTGNNTC CCCCGGGCCT GCAGGAATTC GGNAGAGCAC ACCTTTCNT NTCCTTTTGT | 60 |
| GTGATGAAGG GCCCATTAA GGCCTGCTG CGGTGGCCCT TNANCCAGAA GGTAACCTTA | 120 |
| ATNCTGCTCG ACCAGAATAA CCGGGAAGCA CGTAATTNAG NGCTTTCAGG CCCGAGGTGA | 180 |
| ACTTCATCCT GTTTTAAAAG GCCAGTTAAA CGNCATGTAA CATNGCAAGG NG | 232 |

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

| | |
|---|-----|
| GGNAGAGGTG ACCCTCTGGA ACCTGCNAGG AGCCGGCTCT CCAGGCTGCC CGGCTNANAA | 60 |
| GTACCTAAAG CAGGTAGACT TCANCCGCTA TAACTTCTTC CTGTTGGTCT CCCCCGCGG | 120 |
| CTGTGGGGCC GTCAAAACCC GNCTGGGCGG NTGAGAATCC TGTGCCCAGG GCCAAGAAGT | 180 |
| TCTNACTTTG TGCGCACCAA GGTGGACGAG GACCTGGCGG CCACGGGCAC CTNGTGGNCC | 240 |
| GTGGGGGTTN NAAAAAGGCC G | 261 |

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

| | |
|---|-----|
| CCCGGCTGCA GANTCGAGAG CCGGACACCG AGTCGAGNTT TTNAGGACAT GTTANTAGAC | 60 |
| ATCAAGGCTT CACCGNTTTC TGCACCAGGC CGTGGTGTAT TNACGCAGAA TGTNACGTGG | 120 |
| GATCCTGAGT CTTCCGAATG GGCGGACGAA AGACATGGTC ATCATGCCGG TACTGGTGAG | 180 |
| GGACGTCGGC CAAGTCTCAG GGGAGGGAAG TCGAATGGAG GGGGGAGTGT GGAGTCAGTG | 240 |
| CAGTGGAGTA CATGTNTTCA GGACAGGGAC GCAGGGATCT GCAGTGGTGG GCAGCAGAGC | 300 |
| GAGAGGTGTG TGGTGATGG CGAGGCAGAA GTGGATTCTG AAGCAGAGTC GAGCAGGAGT | 360 |
| CCGGGTCCT GTACATGNCG CCATGGCGAG ACGTGCGTGC CACAAGCCCA GCTGCCNTAG | 420 |

| | |
|---|-----|
| CTCTCGTGGG GTGTGAAGGG GANTGGCGCA GGGTGTNCTG AGGCAGAAGC TGGTCTGAAG | 480 |
| GACCTGTCTG AGGCACAATT CGGTGTGTCT CAAGAGTCTC AAGGTNGNTT NGTT | 534 |

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

| | |
|---|-----|
| GGCACGAGCT CACCATNTCC ATNAACGTGN TCTACAACTA CCTGGAGGCC AACCCCAAGG | 60 |
| TGCCCTGGGA CGATCTCCGN TACCTTTTTG GTGAAATNAT GTATGGNGGC CACATCACAG | 120 |
| ATGACTGGGA ACCGTCGGCT GTGCAGGACC TACCTGGNTG AATACANCCG GACGGNGATG | 180 |
| CTGGAGGGAG ACGTNCTGNT GGCCCCCGGC TTTGCAAAT | 219 |

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

| | |
|---|----|
| ACCAAAGTCC AGCACANACC CTCGGGNCTC ATCANGGCCA GGTAAGCTGA TCCACCTTGN | 60 |
| GATCAAGCCG GCCATCCGGA ACCAG | 85 |

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

| | |
|---|-----|
| GGCAGAGGTG TGGCGAGGTG GTCCGGGACC ACATCATCAG GGCCCTGGGN CAGGCCTTCC | 60 |
| ACCCCTNCTN CTTACGTGT GTAACCTGCG CNNGGTGCAT TGGGGATGAG AGCTTTGCCC | 120 |
| TGGGCAGCCA GAACGAAGGT GTACTGCCTG GACGACTTCT ACAGGNTATT CGCCNCCGTT | 180 |
| TGCAGCATCT GTGAAAAATC CCATGCATCC CTCGGGGATG GGGAAAGATG CCTTCAAAAT | 240 |

CGGAATGCAT GGGAAAGAAA CTTNCATGNA AAATTGCTNA CAGGTGTGAA GGNCTGCAAG 300
ATCCTCCNGT CTGT 314

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

GGCACGAGGG TACNCCATTG CGGCCATGTN TGTNATGCGG CCGGAGCAGA TCATGAAAGT 60
CCATCATCCC AGTGGTCATG GCTGGNATCA GANNCCATCT ACGGCCTGGT GGTGGCAGTC 120
CTCATCGCNA ACTACNCTGA ATGAACGTAC ATCAGCNTCT ACAAGAGCTT CCTCCAGCTG 180
GGNGCCGGCC TGAAGCGTGG GCCTGAAGCG GCCTGGCAGC CGGCTTTGTC ATCGGCATNG 240
TGGGGGAACG CTNGCGTGCG GGNGCACCNC CAG 273

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

GGCACGAGAG GTCATCGGGA CCCTGGAGGA GGTCCACATG CCACAGAATG GGAATCAACC 60
ACNCTGGCAT CACTGCCCTG GCCCAGGCTT TCGCTGTCAA CCCCCTGCTG CGGGTCATCA 120
ACCTGAATGA CAACACCTTC ACTGAGAAGG GCGCCGTGGC CATGGCCGAG AACCTTGNA 180
GACCTTGCGG CAGGTGGAGG TGATTAATTT TGGGGACTGC CTGGTTGCGC TCCAAGGGTG 240
CAGTTGCCAT TGCAGATGCC ATCCGCGGCG GCCTTGCCCA AGTTAAAGGA GCTGAACTTG 300
TCATTTCTGT GAAATCAAGA GGGTTGNTGC CCTGGNTGTT TGTGAGGCC ATGGCAGACA 360
AAGTTNAGTT GGAGAAGTTG GACNTGAATT GGCAACANCC T 401

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

| | |
|---|-----|
| GGCACGAGGT TTGATGAGGG CCGGCTGACA GATGGAAAAG GGAAGACCAT TGATTGCAAG | 60 |
| GACGCCATCT TCATCATGAC CTCCAATGTG GCCAGCGACG AGATCGCACA GCACGCGCTG | 120 |
| CAGCTGTAGG CAGGAAGCTT TGGAGATGAG CCGTAACCGT ATTGGCCGAA AACCTGNNGG | 180 |
| GATGTCCAGA TAAGTGACAA GATCACCATC TCAAAGAACT TCAAGNGAA TNTGATTTCG | 240 |
| CCTATCCTGG AAAGCTTCAC TTCCGGAAGG GATGAGTTTT TNGGGACGGG TNCAATGGAG | 300 |
| GTCGTCTNAC TTT | 313 |

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

| | |
|--|-----|
| AACAACAGGC TGAACAACCG CGCCAGTTTC AAGGGCTGCA CGGCCTTGCA CTATGCTGTT | 60 |
| CTTGCTGATG ACTACCGCAC TGTCAAGGAG CTGCTTGATG GAGGAGCCAA CCCCTGCAG | 120 |
| AGGAATGAAN GNGGACACAC ACCCTTGGAT TATGCCCCGAG AAAGGGGNAA GTGATGAAGC | 180 |
| TTCTGAGGAC TTCTNAAGCC AAGTACCAAG AGAAGCAGCG GAAGNTGNAG GCTGAGGAGC | 240 |
| GGCGCCGCTT CCCCTGGAG CAGCGACTTA AAGNGCACA TCATTNGGCC AGGAGAGCGC | 300 |
| CATCGNCACA GTGGGTGCTT GCGNTTCCGG AGTAAGNGAG AATGGCT | 347 |

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

| | |
|---|-----|
| GGCACGAGAG AAGATGCTGC GTATCCAGAA GGAGCACCGC GNCNAACTTC CCACGCTCCA | 60 |
| AGCACCTGAC AGGCGAGTGC AAGGACCTCA TCTACCACAT GCTGCAGCCN GACGTCAACC | 120 |
| GGCGGCTCCA CATCGACGAG ATCCTCAGCC ACTGCTGGNA TGCAGCCCAA GGCACGGGGA | 180 |
| TCTCCCTCTG TGGCCATCAA CAAGGAGGGG GAGAGTCCCC GGGGAATGGA ACCCTGTGG | 240 |

ACCCCCGAAC CTGGCTCTGA CAAGAAGTCT GCCACCAAGC TGGAGCCTGA GGGAGAGGCA 300
CAGNNCCAGG CACAGTCTNA GNACAAAACC CGAGGGGACA GCAATGCAAA TN 352

(2) INFORMATION FOR SEQ ID NO:1609:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

GGCAGGAGCC AGGTGCGGGT TGCTGCCCAA GGGGTGCAGG GACAGATGAG GGAGGGCACT 60
GCCTTCAGGN ACGACATATG GGGGCCACCA TCGCTTTGTT GGTGGGGACA GGGTCCCCCT 120
TTTTTTTTTT TTNAANATGG GNTNTT 146

(2) INFORMATION FOR SEQ ID NO:1610:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

GGCAGAGCTT TGATTAAGTT CCGGGAGTTT GTCTCTGGGC TAAGTGCTGC ATGCCATGGG 60
GACCTCACAG AGAAGCTCAA ACTCCTGTAC AAAATGCACG TCTTGCCTGA GCCATCCTCT 120
GATCAAGATG AACCAGATTC TGCTTTTGAA AGCAACTCAG TACTTCTTTG AAGATATTAC 180
CCCAGAATGT ACACATGTTG TTGGNATTGG ATAGCAGAAG CAAACAGGGT GCAGATGATG 240
GCTGTGTTAC GGTGAGCCTA AAGCCAGACA AAGGGAAGAG AGCAATTCCC ANGAAANTCG 300
TAATTATTTG NGAAGTGGA CTCCAGAAAA TAATCTAAGT CAAGNTGCAA AGGTTTACCC 360
AANTAAATTC AGGGCATTTC ATTGNACCTT GTTAAGACAT GGTATANCNG GTTCAGCGA 419

(2) INFORMATION FOR SEQ ID NO:1611:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

| | |
|---|-----|
| GGCANGAGGT GACCTCCGTG GGCTGGTCTG AGCGGGGGAA CCTNGTGGCG GTGGGCACAC | 60 |
| ACAAGGGCTT CGTGCAGATC TGGGACGCAN CCGCAGGNAA GAAGCTGTCC ATGTTGGAGG | 120 |
| GCCACACGGC AGCGTCGGGG CGCTGGCCTG GGAATGCTGA GCAGCTNTCG TCCGGGAAGC | 180 |
| CGCGACCGCA TGATCCTGCA NAGGGACATC CGNACCCCGN CACTGCAGTC GGAGCGGCGG | 240 |
| CTTCANGGCC ACCGNCAGGA TGTGTGCGGG CTCAAGTGGT | 280 |

(2) INFORMATION FOR SEQ ID NO:1612:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

| | |
|---|-----|
| NTGGTTNCCC CGGGCTGCAG TANTGGGCAG AGTGAAAGGT GCCTGNGGNG CAGCAGCACC | 60 |
| TGCTTTTCCG TGGCCAGCTC CTGGAGGATG ACAAGCACCT CTNTGACTAC TGCATTGGGC | 120 |
| CCAATGCCTC TATCAATGTC ATCATGCAGC CCTTGGNGAA GATGGCGCTA AAGGAGGCCC | 180 |
| ACCAGCCGCA GACCCAGCCC CTGTGGCACC AGCTGGGACT GGTCCTAGCT AAACACTTTG | 240 |
| AACCACAGGA TGCCAAGGCC GTGCTGCAGC TGCTAAGGCA GGAGCACGAG GAGCGCCTGC | 300 |
| AGAAGNTTAA GCCTGGAGCA CTTGGAGCAG CTGGNCCCAG TACCTNCTGG CAGAGGAGCC | 360 |
| TCACGTGGGA GCCCANTTNG | 380 |

(2) INFORMATION FOR SEQ ID NO:1613:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

| | |
|---|-----|
| GGCACGAGGG GTTCTGCAAA GCGGGNCTGT CTGGGGAGTT TNGACCCCGG CACATGGTCA | 60 |
| GCTCCATCGT GGGGCACCTG GAAATTCCAG GNTCCCTCAG CAGAGGCCCA ACCAGAAGAA | 120 |
| GTACTTTNTG GGGGAGGAGG CCCTGTACAA GCAGGAGGCC CTGCAGCTGC ACTCCCCTTT | 180 |
| CGAGCGTGGC CTGATCACAG GGTGGGATGA CGTGGAGAGA CTNTGGAAGC ACCTNTTTGA | 240 |
| GTGGGAGCTA AGGCGTGAAN CCAGCGACCA GNCCCTGNNT TGCAACGGAG CCCTCCCTGG | 300 |
| G | 301 |

(2) INFORMATION FOR SEQ ID NO:1614:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

| | |
|---|-----|
| GGCACGAGCG GCGGCTGCAC GCTGTGGCCC GGCNCCAGCG CTGTAGGCCT GTGGCAAGAC | 60 |
| CTTCCGCTAC CGCTCCAACC TGCTGGAGCA CCAGGAACTG CACCTGGGCG AGCGCGCCTA | 120 |
| CCGCTGTGAA GCACTGCGGG CAAGGGCTTC TTCTACCTGA GCTCCGTGCT GCGCCACCAG | 180 |
| CGCGCCCATG AAGCCGCCGN GGNCCGAGCT NNCGNTGCCC C | 221 |

(2) INFORMATION FOR SEQ ID NO:1615:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

| | |
|---|-----|
| GGCACGAGGG AAACCTGCAC GACAACCTGT NGGACCTNCG TGCCCAGGTG GCAGCCAACC | 60 |
| AGAAGGGCAT CCAGCTGGTG GGGGAGCTCA TTGGGCAGTA CGGCCTGGAA CGTGGTGCAG | 120 |
| GCCTGACATG GGCCATATTC AGGNAAACGC TGCAGCTGGA CCGTGCGNAG ACATGTTGCG | 180 |
| TGCCTTTTGT AACCTTCCCG GCAGGNNCCG NGG | 213 |

(2) INFORMATION FOR SEQ ID NO:1616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

| | |
|---|-----|
| GGCACGAGGT CAATCTCACG GGGTTGAAGA AGCGGGACCG CTGCGNAAGG CCTGGCCTTT | 60 |
| GCGGAGGAGG TGATGGATGA CATCCTGGAC TCCGCGGACC AACCCTTGAC GGGCCGAAAG | 120 |
| TGGTGGATGG GCGCGGAGGA ACTCTGGCAG ACGCTGGCCT GCTGTATGGA GGTGGCGAAC | 180 |
| GCTGTGGGCG CCTCCAACCC TGAGCGCCTA TGTCTCCCAC CTCCCCGTCC ATCAGGAGNC | 240 |

TTCTTGCAAC GGCCTGCAGC ATTATGCTGT NCTNGGCCGC GGACANTGGG GGCGCCGNCT 300
CCGTTCAACC TGG 313

(2) INFORMATION FOR SEQ ID NO:1617:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

GGCAGGAGGN AAGAGTGTA AACCTGCCTG AACAGACCT GCATGNAGTN CTACG 55

(2) INFORMATION FOR SEQ ID NO:1618:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

AACGGCCTNC ACNGACGGNA TCGGNTTNGC CATCGCCCCG NGTTTGGCCC AGGACAGGGC 60
CCACGTGGTC GTNAGCAGCC GGAAGCAGCA GAATNTGGAC CAGGCGGTGG CCACGCTGCA 120
GGGGGAGGGG CTGAGCGTGA ACGGGCACTG TTTCATNNTG GGAAGGCGG AGNACCGGG 180
AAGCGGCTNG TGGCCATGGC TGTGAAAGTT TCATGGAGGT ATCGATATCC TAGTCTCCAA 240
TGCTGCTGTG CAACCCCTTT TTTGGAAGNC TAATGGGATG TNNACCGNAG GAGGTNTTGG 300
GGACAAGATT TTTGGGACAT T 321

(2) INFORMATION FOR SEQ ID NO:1619:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

AGGTACACAG ACACACGTTA TTACATATGT GCACATGCAT GCATATGCAA ATATGCACAG 60
TACACAGACT GCACAGAGCT CCACAGACAT AACTTGCAC CTTCCGGGTTT AAGCCCTGAG 120
CAAATTGACA TCCCGTGTCT TGTCTCTCCAC AGTGTCTCCA GTGCCAAGCA TGGGGCTGGG 180

| | |
|--|-----|
| TGTGGTAAAT GTTTNTNGAG TCAGTGAATG CATGGNTGGC TCGAACCGTG TCTTGACTCA | 240 |
| GCAACACCGG GNCCAGTGGG GTCTGGAGGT GAGGTTTCAGG AGACAGTCAG CCCTCTGCTT | 300 |
| TTGCTGGAGA CTGGGGAACA CCTTTAGGGA CATTTTCAGAG GAAGGACAGT TGCAGGNACA | 360 |
| ACTTTGGTCT AGCAAATCAC AAGNCTGGGT TGAGGNCTCA GGATTTTCCTT GTACCGTGTT | 420 |
| NCTTTTCCAA TTTGCCCAGA GNTAG | 445 |

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

| | |
|---|-----|
| GGCAGGAGCC AAGGGTGAGC GCCATGGCTC AGCAGCCGAA CGACTTCTGG CAGCTCAGAA | 60 |
| CCCGCTCTCC CAGGCTGATC GCCCTCATCA GCTGTTTGCA GATGCACCTC CTCCACCCTC | 120 |
| TGCTCCCAAT CCTGTGGTAT CATCATTGGG GTCTGGGCTT CCTCCACCAG GCATGCCTCC | 180 |
| TCCTGGCTCC TTCCCACCCC CAGTGCCACC TNCTGGAGCC CTCCCACCTG GGNATACCCN | 240 |
| CAGCCATGNC CCCAACAACT ATGGCTNCTG GGGCTGNAGG ACATGGCCCC CCATNGGCAG | 300 |
| GNACCCCAGG GTAGGACATT CTGGTNANTG GGCATTNANA ANTTNAACNA TTTNCAACGG | 360 |
| GTGGGATNNC CCCNTTCAGG GGTNTTTTAA ATGGAAATTT GAAAAAATG GGGCTTTAAG | 420 |
| GTTTTGGGGA ATNCCAAGGT TGGGACCCCA GTTTTGGGGG GNNAATNAAT GGTC | 474 |

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

| | |
|--|-----|
| AAGCTGGGCT TACAGGATGG AAAAGAATAT TTATTCCAGG CCAAGGATGA GGCAGAGATG | 60 |
| AGCTCGTGGC TACGGGTGGT GAATGCAGCC ATTGCCACAG CGTCTTCTGC CTCTGGAGAG | 120 |
| CCTGAAGAGC CGGTGGTGCC CAGCACNCGN NGGGTCATGA CCCGGGNCAT GACCATGCCN | 180 |
| NCAGTGTCAC CCGTCGGGGC TGAGGGGGCCT GTTGTGCTCC GCAGCAAAGA CGGCAGAGAA | 240 |
| CGAGAGCGAG AAAAACGCTT CAGCTTCTT TAAGGAAGAA CAATAGTTNG GGGCAAGTTC | 300 |

CAGGNCAATT CCTTCCTTNN GTTCAGGAAA NTT

333

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

| | |
|---|-----|
| GCTGCGCTCC TCCGAACCTG CCTGCACGCA GCCTGGGTTC CAGGATCTGG AGGTCGTGCC | 60 |
| CCCAAAACCA CAGCCGAGGC CTACCACGNG GGCATGTGCA GCCGGGAACG GTCGGGTAC | 120 |
| AGCGAAGCCT TCATGCAGGG CCAGTTGCGG GTGGTGGTGG CCACGGTGGC CTTTNGGATG | 180 |
| GGGCTGGACC GGTCAGATGT GCGGGGTGTN CTGCATCTGG GGGTTGCCCC CAAGNTTCGA | 240 |
| GAGCTACGTN CANGCCGTGG GCGTGACCG | 269 |

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

| | |
|---|-----|
| CATGCCCTCC CCGNTATGA GCGGGCCGT GCTGGAGACC AAACAGAGCC TTGAGGCTGC | 60 |
| GGGGCACACG TGGTTCCCTT CTTGCCAAGC AACATACCCC ATGCTCTGGA GACCCTGTCA | 120 |
| ACAGTGGGCT CTTCACTGAA TGGTGGCCAC ACTTGCTTAC AGAACTTCAA AGGTGATTTC | 180 |
| GTGGACCCCT GCCTGGGGGN ACCTGGTCTC AATTCTGNAA GCTTCCCCAA GGCTTAAAGG | 240 |
| TATGCTGGCC TTCCTGGTTG AAGCTNCTGC TGCCANGGCT GTCCAGTTTN NCTCAGCAAC | 300 |
| AT | 302 |

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

| | |
|---|-----|
| GGCANAGGGA GGCTCAGTCT GTAAGTGAAG CAGGGCGNTC TCCCCGATAT CTGCATCGGA | 60 |
| CGCGCCCTCT AGTGGAACC GAGAGTNAAG CGGCCTGGAT TCCGCGATGA ACAGATTCTT | 120 |
| TTGTGTCGCT GGGAACACTG GAGGGTTGTC GTTAATGTCC TTCACCTCCA CGTCCACATG | 180 |
| GGAAAACCTG CAGCGGCCTT TCCACGATCA CCTCCAGGNG GATGCTGCAC TCCGCGCTCC | 240 |
| GCCCGCACAG CTCCTCGCGG TCGATCCGAG AATTCACAAA CAAAATGCCA TTCTGGCAGA | 300 |
| TTTACCTCCA GAAGGTCCCC GGGGNCTTTT GGGATTCCAA TTGGAACAGN GNNGGGCANC | 360 |
| A | 361 |

(2) INFORMATION FOR SEQ ID NO:1625:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

| | |
|---|-----|
| GGCACGAGGA AGGAACTCAC TCTGGGGGCC TCACAGGCCA CCACGGACGA GGTAGCTGCC | 60 |
| TTCTTCGTGG CTGANCTGGG TGCCATAGTG AGGAAGCACT TTNCTTTCT NAAGTGCCTG | 120 |
| CCACGAGTCC GGCCCTTTNA TGCTGTCAAG TGCAACAGCA GCCCAGGTGT GCTGAAGGTT | 180 |
| CTGGCCCAGC TGGGGCTGGG CTTTAGCTGT GCCAACAAGA TTGCTTCCGT NATCAACTCA | 240 |
| GCCTTGGAAC TGTACTTCCC ANAAGGGCTG TGGGCGTGGG ACATCTTTGG CTTGAGCTTG | 300 |
| GGGCGGTTAC TNACGTGNAC CTNGGCCTNT NACTGGTGGG CAGTTCAGCA TTCATTGCCA | 360 |
| AAGAAAGGGA GGTTCCTGNT TAGACCAGGN CTNGGNAGGG GAGGAGGAAA ATGGTTCCAN | 420 |
| CTTCCAAAGA CCATCGTTGT ACCACCTTGG ATGGAGGGGC GTGTATTNGG ATCTTTCAAA | 480 |
| CTTCNAGTCC CTGGT | 495 |

(2) INFORMATION FOR SEQ ID NO:1626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

| | |
|---|-----|
| GGCACGAGGC CAGCAGTGGC TGGAAGCCAC TGGCGTACTC TGACACCGAC GAATTTNACC | 60 |
| CAGTTGCAGG AGGCACAATG AGCCAGCATT TACCTTTGGT CGCCGCACAG CCCGGCATCT | 120 |

| | |
|--|-----|
| GGATGGCAGA AAAACTGTCA GAATTACCCT CCGCCTGGAG CGTGGCGCAT TACGTTGAGT | 180 |
| TAACCGGAGA GGTTGATTCTG CCATTACTGG CCCGCGCGGT GGTGCGCGGA CTAGCGCAAC | 240 |
| AGATACGCTG CGGATGCGTT TTAACGGAAG GATTAACGGC GAAGTCTTGG CAGTGGGTCG | 300 |
| ATGATGCGCT GNACGTTNCG AACTNGCCAG AAATTNATCG ACCTACGGAA CCAACATTTG | 360 |
| ATCCGCACGG TACTN | 375 |

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

| | |
|---|-----|
| GGCAGAGAA AGAGATGACC CCAGGGAACA TCCTGACCAG GCCGGNTTCC TGGATGGCTG | 60 |
| TNTTCAATGC CATGCCCACC ATCTGCTTCG GAATTTNAGT GCCACGTCAG CAGTGTGCCC | 120 |
| GTNTTCAACA GCATGGCAGC AGCCTGAAGT GAAGACCTGG GGTGGTAGTG GTGACAGCTG | 180 |
| CCATGGTCAT AGCCCTCGCT GTCTACATGG GGTGCAGGCA TCTTTGNGGT TCCTGACCTT | 240 |
| TGGNAGCTGC TGTGGGTCCT GACGTGGCTC CTGGTGCTAT CCCTCGGAGG TACATGGNCG | 300 |
| TGGCCGTTGC CCGAGNCTTT CAGCATCCTG AGCGTNGCTC ANCTCNT | 347 |

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

| | |
|---|-----|
| GGCAGAGGC GCCGGTAAAA TCGACCACAA AGGCGATAGT ACCGTCAGGC TGGCGAATCA | 60 |
| GGTTCGACTG CTTACATCC CCCGTTGAAC GACGCGTTN TTGCACCCAT GCGTTATCTG | 120 |
| GCGCATGCAG TTTGTTTTCA TCACGGCTGA AGGTGATGGT GTATTTAAAG TTCATCTCTT | 180 |
| TACCCGGCTC CGGCAGCTGA TCCGGCGTCC AGTAAGCGAC GATGTTATCG TTGGTTTCAT | 240 |
| CGTTGGTTGG AATTTCACC AGCTCAACGC TGCCTTTACC CCACTCCCCT TTCGGAGTCA | 300 |
| CCCATGCGGT TGGGACGGAG NATCGTAAAC GATCATCGAG ATCTTTCAAA GCGGGAGAAA | 360 |
| ATCACGACCC GNGTTGCAAC AGACCCAAAG NCTTGNGGGG TTTTNNCCAT GGGAGNAAGT | 420 |

TGTTT

425

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

| | |
|--|-----|
| GGCACGAGCT TTGCTCCCAC CCCACCCCCA ACCCACAACC CCTGCCTCTG CCCATCAGCC | 60 |
| TGGCCTTGAT GAGGAGCGGG AAGGCCTCCT GCACCCTGGA GACCGTGTGG GAAGACAAGC | 120 |
| ACAAGTATGA GGAGGCCGAG CGGCGCTTCT ACGAACACGA GGCCACACAG GCGGCCGCCT | 180 |
| CCGCCCAGCA GCTGCCAGCC GAGGGGCCAG CCATGAATGG GCCC GGCCAG GACGACCCTN | 240 |
| AGGACGCTGA TGAGGCGGAA GCCCCTNACG GCGGCAGCAG GCGTNGATCC CAGGAAGAGC | 300 |
| CAGGACAGCA GGAAGCCCCT NCAGAAAAAG NAGGAAGCGT TCCCCCAAGA GCGGGTTNGG | 360 |
| CCCCGNGGGA CCTGGCCTTN TTGGCTTTTT GGCCGAA | 397 |

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

| | |
|---|-----|
| GGCACGAGGC GGCTGTGCT NAGCCCACTG CGGGGCGGG AGGCCGGGCC ANACGCCTCA | 60 |
| CCCACAGTNA CCACACCCAC GGTGACCACG CCCTCACTAC CCGCAGAGGT GGGCTTCCCG | 120 |
| CACTCGACCG AGGTGGACGA GTCCCTGTNG GTNTCCTTTN AGCAGGTNNT GCCGCCATCC | 180 |
| GCCCCACCA GTAAAGCTGG GCTGAGCCTC CNGCTGCNTG GCCCCGGGC GCGGCGNTCG | 240 |
| GTTCCTCCAC ACGATGTGGA CCTNTGCCTG GTGTNACCCT GTNAATTTNA AGCATCGCAA | 300 |
| GGTGGTGCCA ATGGCACGNC AACCTGNITT CCCCCGNAG CTTGNAATG AANAGCANTN | 360 |
| CCCGGTTTAC AGGAACGGGG CAGGTGGGCT GGGGGCCGAG NAGACGCCAC CCACATTCGG | 420 |
| TTCAGCAATT CCCTGCCCAA CCTGTTTGAN TTGGATCCNG TTGCCCTNGN CCCGGTTGCG | 480 |
| GNANANTTAG ACGGAGACAA A | 501 |

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

| | |
|---|-----|
| GGGGCAAGAG TATNCCCTCA TGGGGNCAAA TTGGCACCCC TTTGGGTGTTGG NCTTNCAAAG | 60 |
| GGTTTCCAGG GGCCCAGGGT CCCTATTTAC TNTGGGTGTG GGGAGCANAC AGAGGCTTTG | 120 |
| GGCAAGGGGN CCATCGTGGG AGGGCCCCTT TAACCGGGGC CTNCTTTTTT ATNTNTNGGG | 180 |
| TTCAAAANTT GGGGGGGGGC TAATTTCCGG GGGT | 214 |

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

| | |
|---|-----|
| GGCAGAGNCA TACCAAGAAG ACGGTGATGA TCAAAACCAT CGAGAACACG GGATGGGGAG | 60 |
| GTCGTNAGTN AAGGCCACAC AGCAGCAGCA TGAAGTCTCC TAAAGACAGA AACCTCTGC | 120 |
| NACCAGAAAC CGTTCCTCAC CCCTGTTCTT CACTGGCTCC CTGAAGCCAG CNTTCTTCCA | 180 |
| TCCCAGGGAC ACCACACCCA GCCTTCANTC CTCCCCTNAN AGCCTCTGAA CCCCTCTNA | 240 |
| TTGGGCCATC CCTNGTGGTC CCCAACAGCG ACATAGCCCA TCCTTGNTTG GTTCACGGGG | 300 |
| CATGGTCCCG GNCACCTTTG NGGGNNCCTA GTTGTTAAGC TTTTGGGTGT TTGGGA | 356 |

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

| | |
|---|-----|
| GGCAGAGGGA ACAACTCCAT GTTTTTNTAA AGGCCTAGAG AACATATATC CAGTGCCTTT | 60 |
| CCTTTTTGCC TTTGTATTCA TCATTTTGGC AAATTACTGG AAGATGACGG TTCTGGCCAA | 120 |
| AAGGCTGGTT TTNTTTTGG GTCACATTTT CTTGCTTCTC TCGTTAGAA ATCTTGGATT | 180 |

| | |
|---|-----|
| AGATGATGGA CATGGTGAAG ATCTCAGCAA CCTCATTAC TAGAAGATCA TGTGGATTGG | 240 |
| GANTCATACA ATGGGGGAAC AAATGGAAAA GAGTACTTTT GNAAATAGTG GCTGGGNGAC | 300 |
| CACTGTGGAC CACAGANTGT TCAAGACACG TGCTGCCCNT AACTGTTTAC TN | 352 |

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

| | |
|---|-----|
| GGCACGAGCT GGCCCCGTGT TCAAGGGCGT CTGTAAGCAG TTCTCACGCT CACAGGGCCA | 60 |
| TGGCTTCATC ACCCCCGAGA ACGGGTCCGA GGACATCTTC GTACATGTTT NTGACATCGA | 120 |
| GGGGGAGTAC GTGCCANTGG AGGGCGACGA GGTGACCTAC AAGATGTGCC CTATCCCTCC | 180 |
| CAAGAACCAG AAGTTCCAGG CCGTGGAGGT GGTGCTCANT CAGCTGGCCC CCCACACTCC | 240 |
| CCACGNAGAC GTGGTTCTGG CCAGGTCGTG GGCTCCTAGG CTGAGTGGTT CACAGGCCAG | 300 |
| CTGGCCGNGG GTTGGGNGAG CCACACAGGG TGAACGGNCA GCAGCCGGCT CCATGCCCCA | 360 |
| CTGCCTNGNT GATGAGT | 377 |

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

| | |
|---|-----|
| GGCACGAGGN AGAATCTTGC CTAGAGCTTG CGGAGTCCAG CNAGGCCCTT NCTGAAGGGC | 60 |
| CCCAAACCAC CGGCCACTTC TCCCCGTCC ATCTAACCAG CTGGGCCCCCT GCGCCACCT | 120 |
| GGCCTCCACG TTCCCTCTCC TCTAACCAC ACCCCTGGCC ATGGCTAACT ACTATAAAGT | 180 |
| GCTGGGNGTG CAGGCCAGCG CTTCCCCGGA GGACATCAAG AAAGCCTACC GCAAGCTGGC | 240 |
| CCTTCGTTGG CACCCCGACA AGAACCTGA CAATAAGGAG GAGGCGGAGG AAGAAGTTCA | 300 |
| AGCTTGGTGT TTTGAGGCCT ATTAAGGTTT CTGTTNTGGA CTTCCAAGGA AACGNTTCCT | 360 |
| TGTTATGACC GTGTTGGGTT GTAAACAGTT GGGGGGTTT TTTGGCGGGG GCCAGGAANG | 420 |
| GTNTTACCAA AGGCCCTTTT GGGAAACGGG TTANAANTTT CGTAAACCTT TNNGGG | 476 |

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

| | |
|---|-----|
| TGCCTACTCT AAGCGCCTCA AGTTCAATGT GGCTGTNAAG ATCATCGACC GCAAGAAAAC | 60 |
| ACCTACTGAC TTTNTGGAGA GATTCCTTCC TCGGGAGATG GACATCCTGG CAACTNTCAA | 120 |
| CCACGGCTCC ATCATCAAGA CTTACGAGAA TCTTTGAGAA CCTCTGAACG GACGGATCTA | 180 |
| CATCATCATG GAGCTTGGCG TCCAGGGCGA CCTCCTCGAG TTCATCAAGT GCCAGGGAAG | 240 |
| CCCTGCATGA GGACGTGGCA CGCAAGATGT TCCGACAGCT CTCCTCCGNC GTTCAAGTAC | 300 |
| TGNCACGACC TGGGACATTG TTCACCGGGG ACCTTCAAGT TGCGNAGAAC CTTTTTCTTG | 360 |
| GACAAGGANT TTCAACNTCA AGTTGTCTGA CTTTGGGTTT TTCCAGGGGT TGCCTNGGGG | 420 |
| ACAGAATTGG GGGTNT | 436 |

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

| | |
|--|-----|
| CGCACTGTCA AGGAGCTGCT TGATGGAGGA GCCAACCCCC TGCAGAGGAA TGAAATGTGA | 60 |
| CACACACCCT TGGATTATNC CCGANAAGGG GAAGTNATGA AGCTTCTAAG GACTTCTGAA | 120 |
| GCCAAGTACC AAGAGAAGCA GCGGAAGTTN GAGGCTGAGG AGCGGCGCCG CTCCCCCTG | 180 |
| GAGCAGCGAC TAAAGGAGCA CATCATTTGGC CAGGAGAGCG CCATCGCCAC ANTGGGTGCT | 240 |
| GCGATCCGGA GGAAGGAGAA TGGCTGGTAC GATGGAAGGA ACACCCTCTG GTCTTTCTCTC | 300 |
| TTTCTTTGGG GATTCATTCT GGAATTAGGG AAAAACCAGA GCTGGGCCAA GCCAGACAGC | 360 |
| CAATTNTTTN GCACAAGGNT GCTTAAAAAG GGNTTTNATT CAGGTTGG | 408 |

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

| | |
|---|-----|
| ATAATGTNAC GTCAGCCGTA GAAGGCATCA ACAGAATGAC CAGAGCTCTC ATGGACTCGC | 60 |
| TTGGGCGCTGA GTGGCGCCTG AAGCTGCCCT CAATCCCCTT GGTGCCCTGTT TCAGCTCAGA | 120 |
| AGAGGTGGAA TTCCTTGCCT TCGGAGAACC ACAAAGAGAT GGCTAAAAGC AAATCCAAAG | 180 |
| AAACCACAGC TACAAAGAAC AGAGTGCCTT CTGCTGGGGA TGTGGAGAAA GCCAGAGTTC | 240 |
| TGAAGGAAGG AAGGCAATGA GCTTGTAAG AAGGGAAACC ATAAGAAAGC TATTGAGGAA | 300 |
| GTACAGTGG AAGCCTCTTG TGTAGTTAAC CTGGGATTCT TGCCACGTTA CAGGCAACAG | 360 |
| AGGCACTTTG TTATTTTGGT CCCTGAAGGC AGTAACACAG AAGNCAGTGA NGGACTGCAC | 420 |
| ANAGGCCCTG AAGGTNGGNT TGGAAAGACC TTTAAGGG | 458 |

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

| | |
|---|-----|
| CCCGAGGNAT TATTCGATAA AGATAAGCTT ACATTATGAA GAGCAGCATA TTACAGCCGT | 60 |
| ATGGTCTACT TGCNCAGTAA AATTTGAAGA GCATTGGAAG CCTGTTGATG TAGAGGTCGA | 120 |
| GTTTAGATGC AAGTTCCAAG GAGCGAAAGG TGGATGGGTA GGTTATATAG GGATATAGCA | 180 |
| CAGAGATATA TAGCAAAGAG ATACTTTTGA GCCAATGTTT GTGGAAGCGG TATTCGCAAT | 240 |
| ATTTTAAGTA GCTCGTTACA GTCCGGTGCG TTTTGGTTT TTTGNAAATG CCNNTTCCA | 300 |
| AAGCCTTTTG GGTTTTCCAA AGGNTTTTNG GT | 332 |

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

| | |
|---|----|
| CAACCCTTGG ACGTNAGCNC TGAAGGCTAC AACANCTGGN TCTTCATGTC CACCCACTTC | 60 |
|---|----|

| | |
|---|-----|
| TGGAATGAAA ACCCACAGGG CGTGTGGTAC CCTGGGCCTA GAGAACAAGG GCTTACTATT | 120 |
| TNAACACGGG GACGTTGTAC CGCTAACACG CTGCTGCTCC TATGGGAACG GCCGAGGACA | 180 |
| TGANAGCGCC GGCCTTACAG GCCCCCAGG TGAACCAGCA NCGGTNNTTT GCAACGGGAC | 240 |
| ACAGAGGGGC TTNTCCCAGG | 260 |

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

| | |
|--|-----|
| TCCTCACCAA TMTAACNTT NTCCANTTGC TGCAACACCG TGCCCCGGTA ACCAGAGCAC | 60 |
| CGCCCCACC TGAGCCCTAA GGNTGAAGTA GAGCCCCAGC NACAACCAGA GCCCACACCA | 120 |
| NTTAAGGGAG GAAATAAAGC CACCACCGNC ACCACTGCTT CCTNACCCCG NTAACCTCCTC | 180 |
| CTCCTAAGAT TGGTGTCTGT GAGCCCCGGA AGCTGACTGT GGGCATCANT GGTTTTGGAA | 240 |
| CGCATCGNTC GCCTGGTTCC TGNGAGGTTG CNTGGNGGAA GGGTGTTAAG GTGGTGGTTG | 300 |
| TGAAATGATT CCTTTCATTG GACCCGATT ACNGGTGTAC NGTTTAAGTT TGGTTTCCAC | 360 |
| CCAGGGCCGT TACAAGGGAG TTTGGGATTT CAGGATTGGN CAATTGGTTN TGGGCAACCT | 420 |
| GGGTTTTTTT TTTCCNTGN AANGG | 445 |

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

| | |
|---|-----|
| GGCAGAGTGT AAAACCAGAA AATATANTAA TAAAGGATGT CCTGAAATTA GGGGACTTTG | 60 |
| GCTCCTGCCG GAGTGTCTAT TCCAAGCAGC CGTACACGGG AATACATCTC CACCCGCTGG | 120 |
| TACCGGGCCC CGAGTGTCTC CTTACTGAAT GGGTTCTACA CGTACAAGAT GGACCTGTGG | 180 |
| AGCGCCGGCT GTGTGTTCTA CGAGATCGCC AGTNTGCAGC CCCTCTTTCC TGGAGTNAAA | 240 |
| TGAAACTGGA CCAAATCTGC AAAAATCCAC GATGTNCATC GGCACACCCG NTTCAGAAGA | 300 |
| TCCTGCACCA AGTTCCAAAC AGTTCGAGGA GCTATGGAAT TTTGGATTTT TCCTTTTGAA | 360 |

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

| | |
|---|-----|
| GGCACGAGCC AGTTTTCTGT TGCCCTTACC AATTCTGGAG CTGTTTATAC CTGGGGCAAA | 60 |
| GGCGATTATC ACAGGTTGGG CCATGGATCA GATGACCATG TTCGAAGGCC TCGGCAGGTC | 120 |
| CAAGGGTTGC AGGGGAAGAA AGTNATCGCC ATCGCCAATG GCTCCCTGCA CTGTGTGTGN | 180 |
| TGCACAGAGG ATGGTGNGGT TTATACATGG GCGACAATG AATGAGGGAC AANTGGGAGG | 240 |
| ACGGAACCAC CATTGCCATA CAGAAGGCCT CGGTTGGTAG CTGCCCTTNC AGGGTNAAGA | 300 |
| AAGGTNAAAC CGTGTGGNCC TGTGGGTTCA GCACATNACC CTTTCG | 345 |

(2) INFORMATION FOR SEQ ID NO:1660:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

| | |
|---|-----|
| ANGCAACGGA CAGGCCCCTG GAACGAAAGG CATNCCCGNG CCAAGGTGGC TCCCCTAGAG | 60 |
| GTNACAAGTC TTAGGCATTN CGGTCGGGAA ACGCTACCTG CCTGGAGNTC ACT | 113 |

(2) INFORMATION FOR SEQ ID NO:1661:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

| | |
|---|-----|
| CCCNGNGGAT CCCCCGGCCC TGCAGGANTT CGGCANAGTT CTGGTTGGTA CAAACCCACG | 60 |
| GTTTTTGAGG CACCACTGTT TAATGCTAGG NTTCGAAAGA CCTNGCTNGC ATAATGGNCT | 120 |
| TAAAATTGGG CCTT | 134 |

(2) INFORMATION FOR SEQ ID NO:1662:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

| | |
|---|-----|
| GGAAGCCCCA GCGCATTNCT TTCNTCCTG CTA CTCTGGT TCCCAGATAT AACTGGNGAA | 60 |
| ATAGTGATGA CGCATNGCA GTCACCCTGT CTGTTTCGCT AGGTGAAAGA GTCACCCTCT | 120 |
| CCTGCGGGGC CAGTGAAGAG TATTAGCACT AACTTAGCCT GGTACCAGCA GGAAACCTGG | 180 |
| CCAGGCTCCC CGANCTCCTG CATCTATGCT GCATCCACCA GGGNNCACTG GNCATCCCAG | 240 |
| CCAGGTTNCA GTGGCAGTGG GTTTTGGGGA CAANTTGCAC TCTTCACCAG CAGCAGCCTG | 300 |
| CAGTTTNGAA GNTTTGGGGG GTCTNATTAC TGT | 333 |

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

| | |
|---|-----|
| TCCCAGATCC AGGANTTTAA GGGAGGGTTT NAACATGNTT AACCAGTNAC CTTGATGGTT | 60 |
| TCATTAANAA GGGGGGACCT GGGACGGAAA ATGTTGGCTT CGTNGGGGT AAGAACCCCC | 120 |
| | 120 |

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

| | |
|---|-----|
| CATGGGGTTT TNCCTTTGGC CACATATATG CGAATTTTTT ANGAGAAGGT GATATTTTGG | 60 |
| ACATCANGGG AANTGGTTAC TTTCCAAAA GGGTTTGCCC CACANTTTTT ACC | 113 |

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

| | |
|---|-----|
| GGCANAGCCG NCGGTTCCNA GGATGCCAGC GCCATGCTGA GGCGCTTCCT GGGCCGTGAA | 60 |
| CCCCAAGCAG GACGCCTTCC TCCTGAGCAA GGGGCTGCAG GTCGGGGGCT GCAAGCCGNA | 120 |
| GNCCGCAGTN TGNCTGAGGC CTGGTNACTG CGAACTGCCC AGTNTGGCCT GCGCTCCCCG | 180 |
| CGCCCTGGTG CCTTAGCCCC CGGNACAGGT ATGGGGTNAG GCTNTGGGCA CATGNCTGGA | 240 |
| GAAGTGGCA | 249 |

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

| | |
|---|-----|
| AAGAGGCCAA NGTACAGTGG TNGGTGGATA ACGACCTGCA NTCGGGNAAC TCCAAGGAGT | 60 |
| GTCACAGGCA GACACAAGCC AGCACCNACA GACTCAGTAA CA | 102 |

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

| | |
|---|-----|
| NGGGGGTNGG TGACCCNCGG CTGCTGCAGG GAATCTGCNG ANCTTGCAGN CCATGGGGGC | 60 |
| GCACCTGGTC CGGCGCTACC TGGGCGAATG CCTCGGTGGA GCCCGACCCC CTGCAGATGC | 120 |
| CAACCTTCCC GTTCAGACTT ACGGCTTCCC CGAACGGCAA GGAGCGCGAG ATGGTGGCCA | 180 |
| CACAGGCAGG AGGATGATGG ACGTGCCATT NAGGGCTCCA GCTGGGGGGA CTAATTGCGG | 240 |
| CCCACCACCT TCATTCCGGN TGCTTCAAGT GGCAAGTTTT GGACAGTTTT TCCCCAAATT | 300 |
| TNCTTGGGCC TTGNAAAACA NGGAGCNGGG CAGGA | 335 |

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

| | |
|---|-----|
| GGCAGAGNCA CAGATGTCTC AGACGGCCTG TCCATCCGCC TCGGGNCAGC CCTGAAAATC | 60 |
| TACGAGCACC ACATCAAGGT GCTTCAGCAA GGCCACTTTG AAGGATGAAT GACCCCNATG | 120 |
| GCTTCTTAAG GCTGAGCGCC CAGCCTGCAC CCCTGCCCCA GCCCATTCCG GCCCCATCT | 180 |
| NCACCCAAGA ATCCCCCAGA GTCCAGGAGC TGGACGNGGA CACCCTNCAG CCCTCATGAA | 240 |
| CAGAATTCCA AGGAGAGGGC ACCCTCTTGT GCCTTATCTT TGGCCCTTGT GTCTGTTTCA | 300 |
| CACACATNTG CTTCCCTCAG CACGTCGGTG TGGGGAGGGG ATTGCTTCNT AAAACCCAG | 360 |
| TGGNTGNACC TTCCCCACCC ATTCCAGGAC ATTTAGGAAA AAAAAATGNA ATTTGGGGGG | 420 |
| TTTANTTTC CCACTTCTTT T | 441 |

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

| | |
|--|-----|
| GGCAGAGGCG GGTGCAGGTC CAGCCCTTGG AGCTGCCCAT GGTCAACCACC ATCCAGGTGA | 60 |
| TGGTGTCCAG CCAGTTGAGT GGCCGGAGGT GTTGGTCACT GGATTTCCCTG CCAGCCTCAG | 120 |
| GCTNAGCTGN AGGTGGAAGC TGCTGGNACA AGCTCAGAGA ATCTNCTTTG GNCAAGACTA | 180 |
| GGNAACGGTG GTNGNCGGAT GTGGNACGTT CCGGGAAGCT AACTGCCAGG GAAGTNTTCA | 240 |
| TGCTGGGGTT TGCTAGGGAA TGGAGTGGGC TCANCGTCTG TNCCCAAATC GGCCAGTTTC | 300 |
| ACAGTGCCCA CTGGGGTGGG GCAGCAATTC CCTCTGAAGA GTTTTNTCCG TATGTGAAAT | 360 |
| GGGGAGTTCC AAAAGGNTGA GTTCAGTTGN AACCATTTCC CGTTCGGTNA NTGGTG | 416 |

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

| | |
|---|-----|
| NAGCCGCATC CTCAGGGCAG GGGGNAAAAT CCTAACTTTC AACCAGGTGG CCCTGGNACT | 60 |
| CCCCTGAAGG CCTGTGGCAC TGTCCTGTTC TGCCGGTGCT CGCGAAGGCG CGCAAAGCCT | 120 |
| GTGANCGGGC ATTTGGGNNA AGGCCCCCAG GAAGCCCCGG CACAGCCACA CCAAACCTTA | 180 |
| NCGTCNG | 187 |

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

| | |
|--|-----|
| GGCAGAGTAT GATGATGTNA AGAGTATGGA GACCAAGGTT CAGTTCTTAA AGAATTTAAA | 60 |
| CCTGGGAAGG AGCCATGATC TGGTCTATTG ACATGGATGA CTTCACTGGC AAATCCTGCA | 120 |
| ACCAGGGANC CTTACCCTCT TGTCCAAGCA GTCAAGAGAA GCCTTGGCTC CCTGTGAAAG | 180 |
| GATTAACTTA CAGAGAAGCA GGCAAGATGA CCTTGCTGCC TGGGGCCTGC TCTCTNCCCA | 240 |
| GGNAATTCTN CATGTGGGAT TCCCCTTGGC CAGGCCGGCC TTTGGGATCT TCTCTNCCA | 300 |
| AGCCTTTTCCT GGAATTCCTC TTAGATTCAT AGATTGGGAC CGGTTTTGGT TTTNCTGNCA | 360 |
| GTGTTGGANT NGTTGNCCTG GAGTTACATT AAAAAAATT CATTTTGNTC CAAAAAATAA | 420 |
| AAAAAATAA CGGGGGGGGG CCCGTAACCA ANTGGGCC | 458 |

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

| | |
|---|-----|
| GGCANAGGNA CAAGCCCAGC AACACCAAGG TGGNACAAGA AAGTTGAGCC CAAATNTTGT | 60 |
| GAACAAACT CACACATGCC CACCGTGCCC CAGCACCTGA ANCTCCTGGG GGGAACCGTG | 120 |
| NAGTTTTCTT GTTCCCCCA AAACCAAGG ACACCCTCAT GAATCTCNNG GNACCCCTGA | 180 |
| GGTCACATGC NTGGTGGTGG ACGTGAGCCA GATGGACCCT GAGGTCAAGT TCAACTGGTA | 240 |
| CGTGGNACGG CGTGGTAGGT GCATTAATGC CAAGTACAAA GNCGCGGNGA GGGGGNGTNT | 300 |

300

(2) INFORMATION FOR SEQ ID NO:1673:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

| | |
|--|-----|
| GGCAGAGGTT CGCTGCACCG ACCGNCCCCTC AAGGACCTGC TCTNAGGTTC AAAAGCAAAC | 60 |
| CTAACGTGNC AACTGACCG GCCTGAAAAA TGCCTCAGGT GTNACCTTCA CCTGGAACGC | 120 |
| CCTTCAAGTG GGAAAGAGCG CTGTTCAAGG ACCACCTGAA GNCNTGAACC TCTNTGNGCT | 180 |
| GCTAACAGCN TGTGCCAGTG TNCCTGCCGG GGCTGTGCCG NAGCCATGGG AACCATGGGA | 240 |
| AAGACCTTGN ANTTGCACTG CTGCCTTACC CCGAANTCCA AGAACCCCGN TAAACCGNCA | 300 |
| CCCTTTTCAA AATTCCGGAA ACACATTTCC GGGCCCGAGG TTCCAACCTG TTGNGCGTCG | 360 |
| NCGTTNGGAG GGAGTT | 376 |

(2) INFORMATION FOR SEQ ID NO:1674:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

| | |
|---|-----|
| GGCANGAGCC CTGGCGCACA CGNCGNCGTN AAGGGTGAGC ATCCCGCTGT CGATCCTGGA | 60 |
| GGCCCCGCAC CGGTACCACA TCCACCGGCG NAAAGAGCTT TGACGCCTCT NAACACACTG | 120 |
| GGCCCTGCCC CGGCACTGCC TGCTGGGCTG GGAACATTTT TCCTCCGAAG TNTGAGAAAA | 180 |
| GCTCAGCCCC CAGGAACCTG GACCTCTGGT CTNCTGTTTT CCGCTGAGGG CCCAGCAACA | 240 |
| GAAAGNTGTC CGGCAACANC AAGCCTTTTT AAACCGGGCT TNAACAATTG ANATTGTTNC | 300 |
| CCCCGAACCC GACTTGTTAA TT | 322 |

(2) INFORMATION FOR SEQ ID NO:1675:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

| | |
|---|-----|
| GGCAGAGCNA AGGTGGACAA GAAAGTTAAG CCCAAATNTT GTAACAAAAC TAACACATGC | 60 |
| CCACCGTGGC CAGCACCTNA AACTCCTGGG GGGAACCGTA AGTATTCCTC TTCCCCC | 120 |
| AACCCAAGGG ACACCCTGCA TGAATCTCCC GGNACCCCTG AAGAGTTCAC ATGCGNGGTG | 180 |
| GTGGGACGTG AAGCCACGGT GTACCCTGTG GTCAAGTTCC AACTNGGTNA CGTGGGACGG | 240 |
| CGTGGTGGTG CNTNAAT | 257 |

(2) INFORMATION FOR SEQ ID NO:1676:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

| | |
|---|-----|
| GGCANAGTGC ATCACCAAGT TGGAGACCTT TATCCAGGAG CACCTGAGGG TCATTGGGGC | 60 |
| TGTGGGGATC GGCATTGCCT GTNTGCAGTN CTTTGGCATG ATCTTCACGT GNCTGCCTGT | 120 |
| ACGGAAGTCT CAAGCTGGAG CACTACTGAA CCCTGCCTTG GGCCTTNGCT GCTGCTGCAC | 180 |
| CCAACTACTG AGCTGTAGAA CCACTGTAGT NACCAGGNGG TCTGGGNCTT CCCTGAATNG | 240 |
| | 240 |

(2) INFORMATION FOR SEQ ID NO:1677:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

| | |
|---|-----|
| CCTAGCACCT NGTGGATCCC CCGGGCCTGC AGGANTTCGG CAGAGNATTT GGTGACCTTA | 60 |
| AGTNTACAGA NCACTGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA | 120 |
| CAATTACAGG ACTTGGTGGG GAAACTTAAA GATGCTTCGG AAAAGCCTGG NAAAGAGCAA | 180 |
| CTNCANTTGT AAACCTGGGG NAAGTTAAAN NATCCGCCCG AGTGCCAGAG GGAAAACCAG | 240 |
| AAAGNCCTTG CCTTCAGCTG GAACCACCGT TTGTGCGNAG CTGGGATGTN CCTTTTCAGT | 300 |
| AGGAAAAGAA TTTTCCCTTT TGANTTTATA ACCATTCATC AATTTTGAAC ATTTNAAAAA | 360 |

GNGTGAAAAG GGTTAAGAGG GGAAAGATTA TTGCCAGTT TTTTGNATTC GTTTTAGTGG 420
TAAAATGTNC CATTN 435

(2) INFORMATION FOR SEQ ID NO:1678:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

GGCACAGTGA AATACATTTT GGAAGANAGT TTTNATCTT AGAGATTGGT GAACAAGTGT 60
AAGGGTGTNA GAAACTCACA GGAATACAAA TTTNCCTGTA TGTTTTGTGG GTTTTTTTTTT 120
TNCCCCNTCA AGATGTTTNC TATTTC 146

(2) INFORMATION FOR SEQ ID NO:1679:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

GGCAGAGGTG CCTGATACGA CTACCAGGCA GCCGACGACA CANAGATCTC CTTTAACCCC 60
GAGAACCTCA TCACGGGCAT CGAGGTGATC GACGAAGGCT GGTGGCGTGG CTATGGGCCG 120
GATGGCATT TGGCATGTNC CCTGCCAACT ACGTGGAGCT CATTGAGTGA AGGCTGAAGG 180
GCACATCTTG CCCTTGCCCC TCTNCAGACA TGGCTTCCTT ATTGCTGGAA GAGGAGGCCT 240
GGGAAGTTGA CATTACGAC TCTTCAGGA ATAGGACCCC CANTGAAGGA TGAGGCCTCA 300
GGGCTCCCTC CGGNTTTGGN AGATTCAGCC TGTNAACCC AAATGCAGCA ATTGGCCTGG 360
TGATTTCCCA NAATTCNTT CCTGGNAACC CCCGAACCTT TCCCCAAAAA TTTTGGTTTTT 420
NGCCCCTTAA NAGGTTTTTTT GGGCCCAAGC 450

(2) INFORMATION FOR SEQ ID NO:1680:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

| | |
|---|-----|
| ANTCTGGGCC ACGGGANAGA CAAGCTGGAA CCTGCATTG NAACCCTNGC TTCAGNGAAT | 60 |
| ACCACCATTG TTTGCAACTG CATTGGACGG CAGCAACTGG GGGGCAAGTA ACAACGGGNA | 120 |
| GATTNACCNT TGNTTGCCT CCCANGGTTT AAAGGTC | 157 |

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

| | |
|---|-----|
| GGCAGGAGCA CCAGCNACTC TNCCAGCTCA AGGNACCCAC CTGCNAGTAC AGGGCAGCCC | 60 |
| AATCTGGTCC CTCTNAACGG CCAGGACCTC CGCAGAGGGC CCTGCTGGCA CGAGGCACTA | 120 |
| AGTCTCAGGG GCCAGCCAAG CCCCCACCCC CAAGGAAGCC ACTGCNTGCN GACCCCCAGG | 180 |
| GCCGGTGCCC ATCGGGTGAC CTGCCCCGCC CAGGGGCTGG AATCCCGCCC CTAGTGGTAC | 240 |
| CCTCCANACC AGCGTCACCG NCTCCAACAG TGTTCCTCGC TCTTACCTCT GAACCTCTTC | 300 |
| CGGGAGGTTT CCGGTTGCCT TCCAAAGCCG GGACTTTAGG GGTTTCAAAG AAGGCGGGGT | 360 |
| GTTGCCCTTT TGGGNAGTCC CCCTAACCAT TGANTTAAAG GGGGNCAAAA AANTTGGGGG | 420 |
| TTGTTTTNAA GATTCGGGG AAACGCCAAG GGGTTTTT | 458 |

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

| | |
|---|-----|
| GGCAGGAGCA CAGGGGAGCT GCTGGGCGAG TACAAGGGCC ATAAGAACCA GGAATACAAG | 60 |
| CTGGACTGCT GCCTGANCAA GCNTAACACA CATGTGGTCA GCTGTTCTAA GGACGGGAAG | 120 |
| GTGTTCTTCT GGGACCTGGT GGAGGGTGCG CTGGCTCTGG CCCTGCCTGT GGGTTCCGGT | 180 |
| GTGGTGCAGT CGCTGGCCTA CCACCCAACA NAGCCCTGCC TGCTGACCGC CATGGGAAGG | 240 |
| CAGCGTCCAG TGCTGGCGAG NGGAGGCCTA TGAAGGCAGA GGATGGAGCA GGCTGAAGCC | 300 |
| AAGGGACCCA CCAACAGGAC CAAGGACCGA GACACAGACA TGGAAGGACT TCAGTTACCN | 360 |

CTTATTTTTA GAGACGTAGT TGACCCAAAA ATTAGGGGNG GGGGTTNGGT TTNCAAATT 420
NATTAATTAG AGGGGGGGGT AAGACCTTCC TGGGNCCCCA AA 462

(2) INFORMATION FOR SEQ ID NO:1683:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

GGCACGAGGA ATCCTGACAG GGACAGGCAG GCACAAGGCA CAAACCTGG GAAATCTNAG 60
CCACAGAGAA TGCTGTTTTG CTGCGGCAAA GCGCCTCGT NAGTCCTGGG GCCTGTTTGC 120
TCTTGCCCCG GNGCCAGGG CCAGTTTCTG GCACCCCTAG GAGAATGAAT AGGGCTCAGT 180
GTGGTGGCTC CGCTGAAGCT TCAGAGCCCC CTTTNTGCCT GCCTGGGAGT GNGCCGTTAA 240
GGAGTGCAGAA CCAAGGACCT GCCGGTGNGG TGGGCTGTCC CTGCAGGAGC TCTTTNAGTT 300
TGCACTGGGA GGGGCANGTT CANCCCCAGC CCCATGGTTC CCTGTTCTTG NAACAACCCC 360
GAGTGGTTTT TCCTTGNCCT CCAGGCTTTN GGTTTAAGGT TGGGCTTCAA AACCATTGGG 420
GAATTTCAAT TTTNGCCCTT NCCCGGCTTA AGGTTTTTTA AACTCCTTTT GGGATNCCTT 480
AAAGGTTGGG TT 492

(2) INFORMATION FOR SEQ ID NO:1684:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

CAGCACANCC TGTGGCAGGC CCGTAAGTTT TCCTNTTCCC CGCAAAACCA AAGGACACCC 60
TCATAATCTC CCGGGACCCT TAAGGTAACG TNANNGGTGG TGGACGTAAG CCAGAAAAAC 120
CCCAAGGTNC AGTTCAACTG GTCACGTGGN CGGCGT 156

(2) INFORMATION FOR SEQ ID NO:1685:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

GGCANAGGGC CAAGGNGAAG NTCCCGCGCT ACTACANGAA CATCGGNCTG GGCTTCAA 58

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

GGCAGGAGCC CAAATTCAAC ACATTCCACT CATAAGTGTT CTGTACTCTT CAAAAATATT 60
CATTAAAGTC AAAGAGAGGC TGAGGAACTA TTTCAAATC AGGAGACTTG GAAACTAAAT 120
GCAGTGTGTG ATCTTGATT GGATTTTAGA TTAGTAGGAA ACATGACTGT AAAAAAGTGN 180
CTGAAAAATA NCTGGTATTA TTGGGACATC AATGTTAAAT TTCATGAATT TAATATATAT 240
TGGTTATGTA AGTTAAATGT NCTTGTNCTG AGCTGNAAAT TAAGTTTGAN CCTATTAGGG 300
GGGCAAAGCT GTCTAAANCT CCCCAAATAG TTCCTGCAAA ANGTTTTTCC AGTGGGGGTN 360
ACCACACATT GGGAGAGGNG 380

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

GACGCCTTCA GGCCCGACGT GACTTCATCC TCTTTTCAGA GGCCAGTCAA CGACATGAAC 60
ATCGCAAGCG GCTGCCCCCT CTTCTGCCCC GTNTCCAAGA TGGAGGCAAA GAATTCCTAC 120
GTGCGGGACG ATGCCATCTT CATCAAGGCC ATTN TGACAGGGCT CTAAGTGCTC 180
CCTACTGGTG TTTGGGGGTT GGGGCGAGCC AGGCACAGCC GGCTCACGGA GGGGCCACCA 240
CGCTGGGCCA GGGTCTCACT GTACAAGTGG GCAGGGGCG CGCTTGGGCG CTTGGGAAGG 300
GTNTCGGCCT GCAGCCAAGT TCACTGTCCA CGGGGGGAAG GAGCCACCAG CCAGTTCCTC 360
AGATTTTACA GACTNCGGAG GGGTTTNGGC AGACGGTTTT AGNCAAGGGG TTTTGTGGCA 420
TTNGCCGAGG GTTTTTCGGG GTGNTTCCA G 451

(2) INFORMATION FOR SEQ ID NO:1688:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

| | |
|--|-----|
| TTNTTTCCTC ACCNTCCACC AAGGCCCAT NGNTTTTCCG CCTGGGGCCC TGTTTCCAGA | 60 |
| AGCACCTCCA ANAGTGACAG GGCCCTGGG CTGCTTGGTC AAGGACTACT TCCCCGGAAC | 120 |
| CGNTNACGTT TCGTGGAAC TAAGGCGATC TGAACCAAAG GTNTGCACAT TTNCGGGTTG | 180 |
| TCCTANAGTA CT | 192 |

(2) INFORMATION FOR SEQ ID NO:1689:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

| | |
|---|-----|
| GGNAGAAAGG NGCGCACGCC CNATGGCCAG TACATCTNCA GGCTGGAGCC GAACGTGGAG | 60 |
| GAACCTNGCC CGCTTCCTTA ACCTGCCTGC CCGAAAGCCC CTNACCTACC AAACGNANNC | 120 |
| AGCTCATCGC CCGNAAAAAT CCGAGGTGGA GNAAGATGCG GCGGGCGGAG GTTTCTCCCC | 180 |
| GGGNTAGAGG AACAGCCCCC AGGTGGGATG GGAAGCCCCC CAGGGCTCGA AGAGGGTNTG | 240 |
| CTTGGGNGGG GCATTGGGGG AGAAAGGGGG TGCACCGACC TNCCCCACGC AACCTTGNGG | 300 |
| CANCGGTTGG G | 311 |

(2) INFORMATION FOR SEQ ID NO:1690:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

| | |
|---|-----|
| CAGCCCCGAN ACCACAGGT NTATACCCTG CCCCCATCCG GGAATGACCT GACCAAGANC | 60 |
| CAGGTNAGCT TGACCTGCTT GGTCAAAGGT TTCTNTCCNA NCAACATCGC CGTGGAAGTG | 120 |

| | |
|---|-----|
| GGAAGANCAA TGGGCCAGCC GGAGANCAAC TACAAGACCA CGCTTCCGGT GCCTGGANTC | 180 |
| CGAACGGCTN CTTCTTCCTN TNACAGCAAG CTNCACCGTG GGACAAGAGC AGGTGGGCAG | 240 |
| CAGGGGNAAC GTTTTCTAAA TGNTTCCGTG AATGGCATGA GGGTNTTTTG CACAACCAAT | 300 |
| TACAAGGCNG AAGAAGCCTN T | 321 |

(2) INFORMATION FOR SEQ ID NO:1691:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

| | |
|---|-----|
| GGCAGGAGCA AGATCACGTC TCCCGTGCTC ATNATCCACG GCACGGAGGA CGAGGTGATC | 60 |
| GANTTCTCGC ACNGGNTGGC GCTCTACGAG NTCGNCCCCA AGGCGGTGGA GCCCTGTGNG | 120 |
| GTGGAGNGCG CCGGGCACAA CGACATCNAG CTCTACAGCC AGTACCTGGA GCGCCTGNTT | 180 |
| CGCTTTNATC TTCCCAGGAG CTNGCCCAGC CAGCGCCGC | 219 |

(2) INFORMATION FOR SEQ ID NO:1692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

| | |
|---|-----|
| TCCCCGGCNG CCCCTACTGG AAAGTAAGGA GCCCCTCTGC NTGGCCAGCC GCCCGTCCG | 60 |
| GAAGGNCGGT GGGGGGGTCA GCCCCNCCC GNCCAGCNGC CCNATCTGGA AGGTNAGGGG | 120 |
| CACTTNTNCC GGGCCGCCCC TACTGGNAAA GTGAAGGAGC CCTTNTGCCC GGCCAGGACC | 180 |
| CCGTTTGGA GGTGTGCCCA GCGGNTCATT GGGGATGGGG CATGATGACA ATGGCGGTTT | 240 |
| TTGGAATAGA AAGNGGGGAA GGGTGGGGAA AAAATTNAGG AATNGGGTGG TTTNTTGTT | 300 |
| TTTTTTGATA GAAGTAGACN TGGGA | 325 |

(2) INFORMATION FOR SEQ ID NO:1693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

| | |
|--|-----|
| ACCCCAAATG TCCTCATCAT CCCGTAAAN CTGAGGTACT TCGTAAAGGA TGTCTNNGC | 60 |
| TGTTTCTGTT TAAACCCTGG GCGCCTTACC AAAGGGCAGG TGGGAAGGNA CCTTCGCCCCG | 120 |
| ANTNTACCTT AGGAAGGCCG GCAGCGGACG GGNGCAGAAA GGCAGAGCCC ATGCATTGCT | 180 |
| GTGCAGGTCG TNAGGTATCT GAGGGCTTCT TTTNCTCTGC TGTTCTCTGC TGTTTGGGNN | 240 |
| CCTTAAAAGT NTTTAGNCCA AGAG | 264 |

(2) INFORMATION FOR SEQ ID NO:1694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

| | |
|---|-----|
| GCCTGTTGGA GGAGGAGAGA GCTTTNTGGC ATGANCCACA GTTCTTGAT GGNGGGCATC | 60 |
| AACCTTTGGT GAGGGTTNTN TTGGGCCTGA AATTGTTGGC CATGGTGGGT GGGTTTAAGG | 120 |
| TGGCTNTGCT GATAAGGGCC TCCGTTTCTG GGTAAAGTGA NAAGAGAAAA AAGGAGTTAT | 180 |
| TGAAGTNGAC GTTGATAATA GGTTTAANGT GAATCATGAA TGNAGGAATT GGAGNATTTG | 240 |
| TGGTTGGAAA AGGGGAAGGT TTTTNCGGTA ATG | 273 |

(2) INFORMATION FOR SEQ ID NO:1695:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

| | |
|---|-----|
| ANACTACGTG GGCAGCCCCA TCACCTGCAC CTGCTTCACC CGGGATGGGC AGTGCACCCT | 60 |
| GGTGTCCAGC CTGGACTCCA CATTGCGGCT CCTGGACAAA GACACAGGGG AGCTGCTGGG | 120 |
| CGAGTACAAG GGCCATAAGA ACCAGGAATA CAAGCTGGAC TGCTGCCTGG ACCNAGCNTG | 180 |
| ACACACATGT GGTCAGCTGT TCTAAGGACG GGAAGGTGTT CTTCTGGGAC CTGGTGGAGG | 240 |
| GTGCGCTGGC TTCTGGNCCT GNCTGTGGGT TTCCGGTGTG GNTGCAATNG NTGGAC | 296 |

(2) INFORMATION FOR SEQ ID NO:1696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

| | |
|---|-----|
| TCCCGGGGGN CAAGGNAGGN CAGTTCACG CGAAACCGNA NGAACCAGGA AGGTCACGCT | 60 |
| GGAAATGCTC TTTCTAGCC GGACTACGTG GGTGTACTCC ATCAACAACG TTCTCATGTN | 120 |
| TCTTTCAGGA AAGACCCCCC ACCTGTATTC TCATAGCATC CTTGGCCTGC TGGAACGGAA | 180 |
| AGAGACCAGT GCAGGAAACC CCATCGCTCA CATTAGCCCC CACCGCCTAC TGGCAAGGAA | 240 |
| GAACATGGTT TCCACCAAGA TCCAGGACAC CAAAGGCTGC CGGGCGTGCT TGTGTGGCGG | 300 |
| AGGGTGCGAG TTCTNGGGGN CCGTTNCTGT NCGGTGCATT TGAGACGTCC GTTGTCTGT | 360 |
| TNAGTGGTAC CAGCCATGAA CAATTCTTGT T | 391 |

(2) INFORMATION FOR SEQ ID NO:1697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

| | |
|--|-----|
| AAGCCACCT TTTTNGCTGT TCGGGTCCNT GACTCCATAG AANCGGTAGG TGCCGCAGGA | 60 |
| TTAATGGNCC TGNTCCAGAA TCTTGTTGCT ACCGGCAATT AAC | 103 |

(2) INFORMATION FOR SEQ ID NO:1698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

| | |
|---|-----|
| GGCAGAGNCA AGGGCTCTTT NCCCGTGCCC CTGTACGATT ACCAGGCAGC CNACGACACA | 60 |
| AAGATCTCCT TTAACCCCGA GAACCTCATC ACGGGCATCG AGGTGATCGA NGAGGCTGGA | 120 |
| ACACGTGGNT ATGGGCCGGA TGGCATTATT GGNATGTTCC CTGCCAACTA CGTGGATGCT | 180 |
| CATTNANTGA GGCTGAAGGG CACATNTTGC CCTTCCCCTC TAANACATGG TTTCCTTATT | 240 |

GCTGGAAGAG GAGGCCTGGG AAGTTGACAT TTCAGCACTC TTCCAGGAAT AGGNCCCCCA 300
GGAAGGTTNA GGNCTCAGGG GTTCCCNCCG GGT'TTGNAAG 340

(2) INFORMATION FOR SEQ ID NO:1699:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

GGCAGGAGCC AGGATCACGC CATTNCACTC CAGCCTGGGT GATTNANTNA GACTCTGTTT 60
CAAAAAAAAA AAAAAAAAAA CC 82

(2) INFORMATION FOR SEQ ID NO:1700:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

ANAGNCAACA GTTCCNAGTT NAGTGCTCAC CGGCGCATCC AACTGGGGA GAGCCCATAC 60
AAGTNTGCAG TGTGTGAAAA AATCTTCAAC AATAGCTCCC ACTTNAGTGC CCACCGAAAA 120
ACCCACACTG GTGAAAAGCC TTANAGGTGT TCTNACTGTG AAGAGAAGGC TTCACTTAGA 180
ANCTCTGNCC T 191

(2) INFORMATION FOR SEQ ID NO:1701:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

GGCAGAGCAC GCGTGGNTGG TATNTGTTTG TGGCTGCTCC CATTCCTATA ACCTCCGAGA 60
CCTTCACTCC TAGGAATGTC CCAAGGCCAA TTCCCTTGGC AGCAATGAGA AGAAATGCCC 120
TTTTCCAAAT AGCGACTTCT GCAAAACCCG CTGTTGTTTG TGGGTGAGCA CTGCAGTNCC 180
CACCGCATGC CACAGCCAGC CTCCCTCCTG GCTCCTCTGC CACGGTGGCC TTCCCCAGCC 240

| | |
|--|-----|
| CTCACCCAGG CCCCGACTTT CCTCTNANAG GTTTCAGTT TCCTGGGGGC CTNGGAACTT | 300 |
| TTCCTGAGTT CCTTTCNAA NCCAACAGGT CCAG | 334 |

(2) INFORMATION FOR SEQ ID NO:1702:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

| | |
|---|-----|
| GGCAGAGCGG TGACAGCGNC TCCAGGGCCG AAGCCGCNGG GCNCCACTCG GGGGCTGNGN | 60 |
| CTGCGCGTTG GNAGACCGTG CTCCTNAGTC TCGGGTTCCC GANTNATCAG CNGCTGNTCC | 120 |
| CGGAAGTGGG GCCAGTGCTG CGAACCTCTC TATATGGATG TGCAAGCTAC AACTCCTNTG | 180 |
| GACCCCCGGG TGCTTGATGC CATGGTCCCT TACCTAAATC AACTACTATG GGAACCCACA | 240 |
| NTCCCGGACA CATGCTTATG GCTGGGAAGA GTGAGGNAGC CATGGAACGT GCTTGTTNAG | 300 |
| CAAGTTAGCA TCTNTGATTG GGAGTTGATC CTCGTGAGAT TCANTTTTAA TNAGTGGGTG | 360 |
| TTA | 363 |

(2) INFORMATION FOR SEQ ID NO:1703:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

| | |
|---|-----|
| CCTCCCCAGG CCCCAAAGCA CCCCAAGGCT GGTATTCCTT GAGTNATAGG TATTAATAAT | 60 |
| AAAAGCCTCA ATGCAGCTTC TCCATGTAGT TCCTCTCCTA CAAGCCAGGT GGATTCTGGT | 120 |
| CCTAACTAAA GAGATGGGAG TTCACCTGAG GGCAAGAAGT ACCCAGGATG CCCAAACAGC | 180 |
| CGCACAGGTG TCCTGTGCTT CCTGTGAGAC TTCCTGGGGG AAATATACAA ACTTAATATA | 240 |
| TTTTTAAATG TTTACGTCAT TTACACTGCT GCTTTTCTAA TANTCTGNNT TTNATTACTT | 300 |
| GTAGTNAATC ATTTGTTTGG GGTTC AAGC ACTGTCTTCC | 340 |

(2) INFORMATION FOR SEQ ID NO:1704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

| | |
|---|-----|
| GGCAGAGCNA ACGTTGGTGA GGACTNTCCA GTATTCAATG GCCTGTTTAA GTTCTGTNAG | 60 |
| TTGTNTACTG GTGGTTCTGT GGCAAGTGCT GTGAAANTGN AATAAGCAGC AGACGGGACA | 120 |
| TGGNTGTGAA ATTGGGCTGG GGGCCTG | 147 |

(2) INFORMATION FOR SEQ ID NO:1705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

| | |
|---|-----|
| AGGCCCCCTG AAGCTGCAGC CCCCCGAGA ANCTGGCCTG GAACTATGGC CGCCCCCTNAN | 60 |
| CTTCCCTCCA CCCC�ATCC GGAAGAAGNC ATCCAGGAAA G | 101 |

(2) INFORMATION FOR SEQ ID NO:1706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

| | |
|---|-----|
| GGCAGAGGGN ATGGAGGATC TCAACTGTNA ATCCACACTG TTCTCCAGGC CAGGGAAAGC | 60 |
| CTGGGAAGGT AAGCCTGGGA AGAGGCCCAA GCCCACAGTG GGTAATTGGC CCCATGGGCT | 120 |
| NCCAGACTGT NNACTNCCCC AGGTTGAATC ACTGTGGTGC TCCAGCCTGG CTGTGATCTA | 180 |
| GTNAAGGGTG TTGTGGGGGG CATCTNTGGG CCTTCAGGGG CCCCAGGTNA CTTCTGGGT | 240 |
| ATAACTTGNG TNACACGTGT T | 261 |

(2) INFORMATION FOR SEQ ID NO:1707:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

| | |
|---|-----|
| GGCACGAGCG GAGATTGACC TGGGAGGCCA CGCCCCGTTT GATTCATGAC GGTGTGGCTG | 60 |
| CGGCCATCAT GAACAGCGAC TGCCTTGTTT TCGACACAGC CATAGCACAT CTTTTGNCA | 120 |
| GATAATGGGA ACCTTGGGAA TCAATGTTAC TATTTCTACA TGTGTCCAT GNATGTGAAC | 180 |
| TTTCGTAAAC CTTCAAAATT ATTTGGGCAT AGTGCTCTAT GTTTGAATNA AAGGTTTTTA | 240 |
| TAGATGTTTT ATTCCA | 256 |

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

| | |
|---|-----|
| TGTATTAAGT CTGCGCTAAC TAGGTTCCCA GGGCTTCTGT CCCTGGGACG TGGGGTCCCC | 60 |
| ACAGACCTGG AAATTCTCCG GCGTCTTCCT TTGCCAGAG CAAATTGAGA CATCCCCGTG | 120 |
| AAGAGCCCGA GGGTCGCTTC CTTTTGGGTT TAAAGTCGTC CTGAGGCTGG TCTCGTCCCC | 180 |
| GGTCTTTCTG CTATAGGTCA ATGTATACAC TTTCTGTTGA GTANTTTTCC TGCTGTAAAA | 240 |
| CCTTGTTCTG AT | 252 |

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

| | |
|--|-----|
| GGNAGAGGNT AAGACGCCTC CNTNCTGCTT GTGNAACGTC CTAAGCGTAC CCNCTCTTCC | 60 |
| CAGCACCCAG GCCAGTATTA AAATCAATTC TNTCTATGAA AGGGAATCGA CTTCAATACC | 120 |
| TGCCATTAAAC CCGTGCCCCG AATTTGAAAG AACTGAAATG NTGGACCTGT TCCCGTGGGA | 180 |
| ACCCTGGAAC CCAGTAGAGA AAAGCCCTTG GAGAATGCCA AANTGGGGCA AGTGNANAGA | 240 |
| TTTCATGATA TTGCNCCTGG GTTGGTGGTT NTTACTGG | 278 |

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

| | |
|---|-----|
| CAGAAGAGTT AGTTTCCAGG CATCCATTTC CAGGTCCTGG CCTGGNAATC AAAGTAATAT | 60 |
| GTGCCTGAAG AACCTTATAT CTGTAANGNN CTTTCCTGAA AACCAACAAT ATTTTAAAAA | 120 |
| TAGTAGCTGA TTTTTCCTGC CANT | 144 |

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

| | |
|---|-----|
| GTGCGNCATC CTAAGCACCA TCNATCGGGA AGCTGCTCAA GCCCAACGCC TCATTGGCCC | 60 |
| TCCACAAGCA CAGCAATGCA CTGGTGGACG TGCCTGCCCC CCGAAAGCCG ACAGCAGCAT | 120 |
| CATGAATGCT NCACCTTCAA ACCAGAAGCC AGATGTNAAT GTACGCGGAC ATCGNGGGGC | 180 |
| ATGGGACATC CAGAAGCAGG TAGGTGCGGG AAGGCCGTGG AAGCTTCCCG CTCACGCNA | 240 |
| TTTGAAGCT TTACAAGCAG ATTNGGANAT TGTTTTCNNC CCCGAGGG | 288 |

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

| | |
|---|-----|
| ATCTCCCNCG AGAAAGCTTT CTTTCTNAAA ATGGTGGTGG ATGCNGTAAT GATGCTCGAN | 60 |
| GATTTCTGN AGTTTAAAT GATTGGAATC AGGAGGGTAC AGGGTGGNGC CTTGAGGGTT | 120 |
| TCTA | 124 |

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

| | |
|---|-----|
| GNAAGACCAA GGCTCATGGA ATCCTCNAGC AAATGTGGGG AGCTTNCCTC CTCTATGTTT | 60 |
| CCATGANGAT GGAAGGNAC TGNNGGAAAA AGCCTTAACC AGCCCTNTAA GGTGAANAGC | 120 |
| TGTGGAAGGG GCCATTTTCC CGAATAA | 147 |

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

| | |
|---|-----|
| CTAAAGGACC TGCNCGTNTG GACCAGCCAG CTGAAGAGCA CCATCCAAAC GGCCGAGGCG | 60 |
| CTGCGGCTGC CCTACNAGCA GTGGAAGGCN CTCAATNANA TCAACGCGGG CNTNTGNAAG | 120 |
| GAGCTGACCT ACGAGGAGAT CAGGGACACC TACCCTAAGG AGTATGCCCT GCGGGAGCNG | 180 |
| NNCAAGTNCT ATTACCGNTA CCCCACCGGG AAGTCCT | 217 |

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 298 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

| | |
|---|-----|
| GGCAGAGCTT AATGGCAGAA GCTCTGGAAG AGCTCTTNTT GCAAAAAATA AATGGGCTAC | 60 |
| CCACAGAAGA AACCGAGATC ATGATAGTCC AGGCAAAAGG AAGAGGACGT GGGAGGNAAG | 120 |
| AAACAGGGAC AGCAAAACCT GGCGTTTCCA CGGTACCAAA CACAACNAA GCATCGANTC | 180 |
| CTCCGCAGAC CCAGACCCCT CAGCCGAATC CTCCTCCTGT GCCAGGCCAC GGNTTCACCC | 240 |
| CTTCCCTGCG GTNNACCCCG GACCTNATCG TNCAGACCCC TGTTAATGAC ATGGGTGC | 298 |

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

| | |
|---|-----|
| GGAAGAGTGA CCGGCTGGTG GAGGTGCAGT GGGAACAGCA GGAGGCCCGA AGCCTCTGGT | 60 |
| ACCTGCCCCA AGGNCANAAA ACCTAANAGC AGCACANNCA TGGTA | 105 |

(2) INFORMATION FOR SEQ ID NO:1717:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

| | |
|---|-----|
| CGCGGNTACT ACAACCAGAG CAAGGCCGGT TNTAANACCA TCCAAATGAT GTATGGNTGC | 60 |
| AACGTGGGGT CGGACGGGAG NCTTCCTCCG CGGGTACCGT AGGNCGCCTT ACGAACGGCA | 120 |
| AGGTTTACAT CGCCCTGAAG AGGACCTGCG NTTCTTNGAC CGNGGNGGAA CATGGGCAGT | 180 |
| TTCAAACCAC CAAGCACAAG TGGGAAGGNG GGCCCCCT | 217 |

(2) INFORMATION FOR SEQ ID NO:1718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

| | |
|---|----|
| GNAAGACCAC CAAGGCCTCA AAATTAACCT AAAGACCCAC TCCTTNCAAG TGGTGGTAAT | 60 |
| CTCCAANATC T | 71 |

(2) INFORMATION FOR SEQ ID NO:1719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

| | |
|---|----|
| CGGGCAACCC TGAAGGCTGG TGGTGCCGGC AACCCAGTNC GGCTCCNTGA ATTGGGAAAA | 60 |
|---|----|

| | |
|---|-----|
| GGCGGGTNTA ANATCAANGA GAATCCGCAA AAGTACGGGG GCGCNGTCCA GGTGGCGGGG | 120 |
| GAATATGCTG CCCATTCCAC CGAGGGGGCC ATCACCATCG CTGGNGTGCC GCANTTTGTA | 180 |
| ACCGAGTGT TACAGNATTT CCCTGGTCAT GCTGGAGACG GTCTCCCGTT TTCGAAAGGA | 240 |
| AGNGTCATGN CCTTCCGT | 258 |

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

| | |
|---|-----|
| GGNAGANCNA GGTTACNAGG GCTGGCTGGC CGGCTACCAA ATGAATTTNA AAAGTGCAAA | 60 |
| ATCCCGAGTG AACCCAAAGC AACTTTCCAG TTGGCTACAA NACTGNATGA ATTCCAGCTT | 120 |
| CANACTGAAT GTGAAATGAA GGGGANCAAA GTTTGGGGGC TCCATTTACC AGAAAGTGAA | 180 |
| ACAAGAAGTT GGGAGACCGC TGTGNAATTC TTGCCCTGGG NCAGCAGGGN AACAGTTAAC | 240 |
| ACGGGCTTTG GGAAATAGCC AGCCCAAGTT ATCAGAATTG NACCCTGAAC GGCTGTTTTT | 300 |
| TGNGGGTTTA ANGTGNAACA AATT | 324 |

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

| | |
|---|-----|
| AGATCAAGCA CTTTGGNATG CTTGCGCGCT GGAATGANA GCCAAAANTA CCTGTNAAAA | 60 |
| CAACGTCCAC CTGGTGTTCA AGGAGACAGC CAATTACCTG GTCATTTGGT GCATTGNCCT | 120 |
| AGAGGTGGAG GAGAAATGTG CCACTCATGG AGCAGGTGGC CCACCAGAAC AATCGTTAAT | 180 |
| GCAATTTAAT CCTGGGAGCT GGCCAAGAGC CTTAAGGGTG GGACCCCCGG GNNCTGNTTC | 240 |
| CGGNAGTTTT TCCACTAAGN TTAG | 265 |

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

| | |
|---|-----|
| GGNANANACG GAGATTAACC TGGGAAGGCC ACGCCCCGTT CCAATTNATG ACGGTGTGGC | 60 |
| TGCGGCCATG NATGAAACAG CAACTGCCTT GTTTTCAANA CAGCCATAGC ACATCTTTTT | 120 |
| GCCAGATNAA TGGGAAACCT TGGGAATGCA ATGTTAACTN ATTTCTANCA TGTNGTCCCA | 180 |
| TGAATGTGAA CTTTGCGTGA AACCTTNCAA AAATTATTTG GGCCATAGTG CTNCTTATGT | 240 |
| TTAANAAAGG TTTTANTAG ATGTTTNTT CCCATATGTT CTCA | 285 |

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

| | |
|--|-----|
| GGAACAGGCC ATCTCCTTGG CNAAAAATTT CTGGCCGGA NATNCGACCG CCGNNATCTC | 60 |
| CAAGAAGGGC CGTGGCTCCA ATCGAGCCGG GTAAAGCTGC TGTGC | 105 |

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

| | |
|--|-----|
| GGNANAGGNA GNAAGAAGGA GCTGAAGGCC CCCC GGCTCG GANCCAGCCC AAACAAGGAC | 60 |
| AAGGACGAAC CTTTTCCCCC CAAAGCAGAA GGCCGAGCGG NAGAAAGGAG CGCCCGGGTG | 120 |
| GCCAATTAAC GCCCGGGAGA GANTGNGNAG TNCCGTGAAA ATTCAAGAGG CCTTTAAGG | 179 |

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

| | |
|---|-----|
| AACGACACCC TNAGGAAGAT CCTGGACCTA AAATTTTAAG GGGGCCCCC CAGGGCTAGC | 60 |
| NAGCCCTCTG GCCGCCTGCA GGCTNAACCA GTCCCTAAAC AGGATGGACA ACAGCCAGCA | 120 |
| CCCCCAGCCT GCTGANAGCG NACAGAACTG GGTCCTCAAA GGCTCTGGCC CAGAACCCTC | 180 |
| CCACCACCCA CGGTTGCTGG TGAAAGNAAT TCTNTGAACC TGCAACTNTG GCCAGGAGGC | 240 |
| TGTGCTGNTT CACTGTCCGT NAGGAGGGCC CCAACCGGG CGG | 283 |

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

| | |
|---|-----|
| GGCACGAGGG AACAATGCCT TTCCTGAGCC GGGCAGGGTG CCATTTCCCG TGCCTAANAA | 60 |
| AGTGCTGTGG CCGCAGCTGT GTAAGGCGCT CAANATGAAA TTNAAGGCCG AAGTGCAGAG | 120 |
| CAACCGGGGC CTGAACCAAG GAGAAACCTC GTGTTCTTGG CGCAGAACT NTTCAACAAC | 180 |
| AGCAGCAGCC ACCTGGAAGG TATGACAGTG GCCTGTTCCG TNTCCTGGTC CCAGTTCCAA | 240 |
| CAGGGNGGNA CTTGCCGGGC TGGNAATTAN ACCTTTTGGN CAGTGGTTTG AGGGGGTGAT | 300 |
| GGAGGTGTTG AAGANGCACC ANAAGCCCCA TGGAATGATT GGGGCCTTCT AGGTTTTTTG | 360 |
| AATTAGCCAA CAGGCCCAGA ACTGNTNCTT AAACAAGTCC GGGGNACTTT TTGTTTGGCT | 420 |
| TTAAGTGANT TCGAAATTG GGGGGN | 446 |

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

| | |
|---|-----|
| GGCACGAGGG AACTGCCCCT AAAACATCCT GCCCTCTTNA AGGCAATTGG TGTNAAGCCT | 60 |
| CCTAGAGGAA TCCTGCTTTA CGGACCTCCT GGAACAGTAA AGACCCTGAA TTGCTCGAGC | 120 |
| TGTAGCAAAT GAAAACTGGA GCCTTCTTCT TCTTGAATCA ATGGTCCTGA AGAATCATGA | 180 |
| AGNCAAATTG GCTGGTGAGT CTAAGAAGCA ACCTTCGTGA AAGCCTTTGA NGGAGGCTGA | 240 |

GAAAGGAATG CTCCTGCCCC TGCATCTTGC ATTGAATGAA GNTTAGATGC CATCGTNCCC 300
 AAAAGAGGAG NAAAANTCAT GGTGNGGTGG AGCGGTGCAT TGT 343

(2) INFORMATION FOR SEQ ID NO:1728:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

GCAGAGACCC CGACATCANG ATCTTTGGGA AGTGGAGCCC CGATGATGTG CAGATCNTGA 60
 CTTTCCCTGA NGGATTNCTT GAAGTGAGGA NAGTTTGCCA GTCCCTG 107

(2) INFORMATION FOR SEQ ID NO:1729:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

GGCANAGATG AAAGTTCCAC CAGTNTGTGC GGCTATNACG CTCCGAGAAA TAACCGCACC 60
 ATCTCCTTNA TCCCACCCNA CGGCGAAGTT CNAGCTCATG TCCTACCGTN TNAACACCCA 120
 CGTAAAGCCT TTGAANATGG GATCGANTCG GTGAATCGAN AAAGCACTCC CACAGCCGCA 180
 TCGAGTACAT GAATCAAGGG CGGCAAGGGA GTTACCTGAA TGCGGGCCCA CTTNGGCCTG 240
 NCTAAGTGTG GGAGGCCGAA GACAAGGGGG GGCAAGCCCC CGATTCAGTG TCCAGTTTCG 300
 AGATNCCTTN ATTN 314

(2) INFORMATION FOR SEQ ID NO:1730:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

GGCAGAGTNT ATACCAAAAA GCAGCTCTTG GATAGNATGT GTATGAACTT TAGGTGGTCA 60
 AGTCTCTAAA GAAATCTNCT TTGGAAGAAT TACAACGGT GCTCAAAATG AACTTGAGAA 120

AAAGTNAACT NCAAGTGCC ATATGCCCCA AATTNTTCCA GTTTGGN

167

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

| | |
|---|-----|
| CTGGGAGGTG AATCAGTAAT GACCATGGNA TCAACCCAC CGGAACCTAC NACGGGGAAC | 60 |
| AGNGAACCTG NAGCTGGNCC GATTCTTTTT TTACTANAAT GAAGGCCACA GGTGGNAAAT | 120 |
| TTNTNCCTGG TGCCNATCCT GGTGGATTCT NGAAACCTGG GAACCATGGC CTTTTTTCGC | 180 |
| TCAAGGTCCT TTTGGCCA | 198 |

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

| | |
|---|-----|
| GGNACGAGGG AAGGTGTCTN AAAACTGGAG ACTGGGGCGC TGCCGAAAGG GGATTCTCCT | 60 |
| GAAGTGGAGA TGCAGTCAAA TGCCCTGGAA TGCAGCTAGA GGATGATTCT TTGTNCATAA | 120 |
| TCCCAGGCTA ATTNNAATCC TGGCCTACCA GTTCCGTCCA AATGGTGCCA GCTTGAATTC | 180 |
| GTCGGCCTCT GGGAGTCTTT NNTGGGGCAT GATNAGGACG TTTGCNACTT TNTCCTGGCC | 240 |
| AATTCG | 246 |

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

| | |
|---|-----|
| GGCACAGTGG TGGCTCATGC CTGCAGTCCC AGCCACTCAG GAGGCTTAGG CAGGAGAACC | 60 |
| ACCTAACCGG GAGGTGGNAG GCCGCGGTGA GTCGAGACCG GAAAACACTC TAGCCTGGGA | 120 |

AAACAAGAGC GAAACTCCGC TCAAAAAAAAAA AAAAAAAAAA AAAAAANNTNG GGGGGGNCCC 180
CNT 183

(2) INFORMATION FOR SEQ ID NO:1734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

GGTAGTATTC CNGGCGTACA GGTGCGCAGC TCGCGGCTCC AGTNATAACC AAAGCCCAGC 60
ATTTTAAGCT GGTTTTNAAT ATACGCAATG TTGTCGTACG TCCACGGTGC CGGAGCGGTG 120
TTGTTTTTAA CCGCCGCGCC TTCCGCAGGC AGACCAAACG NGTCCNAGCC GATCGGCTGC 180
AGGACGTTTT TCCCCAGCAT ACGCTGGTAG CGGGCAATCA CGTNACCNAT GGTGTAGTTA 240
CGTACGTGGC CCATGTNTAG TCGACCAGAA GGNTTAGGGA NAGCATAGAC AGGCAGTAAT 300
AATTCTNTTT GATCTTCGTC TTCGGTTAAC TTNAAATGTG CGGTTTTAAT NCCCATGAAA 360
GT 362

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

CACTTTATNA NCCGGGAAAT AATGCGGGCA ACGGTGTTTA ATTATNTCGA TTGTNATTNC 60
AATCGGTGGC GGCGGCACAG TTGGTGTGGC GGCTCAGTC CGGAACANTT TGAAANCAAG 120
ACCCTCGCTT AGGCCTGTNT TCCATATTAN GTGGGTAGGT TCAAAATGCC GTTTNTGGTG 180
180

(2) INFORMATION FOR SEQ ID NO:1736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

| | |
|---|-----|
| GGCANAGGNA GAGAGAGAGA GAACTAGTCT CGAGCGGGAG TCCGGCGGGT TACAGCGGAG | 60 |
| GCCTAGGTGG CAGACAGGGG GCCCGGGCCG CTGCGTGTG TCCACCCAAA ATGGAGTTCC | 120 |
| TCCTGGGGAA CCGTTNCAGC ACACCANTGG GGCAGTGCCT CGAAAAGGCA ACAAATGGCT | 180 |
| CCCTGCAAAG TGAAGGNTTG GACGTTGAAA TATGGAGATC TGTGAACATC ATCCAATGAG | 240 |
| AACGGAGGNA AGGGCCAAAG GATGCCATTC GAGCCCTGNA AGAAGCGGCT TCAACGGGGA | 300 |
| ACCGATACTT ACAGAGAAGG TTGATGCTGG NATTTAANCA GTGNCTGGNA G | 351 |

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

| | |
|---|-----|
| AGCACGAGGT GGA CTCACAA TTCCAAATAT TACCAGAAAG GGAGCCATGT NAGACAGGAC | 60 |
| AGCATGGAGC CCAGCGACGC TCTGGGAATG AATGTGTCTA ACTGTCCGTG TGGGGACAGG | 120 |
| CTGAAGACCC TAGAGCAGAG GGC GCGGTAG CAGNCACGCA GAGC NCTGNG NNACATTGCA | 180 |
| CTGGTGGGGA CTCCAAACTA CATNGCACCC NAGGTCTNCC TCCGCAAAGG GTACACTCAA | 240 |
| CTTTNTGACT GGTGGAGTNT TGGAGTGATT CTTTTCGAGA TGCTGGTGGG GGCA | 294 |

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

| | |
|---|-----|
| GGCACGAGGG ANCANNCTCA ATAAGGTTGT NACACGACAC CCTNATCTNA AAGACTGCAT | 60 |
| GGTTTTGGCA NTGNACATG TCGCAGCATG GTGGCCGTGA ANGGCATAGC GAACACCACA | 120 |
| GGGCAAGCTG G | 131 |

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

| | |
|---|-----|
| GGCAGAGCCA ATNAGGGNTA TTTTNATNAT TCCCACAAAT CCACCACCAA CATTCAGAAA | 60 |
| GCCAGANCTT TGGTCCGATG ATTCACCGA TTTTTTTAAA AAGTGTTTGG TGAAGAATCC | 120 |
| TGAGCAGAGA GCTACTGNAA CACAACTTTT ACAGCATCCT TTTATCANGG NTGCCCAAAC | 180 |
| CTGTATCAAT ATTAAGAGAC CTGATCACAG AAGCTATGGN GATCAAAGCT AAAAGNNCAT | 240 |
| GNGGAACCAG CAACGGGANT TGGAAGGAGG AAG | 273 |

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:

| | |
|---|-----|
| GGCAGAGGGC GACCANAGGC ACTTTTCCCC ACAGACCGGC GGCAGTANGG CAAAGGCTGT | 60 |
| GGGCAGCNGT TCGCTGGGAA GAAGTGCCTN CTGTGGTGGG CCANGCGCTG CTCGGAAGGG | 120 |
| CCTGTNTGCC CNCTGCTTTG GCCATTGCTT GGGGT | 155 |

(2) INFORMATION FOR SEQ ID NO:1741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

| | |
|---|-----|
| GGCACAGGGN TCATCGGTGC AGGGGAGTTT GGAGAAGTGT ACAAGGGGCG TTTGAAACTN | 60 |
| CCNGGCAAGA GGGAAATCTA CGTGGCCATC AAGACCCTGA AGGCAGGGTN CTCGGAGAAG | 120 |
| CAGCGTCGGG ACTTTNTGAA GTNAAGGCGA GCATCATGGG CCAGTTCGAC CATCCTAANA | 180 |
| TCATTGCGCT GGNNGGTGTG GTCACCAAGA GTCGGCCTGT NCATGATCAT CACAGAGTTC | 240 |
| ATGGAGAATG GTGCATTGGG ATTCTTTCCT CAGGC AAAAT GACGGGCAGT TCACCGTGAT | 300 |
| CCAGCTTG TG GGTATGCTCA NGGGCATCGC TGCTGGCATG GAAGTACCTG GCTGN NATGA | 360 |
| ATTANGTGCA TCNNGGACCT GGG | 383 |

(2) INFORMATION FOR SEQ ID NO:1742:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

| | |
|--|-----|
| GGTANAGGTT GTNCCGAGGT GACACAGTGT TGCTGAANGN AAAGAAGAGA CGAGAAGCTG | 60 |
| TTTGCATCGT CCTTNCTAAT GATACTTGTN CTGATGAGAA GTATTCGGNA TGNAATAGAA | 120 |
| GTTGTTCCGG GAATAACCTT CGTGGACGCC TGAGGGGGTG TNATCAGCAT CCAGCCATGC | 180 |
| CCTGATGTGA AAGTACGGGA AACGTNATCC AGTGNTNGCC ATTGGTGACA CATTTGGGAGG | 240 |
| GCATTACTNG GTAATCTCTT CGAGGGTATA CCTNAAAGG | 279 |

(2) INFORMATION FOR SEQ ID NO:1743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

| | |
|---|-----|
| GNAAGACCNA AGGCCAAGAC CATAATCGTG GCGGGCNTGG TGTNCCTGTT GGCCGGCCTT | 60 |
| ATGGTGATAG TGCCCGGTTT CCTGGAACGG CCCANAAAAT CATCCAAAAT TTCTANAATC | 120 |
| CGNTGGTGGC CTCCGGGCCA GAAGCGGGAA ATGGGTGCTT CGTTCTACGT GGGNTGGGCC | 180 |
| GNTTCCGACC TT | 192 |

(2) INFORMATION FOR SEQ ID NO:1744:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

| | |
|---|-----|
| TNGGGNTGCA GGAATTGGGN AGAGCGTGGG CAGCAAGGGT GGGTAAAGGA TCCAAANATG | 60 |
| GCTGGGCGAA AAATTGCTCT AAAAAGAATT NATTGGGTAG CTTTTCAGN GATAATANNC | 120 |
| | 120 |

(2) INFORMATION FOR SEQ ID NO:1745:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

GGCANAGGCG CGCCCGAAAN CCCGNGNTGA TCCGCCGCCG CTGCCTTGAG TCGACTCTG 59

(2) INFORMATION FOR SEQ ID NO:1746:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

GGCAGAGCCC GGGGTGGAGG AGCTGCTGAA CAAGGGGCAG GACCCTCTGG CAGACAGGGG 60
TGAGAAGGAC ACAGCTAAGA GCCTCCAGCC CTTGGCGCCC CGGAACAAGA CCCGTGTGGT 120
CAGCTACCGG TGCCCCACAA CGCTGCGGTG CAGTNTACGA CTACCGANAG AAGCGAGCCC 180
GCNTGGTCTT CGGGCCTNAG CTGGTGTGCG TGGGTCCTGA GGAGCAGTTC ACAGTGTGTG 240
CCCTCTNAGC TGGGCGGCCC AAGCNTCCCC ATGCCCGCCG TGGGCTTCTG CCTGCTTGCT 300
GGGGCCTGAC TTCTTCACAG ACGTNATCAC CATCGAAACG GNGGATCATG CCAGGNTGCA 360
ATTGCATTGG NTTACAATTG GNATTTAAGG TGAATTAACC GNAGGACCCC CAAGAGACGG 420
CCAAGTTTTT TTAANTGCCA ATTTTATAGN ATGCTNAAAA CCNTGNATCC CGGTNGGGGG 480
NCCTGGGTT 489

(2) INFORMATION FOR SEQ ID NO:1747:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

GGCAGAGTTT AATCATCCAG CGCACATTTA TTGAGCCTGG CTTTCAGCCT TCGTGTGGT 60
GCAGTGTGAG CCCCCGGCTT GAGTTCACCT CCTTGGCCCT GCACTCTNAG TGGCGGCTCG 120

| | |
|---|-----|
| TGGCCTTCGG CACCAGCCAT GGCTTTGGCC TCTTTGAACC ACCAGCAGCG GCGGCAGGTC | 180 |
| TTTGTTAAGT GCACACTGCA CCCCAGTNAC CAGCTGGCCT TGGAGGGCCC ACTCTCCCGC | 240 |
| GTCAAGTCCC TCAAGAAGTC CTTGCGTCAT NATTCGCGG GATGCGTCGG NGCCGGGTGT | 300 |
| CCAGCCGGAA GCGGCACCCG TTGGCCCCC AGNAGAGGCA CAGNAGGGGA NTGCCAAGGT | 360 |
| TNAGCGGCCA GGCTTCCAGA ACATGGGAGT TTGNNGGCTTT | 400 |

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

| | |
|--|-----|
| GGAAGACCTG ACGGGCATTG TAAGCTGGGN ANATGCCTGT GNGGCCCCGAA ANAGGCCTGG | 60 |
| NGTGTACATN CTGGCCTCCA GCTATGCCTC CTGGAATCCA AAGCAAGGTG AACAAANCTC | 120 |
| CAGCCTCGTN TGGTGCCCCA AACCCAGGGG TCCCAGCCCG AAAGAAACCT TTTTGGCAGC | 180 |
| CACCTGGCCT TAAAGNTNTG CCCCAGCCCA GGGNTTNNTG AGGCCCCATCC TTTTCCTG | 238 |

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

| | |
|--|-----|
| GGCAGAGNCA GCAGGCACAG TCTCGCCATC TGCATCCATC TTGTTTGGGC TCCCTACCCT | 60 |
| TAAAAAGTGC CTCAAATAAT ACCCTGGTGG CCATGGACTT CTCTGGCCAT GCTGGGCGTG | 120 |
| TNATTGAAGA AACCCCCGGG AAGGCTCTGA AGTGTGGCCC TGGAGGAGGC CCAGGCCTGG | 180 |
| NAGGNAAGAA GACAAACCAC CGCCTTCAGC CTGCCCCATGC CAGCCTCCGG NAAGAGCCTC | 240 |
| AGTGGCAGCC ATCCACCGNA CCCAACTTTG GTTCCACGGG GCGGCATTTT CCGTGAAGGA | 300 |
| GAGCCAGGGT TNATTTGGGA CAGCAGGGTT TNGTTAGACG GNCTGTTCTT GGTNCGGGAA | 360 |
| GAGTCANGGG AACCCCCAGG GTTTTGTCC | 389 |

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

GGNAGAGCCN AGTCTTAAGT TTTTNTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTNAAA 60
AAAACCCCTT TTTTTTTN 79

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

CAACGNGNGN GGNCCAAGTA AGCAAGGGCG GGCAACTCCG GAGATNCAAC GGGGAGCTGT 60
ACGCCCCGCT GCAGCATGTG AAGCCCCGTG CTGCCCGGGG GGGCGGCCGA ATCGGGCCCCG 120
GNNTGCGCAA GGGGGACCGC ATCCTGGAAG GTGAACCACG TGAATTTTGA GGGGGCGACA 180
CACAAGCAGG TGGTGGGACC TNATTCGAGC AGGCGNNNAA GGAATTGAAT CCTTGAACAG 240
TTTTATCTGT ACCTCCTCAT GAGGCAGATT AACCTTAGAT CCCAGTGAAC GGATTCGTTN 300
NGGGACAATT NATTTTAATG NTTTTACAAC AGAAAAGCNA AGG 343

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

GGCANAGCTC GAGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTNNNC N 101

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

| | |
|---|----|
| GGAAGANCCC TCTCCCAGTN TCCGAAAGGA AGAGTAATGA CCATTCCGTA CCAGCCCATG | 60 |
| CNGGCNAG | 68 |

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

| | |
|---|-----|
| GGCAGAGACT GGGAAGGAAA GAACATGGCC TGTGTGCAGC GGACGCTTAT GAAATCTGGG | 60 |
| TGGGCTGGCA GTAGCCCGAA ATGATGGGCT CTTCTCTGGG GTATCCCAAC TGGTTCCCTA | 120 |
| AGAAATCCAA GGTAGAATCC TCGGNAACTT CTCGGATAAC CAGCTGCANG AGGGTCAAGA | 180 |
| ACGTGAATCG GGTTACAGAT GGGACCAAC CGCGGGGCGT CTTCAGGCAG GCATGNACTG | 240 |
| GNCTTACGGG AATGCCACGN CAGATCCTTT GAATCCCACC CCAGGCCTTN GCCCCTGNC | 299 |

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

| | |
|---|-----|
| GGCANAGGTT TCCCGAAGTA AGTNCCCANA GAGCTGGCTG TGGAACGTTG AAGGACTTGA | 60 |
| AANAGCCACC GAAAAATGGG AATCTNTACG AAGGCTCATG AAATATATTT TTAAAAGACT | 120 |
| CCATCACCAC GTGGGAAGAA TTCTGNGCTG TGANGCATGT NGGACAAGA AAGGGAATCT | 180 |
| NTNTGGCAAA CCCCTTCAAG GTTCACAGTT ATG | 213 |

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

| | |
|---|-----|
| GGCAGAGTGA AAGTCACTGT GGATCGAGCT CACAGGGGGC ACCCATGCCT GTTGTNAACA | 60 |
| GAGTCTNAAG CAGTCAGGGT GTTGAATTC CTCTGTTGTT GTNATCAATT CCTGCTGAGG | 120 |
| GGTTTCTGGG GTTTTNTTTT TAATAAATGA ACTCCTTTGT AGCCTTTGTN ACATAATCTT | 180 |
| CACTTTGGTT GTTGGTACCA AACAGAGCTC CCAGCCATCT CCTCCCTGTT CCTGAAAGAC | 240 |
| TAAAAATCCA CTTNCGGACT CTCCCTTCCT TCCTTCTTNA GCCCTCGAGG GTGCATATTA | 300 |
| GCTAATTAAG CAGGNCCAGA GNCAGAGAGG GGGGGTTCCA AAATGAANTC GGNTTTAAGG | 360 |
| GGCAAGTGNC CATTNATTGG GTTGAATTA ACGGTTATCC TTCATGGNCC GTAAATCCCA | 420 |
| GCATTTTGG GGGGCCNNG CANGTGGGTC CCNAGGTTGG GGGTTCGGGA CCAACNGGGC | 480 |
| CAAC | 484 |

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

| | |
|---|-----|
| GGCAGAGCTT TGGAGAGAAG GGAACAGAAG GTGACATCGG CTTCCCTGGG AATAACAGGC | 60 |
| GTAANTGGAG TCCACGGCCC TCCAGGGTCG CAGGGAGAGC TGGGGCGAAT TGGAAGTGCC | 120 |
| TGGTGGCAAA GGAAGATGAT GGCTGGCCGG GAAGCTCCGG GNTTNACCAG GTTTTCCGGG | 180 |
| NACTCCGTGG GAATCCGCGG NNTTACACGG ATT | 213 |

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

| | |
|---|----|
| TTTTTTTTTT TTTTTTTTTT TTTTTTNAAA GGGGGGGGGG GGGGGNAATT TT | 52 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

| | |
|---|-----|
| TCCGGNATGT GCCAAAGCTG GTTTTCCTGG GGAACGAACG CTCCCGAAGN NGANGTTTCC | 60 |
| TTCCATCGTC GGGNGCCCCA AACACCAGGG CCGTGCATGG TGGGTCATGG TNCCAGTAAG | 120 |
| GACTCCTGAC G | 131 |

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

| | |
|---|-----|
| GGCAGAGGNA ACCATATACA AGTTCTGCCC GACCATTGTA ACGCAAGGTT GGAAAGTCCT | 60 |
| AAATTCAATC ACAATCTTCT GCCAAGTGNA ACTGGNACAT AAACCTGGAC TTGTCTTCAA | 120 |
| AAACTCCAC TTCTCCAAAA ACTCTTGTA AAATCGCACA GTTTGGGCAC AGCCTNCCTG | 180 |
| AGTTTGAACA GTGGAGTTGA AACTTTCTCT ATCCCATGCA GAGGAAGCCT AAATNATGCA | 240 |
| AATAAATAAT TATCCAGCAC AGTGCCTNAA AGCTATTTCC TGTGAAGTCC CTTTCAGCTG | 300 |
| TGGGAAGAGG GATGGAAGGA TGGAAGATGG GTNCATAACT GTGGGTGGGC CACAANCCCG | 360 |
| AGGGNATNNT TTAACAGCAA TGGGGGGCGT GCTGAGTTCC CTAGGAAACT GGTGTTTAGT | 420 |
| | 420 |

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

| | |
|---|-----|
| GGCANAGTAA GAACAGGGTG ATTTTNAATC AGAGAACTC TGGGAACGGG TAACTCGAGC | 60 |
| CATAAATGCC AAAGACCAA CTGAAGCTAC CCAAGAGAAG TATGTTTTGG ANGAAGCTCA | 120 |
| AAGACAAGCT GCCACGGATC GGAANACANA AANTGTNAGA GTGGTCTTTC AAATTATTTG | 180 |
| | 180 |

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

| | |
|---|-----|
| GGCAGAGAGN ATGCTTCCTT TAAATACCAA TATTCGACTT GCGTACTCAA ATGGAAAAGA | 60 |
| TGATGAACAG AACTTCATTC AAAATCTCAG TTTGTTTCTC TGCACCTTTC TTAAGGAACA | 120 |
| TGNTCAACTT GATGAGGAAA AAAGGTAAA TCTCAGGGAA ACTCTTATGG GAGGCCCTTN | 180 |
| CATTATATGT TGTGGGTAT CTGGAAGTGA GNAAGAACT GGAAAATTCT TTGAAAATTT | 240 |
| GTNCTTGGA TGACTGGNAA TCCATNTAGG GCTGGCTGGA ACNCTATAGG AG | 292 |

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

| | |
|---|-----|
| GGCAGAGNAG AAGTTTAAGA TCAAGCTCAT GAGTNANTTG GTCAGCAATG GCGTCCAGAT | 60 |
| ATACCANTTC CCAACGGATG ATGACACTAT TGCNANGGTC AACGCTGCAA TGAAATGGNA | 120 |
| CAGTTGCCGT TTGCTGTTGT GGGAAGTATG GTTGAGGTAA AAGTCGGAAA CAANTGGTCA | 180 |
| AAGCTCGCCA GTTACCCTTG GGGTGTGTA CAAGTGAAA ATGAAAACCA CTGTGAACTT | 240 |
| TGTAAAAGCT GCGGGAAATG CTCCATTTGT ACAAATATGG NGGTNCCTGC GNGAGNAANC | 300 |
| CCATACCAGG CACTATGAGG TTTTACAGGC GCTGCAANCT GGAGGAAATG GGGTTTTACA | 360 |
| GTGTGGGCCC AGNAAANCAA GCCATTCATT TTTCAGGGGA CNTTGNGGCC AAAG | 414 |

(2) INFORMATION FOR SEQ ID NO:1764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

| | |
|--|-----|
| AATGGCGGNA AATTNTTGAT TACAAGGNTA TTNAGCTTAG TTGGAAAGCA AGAAATTTCA | 60 |
| ACTTTTTTATT GTTTAGAGCN TCATAAAGTT TTGTGAAAGA GNGAAGNATT TTTGGTTCCA | 120 |
| AGNTTATATG GTTNGGG | 137 |

(2) INFORMATION FOR SEQ ID NO:1765:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

| | |
|--|-----|
| GGCAGANAAG TNTAAATGCA CATNANTGGC AGCTTATAGA GAACCACCTT GTAACCAGTA | 60 |
| TACAGGTACA ACTACAGCTC TTCAGAAATT GGAAGGTTTT GCTAGCCGGT TATTTTCATAG | 120 |
| ACACTCTAAA GGTACTGCNA CATGAATCAG AAAACAGCTC TGGNAAAATG AACAGCCTTT | 180 |
| CATTTCTTTG AAACATACTG CCTTTATGGG AACAGATTCA ATGNAAAGAN TTTCTAGCCA | 240 |
| AAGCCAAAGA AGGACTTTTT GAAAAAATG GGGNGATTCC AACTCNGAAG TTAATGCCGG | 300 |
| ACTTGNAAG | 309 |

(2) INFORMATION FOR SEQ ID NO:1766:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

| | |
|---|-----|
| GGCAGAGGGC ANCATCCACA ATAAAGAGAA GCCATTTAAG TNTCACTTAT GTAATAGGTG | 60 |
| TTTTGGTCAA CAAACCANTT TAGACAGNCA CCTAAAGAAA CATGAGAATG GGAAACATGT | 120 |
| TCCGGTACAG CAACANCGTC GACTCATTCT AAACNGTAA AGTACAGGTG NGAATTCTGG | 180 |
| TTGTACAAAG ATGAATGNNTT ACTTTACAG AAATTCCGAA ATTTTCATTGG GNAACANCA | 240 |
| CCATGGGCAG CCAATCTCCC AGGTATTNTG GGTGGAGAGN ATGA | 284 |

(2) INFORMATION FOR SEQ ID NO:1767:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

| | |
|--|-----|
| GGCAGAGCTC GTCNTNNGNN ATCAAAAGAA ATTTGGTTGC CACCCCCACA GTTCTACGAA | 60 |
| GGAGNAAGAC TTGCAAACCTT TGCCTCTCTC TCTGACTTGC ACAAATTTTG TTTGGGTCGT | 120 |
| GCATTAGAAG GACTGGTAAA GGTGGCTGCC GATCATCTNG TTAAGTCTG ATGGGATGGT | 180 |
| CCATCTTTTA CCAGGTGATG AGCTATATTT AGAAGATTCA NACTTTTTTG AAAATCTTAT | 240 |
| GTCTACTGAA AAAAAGACTG AGGAAATCAT GAAGGAAGGC AAGCAGTTTC ACCGGGNTAG | 300 |
| TGACATACCA TCGNCACCTT TATGGATATC CCCGNGGACT GTTCCAGCCA AAGTTTAAAA | 360 |
| CCAGGTTTTT CCNCANGAAC | 380 |